

NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS

This application is a continuation-in-part of the following U.S. Provisional Patent applications, from each of which priority is claimed, and each of which is incorporated by reference in its entirety: 60/083,758 (filed May 1, 1998); 60/094,869 (filed July 31, 1998); 60/098,994 (filed September 2, 1998); 60/099,062 (filed September 2, 1998); 60/103,749 (filed October 9, 1998); 60/103,794 (filed October 9, 1998); 60/103,796 (filed October 9, 1998); and 60/121,528 (filed February 25, 1999).

This invention relates to antigens from the bacterial species: *Neisseria meningitidis* and *Neisseria gonorrhoeae*.

BACKGROUND

Neisseria meningitidis is a non-motile, gram negative diplococcus human pathogen. It colonizes the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. It is closely related to *N. gonorrhoea*, although one feature that clearly differentiates meningococcus from gonococcus is the presence of a polysaccharide capsule that is present in all pathogenic meningococci.

N. meningitidis causes both endemic and epidemic disease. In the United States the attack rate is 0.6-1 per 100,000 persons per year, and it can be much greater during outbreaks. (see Lieberman *et al.* (1996) Safety and Immunogenicity of a Serogroups A/C *Neisseria meningitidis* Oligosaccharide-Protein Conjugate Vaccine in Young Children. *JAMA* 275(19):1499-1503; Schuchat *et al* (1997) Bacterial Meningitis in the United States in 1995. *N Engl J Med* 337(14):970-976). In developing countries, endemic disease rates are much higher and during epidemics incidence rates can reach 500 cases per 100,000 persons per year. Mortality is extremely high, at 10-20% in the United States, and much higher in developing countries. Following the introduction of the conjugate vaccine against *Haemophilus influenzae*, *N. meningitidis* is the major cause of bacterial meningitis at all ages in the United States (Schuchat *et al* (1997) *supra*).

Based on the organism's capsular polysaccharide, 12 serogroups of *N. meningitidis* have been identified. Group A is the pathogen most often implicated in epidemic disease in sub-Saharan Africa. Serogroups B and C are responsible for the vast majority of cases in the

United States and in most developed countries. Serogroups W135 and Y are responsible for the rest of the cases in the United States and developed countries. The meningococcal vaccine currently in use is a tetravalent polysaccharide vaccine composed of serogroups A, C, Y and W135. Although efficacious in adolescents and adults, it induces a poor immune response and short duration of protection, and cannot be used in infants [eg. Morbidity and Mortality weekly report, Vol.46, No. RR-5 (1997)]. This is because polysaccharides are T-cell independent antigens that induce a weak immune response that cannot be boosted by repeated immunization. Following the success of the vaccination against *H.influenzae*, conjugate vaccines against serogroups A and C have been developed and are at the final stage of clinical testing (Zollinger WD "New and Improved Vaccines Against Meningococcal Disease". In: *New Generation Vaccines, supra*, pp. 469-488; Lieberman *et al* (1996) *supra*; Costantino *et al* (1992) Development and phase I clinical testing of a conjugate vaccine against meningococcus A and C. *Vaccine* 10:691-698).

Meningococcus B (menB) remains a problem, however. This serotype currently is responsible for approximately 50% of total meningitis in the United States, Europe, and South America. The polysaccharide approach cannot be used because the menB capsular polysaccharide is a polymer of $\alpha(2-8)$ -linked *N*-acetyl neuraminic acid that is also present in mammalian tissue. This results in tolerance to the antigen; indeed, if an immune response were elicited, it would be anti-self, and therefore undesirable. In order to avoid induction of autoimmunity and to induce a protective immune response, the capsular polysaccharide has, for instance, been chemically modified substituting the *N*-acetyl groups with *N*-propionyl groups, leaving the specific antigenicity unaltered (Romero & Outschoorn (1994) Current status of Meningococcal group B vaccine candidates: capsular or non-capsular? *Clin Microbiol Rev* 7(4):559-575).

Alternative approaches to menB vaccines have used complex mixtures of outer membrane proteins (OMPs), containing either the OMPs alone, or OMPs enriched in porins, or deleted of the class 4 OMPs that are believed to induce antibodies that block bactericidal activity. This approach produces vaccines that are not well characterized. They are able to protect against the homologous strain, but are not effective at large where there are many antigenic variants of the outer membrane proteins. To overcome the antigenic variability, multivalent vaccines containing up to nine different porins have been constructed (eg. Poolman JT (1992) Development of a meningococcal vaccine. *Infect. Agents Dis.* 4:13-28).

Additional proteins to be used in outer membrane vaccines have been the opa and opc proteins, but none of these approaches have been able to overcome the antigenic variability (eg. Ala'Aldeen & Borriello (1996) The meningococcal transferrin-binding proteins 1 and 2 are both surface exposed and generate bactericidal antibodies capable of killing homologous and heterologous strains. *Vaccine* 14(1):49-53).

A certain amount of sequence data is available for meningococcal and gonococcal genes and proteins (e.g. EP-A-0467714, WO96/29412), but this is by no means complete. Other men B proteins may include those listed in WO 97/28273, WO 96/29412, WO 95/03413, US 5,439,808, and US 5,879,686.

The provision of further sequences could provide an opportunity to identify secreted or surface-exposed proteins that are presumed targets for the immune system and which are not antigenically variable. For instance, some of the identified proteins could be components of efficacious vaccines against meningococcus B, some could be components of vaccines against all meningococcal serotypes, and others could be components of vaccines against all pathogenic *Neisseriae* including *Neisseria meningitidis* or *Neisseria gonorrhoeae*. Those sequences specific to *N. meningitidis* or *N. gonorrhoeae* that are more highly conserved are further preferred sequences.

It is thus an object of the invention is to provide Neisserial DNA sequences which encode proteins that are antigenic or immunogenic.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 illustrates the products of protein expression and purification of the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 2 illustrates the products of protein expression and purification of the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 3 illustrates the products of protein expression and purification of the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 4 illustrates the products of protein expression and purification of the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 5 illustrates the products of protein expression and purification of the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 6 illustrates the products of protein expression and purification of the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 7 illustrates the products of protein expression and purification of the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 8 illustrates the products of protein expression and purification of the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 9 illustrates the products of protein expression and purification of the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 10 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 11 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 12 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 13 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 14 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 15 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 16 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 17 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 18 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 19 shows an alignment comparison of amino acid sequences for ORF 225 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 20 shows an alignment comparison of amino acid sequences for ORF 235 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 21 shows an alignment comparison of amino acid sequences for ORF 287 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 22 shows an alignment comparison of amino acid sequences for ORF 519 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 23 shows an alignment comparison of amino acid sequences for ORF 919 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

THE INVENTION

The invention provides proteins comprising the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples.

It also provides proteins comprising sequences homologous (i.e., those having sequence identity) to the *N. meningitidis* amino acid sequences disclosed in the examples. Depending on the particular sequence, the degree of homology (sequence identity) is preferably greater than 50% (eg. 60%, 70%, 80%, 90%, 95%, 99% or more). These proteins include mutants and allelic variants of the sequences disclosed in the examples. Typically, 50% identity or more between two proteins is considered to be an indication of functional equivalence. Identity between proteins is preferably determined by the Smith-Waterman

homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with parameters: gap penalty 12, gap extension penalty 1.

The invention further provides proteins comprising fragments of the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples. The fragments should comprise at least n consecutive amino acids from the sequences and, depending on the particular sequence, n is 7 or more (eg. 8, 10, 12, 14, 16, 18, 20 or more). Preferably the fragments comprise an epitope from the sequence.

The proteins of the invention can, of course, be prepared by various means (eg. recombinant expression, purification from cell culture, chemical synthesis *etc.*) and in various forms (eg. native, fusions *etc.*). They are preferably prepared in substantially pure or isolated form (*ie.* substantially free from other *N. meningitidis* or *N. gonorrhoeae* host cell proteins).

According to a further aspect, the invention provides antibodies which bind to these proteins. These may be polyclonal or monoclonal and may be produced by any suitable means.

According to a further aspect, the invention provides nucleic acid comprising the *N. meningitidis* nucleotide sequences and *N. gonorrhoeae* nucleotide sequences disclosed in the examples.

According to a further aspect, the invention comprises nucleic acids having sequence identity of greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) to the nucleic acid sequences herein. Sequence identity is determined as above-discussed.

According to a further aspect, the invention comprises nucleic acid that hybridizes to the sequences provided herein. Conditions for hybridization are set forth herein.

Nucleic acid comprising fragments of these sequences are also provided. These should comprise at least n consecutive nucleotides from the *N. meningitidis* sequences or *N. gonorrhoeae* sequences and depending on the particular sequence, n is 10 or more (eg 12, 14, 15, 18, 20, 25, 30, 35, 40 or more).

According to a further aspect, the invention provides nucleic acid encoding the proteins and protein fragments of the invention.

It should also be appreciated that the invention provides nucleic acid comprising sequences complementary to those described above (eg. for antisense or probing purposes).

Nucleic acid according to the invention can, of course, be prepared in many ways (eg. by chemical synthesis, in part or in whole, from genomic or cDNA libraries, from the

organism itself *etc.*) and can take various forms (*eg.* single stranded, double stranded, vectors, probes *etc.*).

In addition, the term "nucleic acid" includes DNA and RNA, and also their analogues, such as those containing modified backbones, and also protein nucleic acids (PNA) *etc.*

According to a further aspect, the invention provides vectors comprising nucleotide sequences of the invention (*eg.* expression vectors) and host cells transformed with such vectors.

According to a further aspect, the invention provides compositions comprising protein, antibody, and/or nucleic acid according to the invention. These compositions may be suitable as vaccines, for instance, or as diagnostic reagents or as immunogenic compositions.

The invention also provides nucleic acid, protein, or antibody according to the invention for use as medicaments (*eg.* as vaccines) or as diagnostic reagents. It also provides the use of nucleic acid, protein, or antibody according to the invention in the manufacture of (i) a medicament for treating or preventing infection due to Neisserial bacteria (ii) a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria or (iii) for raising antibodies. Said Neisserial bacteria may be any species or strain (such as *N. gonorrhoeae*) but are preferably *N. meningitidis*, especially strain B or strain C.

The invention also provides a method of treating a patient, comprising administering to the patient a therapeutically effective amount of nucleic acid, protein, and/or antibody according to the invention.

According to further aspects, the invention provides various processes.

A process for producing proteins of the invention is provided, comprising the step of culturing a host cell according to the invention under conditions which induce protein expression.

A process for detecting polynucleotides of the invention is provided, comprising the steps of: (a) contacting a nucleic probe according to the invention with a biological sample under hybridizing conditions to form duplexes; and (b) detecting said duplexes.

A process for detecting proteins of the invention is provided, comprising the steps of: (a) contacting an antibody according to the invention with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

Methodology - Summary of standard procedures and techniques.

General

This invention provides *Neisseria meningitidis* menB nucleotide sequences, amino acid sequences encoded therein. With these disclosed sequences, nucleic acid probe assays and expression cassettes and vectors can be produced. The expression vectors can be transformed into host cells to produce proteins. The purified or isolated polypeptides (which may also be chemically synthesized) can be used to produce antibodies to detect menB proteins. Also, the host cells or extracts can be utilized for biological assays to isolate agonists or antagonists. In addition, with these sequences one can search to identify open reading frames and identify amino acid sequences. The proteins may also be used in immunogenic compositions, antigenic compositions and as vaccine components.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature e.g., Sambrook *Molecular Cloning; A Laboratory Manual, Second Edition* (1989); *DNA Cloning, Volumes I and ii* (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); *Transcription and Translation* (B.D. Hames & S.J. Higgins eds. 1984); *Animal Cell Culture* (R.I. Freshney ed. 1986); *Immobilized Cells and Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide to Molecular Cloning* (1984); the *Methods in Enzymology* series (Academic Press, Inc.), especially volumes 154 & 155; *Gene Transfer Vectors for Mammalian Cells* (J.H. Miller and M.P. Calos eds. 1987, Cold Spring Harbor Laboratory); Mayer and Walker, eds. (1987), *Immunochemical Methods in Cell and Molecular Biology* (Academic Press, London); Scopes, (1987) *Protein Purification: Principles and Practice*, Second Edition (Springer-Verlag, N.Y.), and *Handbook of Experimental Immunology, Volumes I-IV* (D.M. Weir and C.C. Blackwell eds 1986).

Standard abbreviations for nucleotides and amino acids are used in this specification.

All publications, patents, and patent applications cited herein are incorporated in full by reference.

Expression systems

The *Neisseria menB* nucleotide sequences can be expressed in a variety of different expression systems; for example those used with mammalian cells, plant cells, baculoviruses, bacteria, and yeast.

i. Mammalian Systems

Mammalian expression systems are known in the art. A mammalian promoter is any DNA sequence capable of binding mammalian RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiating region, which is usually placed proximal to the 5' end of the coding sequence, and a TATA box, usually located 25-30 base pairs (bp) upstream of the transcription initiation site. The TATA box is thought to direct RNA polymerase II to begin RNA synthesis at the correct site. A mammalian promoter will also contain an upstream promoter element, usually located within 100 to 200 bp upstream of the TATA box. An upstream promoter element determines the rate at which transcription is initiated and can act in either orientation (Sambrook et al. (1989) "Expression of Cloned Genes in Mammalian Cells." In *Molecular Cloning: A Laboratory Manual*, 2nd ed.).

Mammalian viral genes are often highly expressed and have a broad host range; therefore sequences encoding mammalian viral genes provide particularly useful promoter sequences. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter (Ad MLP), and herpes simplex virus promoter. In addition, sequences derived from non-viral genes, such as the murine metallothionein gene, also provide useful promoter sequences. Expression may be either constitutive or regulated (inducible). Depending on the promoter selected, many promoters may be inducible using known substrates, such as the use of the mouse mammary tumor virus (MMTV) promoter with the glucocorticoid responsive element (GRE) that is induced by glucocorticoid in hormone-responsive transformed cells (see for example, U.S. Patent 5,783,681).

The presence of an enhancer element (enhancer), combined with the promoter elements described above, will usually increase expression levels. An enhancer is a

regulatory DNA sequence that can stimulate transcription up to 1000-fold when linked to homologous or heterologous promoters, with synthesis beginning at the normal RNA start site. Enhancers are also active when they are placed upstream or downstream from the transcription initiation site, in either normal or flipped orientation, or at a distance of more than 1000 nucleotides from the promoter (Maniatis et al. (1987) *Science* 236:1237; Alberts et al. (1989) *Molecular Biology of the Cell*, 2nd ed.). Enhancer elements derived from viruses may be particularly useful, because they usually have a broader host range. Examples include the SV40 early gene enhancer (Dijkema et al (1985) *EMBO J.* 4:761) and the enhancer/promoters derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus (Gorman et al. (1982b) *Proc. Natl. Acad. Sci.* 79:6777) and from human cytomegalovirus (Boshart et al. (1985) *Cell* 41:521). Additionally, some enhancers are regulatable and become active only in the presence of an inducer, such as a hormone or metal ion (Sassone-Corsi and Borelli (1986) *Trends Genet.* 2:215; Maniatis et al. (1987) *Science* 236:1237).

A DNA molecule may be expressed intracellularly in mammalian cells. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in mammalian cells. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The adenovirus tripartite leader is an example of a leader sequence that provides for secretion of a foreign protein in mammalian cells.

Usually, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. The 3' terminus of the mature mRNA is formed by site-specific post-transcriptional cleavage and polyadenylation (Birnstiel et al. (1985) *Cell* 41:349; Proudfoot and Whitelaw (1988) "Termination and 3' end processing of eukaryotic RNA. In *Transcription and splicing* (ed. B.D. Hames and D.M.

Glover); Proudfoot (1989) *Trends Biochem. Sci.* 14:105). These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator/polyadenylation signals include those derived from SV40 (Sambrook et al (1989) "Expression of cloned genes in cultured mammalian cells." In *Molecular Cloning: A Laboratory Manual*).

Usually, the above described components, comprising a promoter, polyadenylation signal, and transcription termination sequence are put together into expression constructs. Enhancers, introns with functional splice donor and acceptor sites, and leader sequences may also be included in an expression construct, if desired. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as mammalian cells or bacteria. Mammalian replication systems include those derived from animal viruses, which require trans-acting factors to replicate. For example, plasmids containing the replication systems of papovaviruses, such as SV40 (Gluzman (1981) *Cell* 23:175) or polyomavirus, replicate to extremely high copy number in the presence of the appropriate viral T antigen. Additional examples of mammalian replicons include those derived from bovine papillomavirus and Epstein-Barr virus. Additionally, the replicon may have two replication systems, thus allowing it to be maintained, for example, in mammalian cells for expression and in a prokaryotic host for cloning and amplification. Examples of such mammalian-bacteria shuttle vectors include pMT2 (Kaufman et al. (1989) *Mol. Cell. Biol.* 9:946) and pHEBO (Shimizu et al. (1986) *Mol. Cell. Biol.* 6:1074).

The transformation procedure used depends upon the host to be transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to, Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (e.g., Hep G2), and a number of other cell lines.

ii. Plant Cellular Expression Systems

There are many plant cell culture and whole plant genetic expression systems known in the art. Exemplary plant cellular genetic expression systems include those described in patents, such as: U.S. 5,693,506; US 5,659,122; and US 5,608,143. Additional examples of genetic expression in plant cell culture has been described by Zenk, *Phytochemistry* 30:3861-3863 (1991). Descriptions of plant protein signal peptides may be found in addition to the references described above in Vaulcombe et al., *Mol. Gen. Genet.* 209:33-40 (1987); Chandler et al., *Plant Molecular Biology* 3:407-418 (1984); Rogers, *J. Biol. Chem.* 260:3731-3738 (1985); Rothstein et al., *Gene* 55:353-356 (1987); Whittier et al., *Nucleic Acids Research* 15:2515-2535 (1987); Wirsal et al., *Molecular Microbiology* 3:3-14 (1989); Yu et al., *Gene* 122:247-253 (1992). A description of the regulation of plant gene expression by the phytohormone, gibberellic acid and secreted enzymes induced by gibberellic acid can be found in R.L. Jones and J. MacMillin, *Gibberellins*: in: *Advanced Plant Physiology*, Malcolm B. Wilkins, ed., 1984 Pitman Publishing Limited, London, pp. 21-52. References that describe other metabolically-regulated genes: Sheen, *Plant Cell*, 2:1027-1038(1990); Maas et al., *EMBO J.* 9:3447-3452 (1990); Benkel and Hickey, *Proc. Natl. Acad. Sci.* 84:1337-1339 (1987)

Typically, using techniques known in the art, a desired polynucleotide sequence is inserted into an expression cassette comprising genetic regulatory elements designed for operation in plants. The expression cassette is inserted into a desired expression vector with companion sequences upstream and downstream from the expression cassette suitable for expression in a plant host. The companion sequences will be of plasmid or viral origin and provide necessary characteristics to the vector to permit the vectors to move DNA from an original cloning host, such as bacteria, to the desired plant host. The basic bacterial/plant vector construct will preferably provide a broad host range prokaryote replication origin; a prokaryote selectable marker; and, for *Agrobacterium* transformations, T DNA sequences for *Agrobacterium*-mediated transfer to plant chromosomes. Where the heterologous gene is not readily amenable to detection, the construct will preferably also have a selectable marker gene suitable for determining if a plant cell has been transformed. A general review of suitable markers, for example for the members of the grass family, is found in Wilmink and Dons, 1993, *Plant Mol. Biol. Reprtr*, 11(2):165-185.

Sequences suitable for permitting integration of the heterologous sequence into the plant genome are also recommended. These might include transposon sequences and the like for homologous recombination as well as Ti sequences which permit random insertion of a heterologous expression cassette into a plant genome. Suitable prokaryote selectable markers include resistance toward antibiotics such as ampicillin or tetracycline. Other DNA sequences encoding additional functions may also be present in the vector, as is known in the art.

The nucleic acid molecules of the subject invention may be included into an expression cassette for expression of the protein(s) of interest. Usually, there will be only one expression cassette, although two or more are feasible. The recombinant expression cassette will contain in addition to the heterologous protein encoding sequence the following elements, a promoter region, plant 5' untranslated sequences, initiation codon depending upon whether or not the structural gene comes equipped with one, and a transcription and translation termination sequence. Unique restriction enzyme sites at the 5' and 3' ends of the cassette allow for easy insertion into a pre-existing vector.

A heterologous coding sequence may be for any protein relating to the present invention. The sequence encoding the protein of interest will encode a signal peptide which allows processing and translocation of the protein, as appropriate, and will usually lack any sequence which might result in the binding of the desired protein of the invention to a membrane. Since, for the most part, the transcriptional initiation region will be for a gene which is expressed and translocated during germination, by employing the signal peptide which provides for translocation, one may also provide for translocation of the protein of interest. In this way, the protein(s) of interest will be translocated from the cells in which they are expressed and may be efficiently harvested. Typically secretion in seeds are across the aleurone or scutellar epithelium layer into the endosperm of the seed. While it is not required that the protein be secreted from the cells in which the protein is produced, this facilitates the isolation and purification of the recombinant protein.

Since the ultimate expression of the desired gene product will be in a eucaryotic cell it is desirable to determine whether any portion of the cloned gene contains sequences which will be processed out as introns by the host's splicosome machinery. If so, site-directed mutagenesis of the "intron" region may be conducted to prevent losing a portion of the genetic message as a false intron code, Reed and Maniatis, *Cell* 41:95-105, 1985.

The vector can be microinjected directly into plant cells by use of micropipettes to mechanically transfer the recombinant DNA. Crossway, *Mol. Gen. Genet*, 202:179-185, 1985. The genetic material may also be transferred into the plant cell by using polyethylene glycol, Krens, et al., *Nature*, 296, 72-74, 1982. Another method of introduction of nucleic acid segments is high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface, Klein, et al., *Nature*, 327, 70-73, 1987 and Knudsen and Muller, 1991, *Planta*, 185:330-336 teaching particle bombardment of barley endosperm to create transgenic barley. Yet another method of introduction would be fusion of protoplasts with other entities, either minicells, cells, lysosomes or other fusible lipid-surfaced bodies, Fraley, et al., *Proc. Natl. Acad. Sci. USA*, 79, 1859-1863, 1982.

The vector may also be introduced into the plant cells by electroporation. (Fromm et al., *Proc. Natl Acad. Sci. USA* 82:5824, 1985). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the gene construct. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and form plant callus.

All plants from which protoplasts can be isolated and cultured to give whole regenerated plants can be transformed by the present invention so that whole plants are recovered which contain the transferred gene. It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to all major species of sugarcane, sugar beet, cotton, fruit and other trees, legumes and vegetables. Some suitable plants include, for example, species from the genera *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*, *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersion*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Cichorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Hererocallis*, *Nemesia*, *Pelargonium*, *Panicum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Glycine*, *Lolium*, *Zea*, *Triticum*, *Sorghum*, and *Datura*.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts containing copies of the heterologous gene is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced from the protoplast suspension.

These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Shoots and roots normally develop simultaneously. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is fully reproducible and repeatable.

In some plant cell culture systems, the desired protein of the invention may be excreted or alternatively, the protein may be extracted from the whole plant. Where the desired protein of the invention is secreted into the medium, it may be collected. Alternatively, the embryos and embryoless-half seeds or other plant tissue may be mechanically disrupted to release any secreted protein between cells and tissues. The mixture may be suspended in a buffer solution to retrieve soluble proteins. Conventional protein isolation and purification methods will be then used to purify the recombinant protein. Parameters of time, temperature pH, oxygen, and volumes will be adjusted through routine methods to optimize expression and recovery of heterologous protein.

iii. Baculovirus Systems

The polynucleotide encoding the protein can also be inserted into a suitable insect expression vector, and is operably linked to the control elements within that vector. Vector construction employs techniques which are known in the art. Generally, the components of the expression system include a transfer vector, usually a bacterial plasmid, which contains both a fragment of the baculovirus genome, and a convenient restriction site for insertion of the heterologous gene or genes to be expressed; a wild type baculovirus with a sequence homologous to the baculovirus-specific fragment in the transfer vector (this allows for the homologous recombination of the heterologous gene in to the baculovirus genome); and appropriate insect host cells and growth media.

After inserting the DNA sequence encoding the protein into the transfer vector, the vector and the wild type viral genome are transfected into an insect host cell where the vector and viral genome are allowed to recombine. The packaged recombinant virus is expressed and recombinant plaques are identified and purified. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *inter alia*, Invitrogen, San Diego CA ("MaxBac" kit). These techniques are generally known to

those skilled in the art and fully described in Summers and Smith, *Texas Agricultural Experiment Station Bulletin No. 1555* (1987) (hereinafter "Summers and Smith").

Prior to inserting the DNA sequence encoding the protein into the baculovirus genome, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are usually assembled into an intermediate transplacement construct (transfer vector). This construct may contain a single gene and operably linked regulatory elements; multiple genes, each with its own set of operably linked regulatory elements; or multiple genes, regulated by the same set of regulatory elements. Intermediate transplacement constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as a bacterium. The replicon will have a replication system, thus allowing it to be maintained in a suitable host for cloning and amplification.

Currently, the most commonly used transfer vector for introducing foreign genes into AcNPV is pAc373. Many other vectors, known to those of skill in the art, have also been designed. These include, for example, pVL985 (which alters the polyhedrin start codon from ATG to ATT, and which introduces a BamHI cloning site 32 basepairs downstream from the ATT; see Luckow and Summers, *Virology* (1989) 17:31.

The plasmid usually also contains the polyhedrin polyadenylation signal (Miller et al. (1988) *Ann. Rev. Microbiol.*, 42:177) and a prokaryotic ampicillin-resistance (*amp*) gene and origin of replication for selection and propagation in *E. coli*.

Baculovirus transfer vectors usually contain a baculovirus promoter. A baculovirus promoter is any DNA sequence capable of binding a baculovirus RNA polymerase and initiating the downstream (5' to 3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A baculovirus transfer vector may also have a second domain called an enhancer, which, if present, is usually distal to the structural gene. Expression may be either regulated or constitutive.

Structural genes, abundantly transcribed at late times in a viral infection cycle, provide particularly useful promoter sequences. Examples include sequences derived from the gene encoding the viral polyhedron protein, Friesen et al., (1986) "The Regulation of Baculovirus Gene Expression," in: *The Molecular Biology of Baculoviruses* (ed. Walter Doerfler); EPO

Publ. Nos. 127 839 and 155 476; and the gene encoding the p10 protein, Vlak et al., (1988), *J. Gen. Virol.* 69:765.

DNA encoding suitable signal sequences can be derived from genes for secreted insect or baculovirus proteins, such as the baculovirus polyhedrin gene (Carbonell et al. (1988) *Gene*, 73:409). Alternatively, since the signals for mammalian cell posttranslational modifications (such as signal peptide cleavage, proteolytic cleavage, and phosphorylation) appear to be recognized by insect cells, and the signals required for secretion and nuclear accumulation also appear to be conserved between the invertebrate cells and vertebrate cells, leaders of non-insect origin, such as those derived from genes encoding human (alpha) α -interferon, Maeda et al., (1985), *Nature* 315:592; human gastrin-releasing peptide, Lebacqz-Verheyden et al., (1988), *Molec. Cell. Biol.* 8:3129; human IL-2, Smith et al., (1985) *Proc. Nat'l Acad. Sci. USA*, 82:8404; mouse IL-3, (Miyajima et al., (1987) *Gene* 58:273; and human glucocerebrosidase, Martin et al. (1988) *DNA*, 7:99, can also be used to provide for secretion in insects.

A recombinant polypeptide or polyprotein may be expressed intracellularly or, if it is expressed with the proper regulatory sequences, it can be secreted. Good intracellular expression of nonfused foreign proteins usually requires heterologous genes that ideally have a short leader sequence containing suitable translation initiation signals preceding an ATG start signal. If desired, methionine at the N-terminus may be cleaved from the mature protein by *in vitro* incubation with cyanogen bromide.

Alternatively, recombinant polyproteins or proteins which are not naturally secreted can be secreted from the insect cell by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in insects. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the translocation of the protein into the endoplasmic reticulum.

After insertion of the DNA sequence and/or the gene encoding the expression product precursor of the protein, an insect cell host is co-transformed with the heterologous DNA of the transfer vector and the genomic DNA of wild type baculovirus -- usually by co-transfection. The promoter and transcription termination sequence of the construct will usually comprise a 2-5kb section of the baculovirus genome. Methods for introducing heterologous DNA into the desired site in the baculovirus virus are known in the art. (See

Summers and Smith *supra*; Ju et al. (1987); Smith et al., *Mol. Cell. Biol.* (1983) 3:2156; and Luckow and Summers (1989)). For example, the insertion can be into a gene such as the polyhedrin gene, by homologous double crossover recombination; insertion can also be into a restriction enzyme site engineered into the desired baculovirus gene. Miller et al., (1989), *Bioessays* 4:91. The DNA sequence, when cloned in place of the polyhedrin gene in the expression vector, is flanked both 5' and 3' by polyhedrin-specific sequences and is positioned downstream of the polyhedrin promoter.

The newly formed baculovirus expression vector is subsequently packaged into an infectious recombinant baculovirus. Homologous recombination occurs at low frequency (between about 1% and about 5%); thus, the majority of the virus produced after cotransfection is still wild-type virus. Therefore, a method is necessary to identify recombinant viruses. An advantage of the expression system is a visual screen allowing recombinant viruses to be distinguished. The polyhedrin protein, which is produced by the native virus, is produced at very high levels in the nuclei of infected cells at late times after viral infection. Accumulated polyhedrin protein forms occlusion bodies that also contain embedded particles. These occlusion bodies, up to 15 μm in size, are highly refractile, giving them a bright shiny appearance that is readily visualized under the light microscope. Cells infected with recombinant viruses lack occlusion bodies. To distinguish recombinant virus from wild-type virus, the transfection supernatant is plaqued onto a monolayer of insect cells by techniques known to those skilled in the art. Namely, the plaques are screened under the light microscope for the presence (indicative of wild-type virus) or absence (indicative of recombinant virus) of occlusion bodies. *Current Protocols in Microbiology* Vol. 2 (Ausubel et al. eds) at 16.8 (Supp. 10, 1990); Summers and Smith, *supra*; Miller et al. (1989).

Recombinant baculovirus expression vectors have been developed for infection into several insect cells. For example, recombinant baculoviruses have been developed for, *inter alia*: *Aedes aegypti*, *Autographa californica*, *Bombyx mori*, *Drosophila melanogaster*, *Spodoptera frugiperda*, and *Trichoplusia ni* (PCT Pub. No. WO 89/046699; Carbonell et al., (1985) *J. Virol.* 56:153; Wright (1986) *Nature* 321:718; Smith et al., (1983) *Mol. Cell. Biol.* 3:2156; and see generally, Fraser, et al. (1989) *In Vitro Cell. Dev. Biol.* 25:225).

Cells and cell culture media are commercially available for both direct and fusion expression of heterologous polypeptides in a baculovirus/expression system; cell culture technology is generally known to those skilled in the art. See, e.g., Summers and Smith *supra*.

The modified insect cells may then be grown in an appropriate nutrient medium, which allows for stable maintenance of the plasmid(s) present in the modified insect host. Where the expression product gene is under inducible control, the host may be grown to high density, and expression induced. Alternatively, where expression is constitutive, the product will be continuously expressed into the medium and the nutrient medium must be continuously circulated, while removing the product of interest and augmenting depleted nutrients. The product may be purified by such techniques as chromatography, e.g., HPLC, affinity chromatography, ion exchange chromatography, etc.; electrophoresis; density gradient centrifugation; solvent extraction, or the like. As appropriate, the product may be further purified, as required, so as to remove substantially any insect proteins which are also secreted in the medium or result from lysis of insect cells, so as to provide a product which is at least substantially free of host debris, e.g., proteins, lipids and polysaccharides.

In order to obtain protein expression, recombinant host cells derived from the transformants are incubated under conditions which allow expression of the recombinant protein encoding sequence. These conditions will vary, dependent upon the host cell selected. However, the conditions are readily ascertainable to those of ordinary skill in the art, based upon what is known in the art.

iv. Bacterial Systems

Bacterial expression techniques are known in the art. A bacterial promoter is any DNA sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A bacterial promoter may also have a second domain called an operator, that may overlap an adjacent RNA polymerase binding site at which RNA synthesis begins. The operator permits negative regulated (inducible) transcription, as a gene repressor protein may bind the operator and thereby inhibit transcription of a specific gene. Constitutive expression may occur in the absence of negative regulatory elements, such as the operator. In addition, positive regulation may be achieved by a gene activator protein binding sequence, which, if present is usually proximal (5') to the RNA polymerase binding sequence. An example of a gene activator protein is the catabolite activator protein (CAP), which helps

initiate transcription of the lac operon in *Escherichia coli* (*E. coli*) (Raibaud *et al.* (1984) *Annu. Rev. Genet.* 18:173). Regulated expression may therefore be either positive or negative, thereby either enhancing or reducing transcription.

Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose (*lac*) (Chang *et al.* (1977) *Nature* 198:1056), and maltose. Additional examples include promoter sequences derived from biosynthetic enzymes such as tryptophan (*trp*) (Goeddel *et al.* (1980) *Nuc. Acids Res.* 8:4057; Yelverton *et al.* (1981) *Nucl. Acids Res.* 9:731; U.S. Patent 4,738,921; EPO Publ. Nos. 036 776 and 121 775). The beta-lactamase (*bla*) promoter system (Weissmann (1981) "The cloning of interferon and other mistakes." In *Interferon 3* (ed. I. Gresser)), bacteriophage lambda PL (Shimatake *et al.* (1981) *Nature* 292:128) and T5 (U.S. Patent 4,689,406) promoter systems also provide useful promoter sequences.

In addition, synthetic promoters which do not occur in nature also function as bacterial promoters. For example, transcription activation sequences of one bacterial or bacteriophage promoter may be joined with the operon sequences of another bacterial or bacteriophage promoter, creating a synthetic hybrid promoter (U.S. Patent 4,551,433). For example, the *tac* promoter is a hybrid *trp-lac* promoter comprised of both *trp* promoter and *lac* operon sequences that is regulated by the *lac* repressor (Amann *et al.* (1983) *Gene* 25:167; de Boer *et al.* (1983) *Proc. Natl. Acad. Sci.* 80:21). Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. A naturally occurring promoter of non-bacterial origin can also be coupled with a compatible RNA polymerase to produce high levels of expression of some genes in prokaryotes. The bacteriophage T7 RNA polymerase/promoter system is an example of a coupled promoter system (Studier *et al.* (1986) *J. Mol. Biol.* 189:113; Tabor *et al.* (1985) *Proc Natl. Acad. Sci.* 82:1074). In addition, a hybrid promoter can also be comprised of a bacteriophage promoter and an *E. coli* operator region (EPO Publ. No. 267 851).

In addition to a functioning promoter sequence, an efficient ribosome binding site is also useful for the expression of foreign genes in prokaryotes. In *E. coli*, the ribosome binding site is called the Shine-Dalgarno (SD) sequence and includes an initiation codon (ATG) and a sequence 3-9 nucleotides in length located 3-11 nucleotides upstream of the initiation codon

(Shine *et al.* (1975) *Nature* 254:34). The SD sequence is thought to promote binding of mRNA to the ribosome by the pairing of bases between the SD sequence and the 3' end of *E. coli* 16S rRNA (Steitz *et al.* (1979) "Genetic signals and nucleotide sequences in messenger RNA." In *Biological Regulation and Development: Gene Expression* (ed. R.F. Goldberg)). To express eukaryotic genes and prokaryotic genes with weak ribosome-binding site, it is often necessary to optimize the distance between the SD sequence and the ATG of the eukaryotic gene (Sambrook *et al.* (1989) "Expression of cloned genes in *Escherichia coli*." In *Molecular Cloning: A Laboratory Manual*).

A DNA molecule may be expressed intracellularly. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide or by either *in vivo* or *in vitro* incubation with a bacterial methionine N-terminal peptidase (EPO Publ. No. 219 237).

Fusion proteins provide an alternative to direct expression. Usually, a DNA sequence encoding the N-terminal portion of an endogenous bacterial protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the bacteriophage lambda cell gene can be linked at the 5' terminus of a foreign gene and expressed in bacteria. The resulting fusion protein preferably retains a site for a processing enzyme (factor Xa) to cleave the bacteriophage protein from the foreign gene (Nagai *et al.* (1984) *Nature* 309:810). Fusion proteins can also be made with sequences from the *lacZ* (Jia *et al.* (1987) *Gene* 60:197), *trpE* (Allen *et al.* (1987) *J. Biotechnol.* 5:93; Makoff *et al.* (1989) *J. Gen. Microbiol.* 135:11), and *Chey* (EPO Publ. No. 324 647) genes. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin specific processing-protease) to cleave the ubiquitin from the foreign protein. Through this method, native foreign protein can be isolated (Miller *et al.* (1989) *Bio/Technology* 7:698).

Alternatively, foreign proteins can also be secreted from the cell by creating chimeric DNA molecules that encode a fusion protein comprised of a signal peptide sequence fragment that provides for secretion of the foreign protein in bacteria (U.S. Patent 4,336,336). The

signal sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). Preferably there are processing sites, which can be cleaved either *in vivo* or *in vitro* encoded between the signal peptide fragment and the foreign gene.

DNA encoding suitable signal sequences can be derived from genes for secreted bacterial proteins, such as the *E. coli* outer membrane protein gene (*ompA*) (Masui *et al.* (1983), in: *Experimental Manipulation of Gene Expression*; Ghayeb *et al.* (1984) *EMBO J.* 3:2437) and the *E. coli* alkaline phosphatase signal sequence (*phoA*) (Oka *et al.* (1985) *Proc. Natl. Acad. Sci.* 82:7212). As an additional example, the signal sequence of the alpha-amylase gene from various *Bacillus* strains can be used to secrete heterologous proteins from *B. subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. No. 244 042).

Usually, transcription termination sequences recognized by bacteria are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Transcription termination sequences frequently include DNA sequences of about 50 nucleotides capable of forming stem loop structures that aid in terminating transcription. Examples include transcription termination sequences derived from genes with strong promoters, such as the *trp* gene in *E. coli* as well as other biosynthetic genes.

Usually, the above described components, comprising a promoter, signal sequence (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as bacteria. The replicon will have a replication system, thus allowing it to be maintained in a prokaryotic host either for expression or for cloning and amplification. In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably contain at least about 10, and more preferably at least about 20 plasmids. Either a high or low copy number

vector may be selected, depending upon the effect of the vector and the foreign protein on the host.

Alternatively, the expression constructs can be integrated into the bacterial genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to the bacterial chromosome that allows the vector to integrate. Integrations appear to result from recombinations between homologous DNA in the vector and the bacterial chromosome. For example, integrating vectors constructed with DNA from various *Bacillus* strains integrate into the *Bacillus* chromosome (EPO Publ. No. 127 328). Integrating vectors may also be comprised of bacteriophage or transposon sequences.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of bacterial strains that have been transformed. Selectable markers can be expressed in the bacterial host and may include genes which render bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin (neomycin), and tetracycline (Davies *et al.* (1978) *Annu. Rev. Microbiol.* 32:469). Selectable markers may also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways.

Alternatively, some of the above described components can be put together in transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extra-chromosomal replicons or integrating vectors, have been developed for transformation into many bacteria. For example, expression vectors have been developed for, *inter alia*, the following bacteria: *Bacillus subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541), *Escherichia coli* (Shimatake *et al.* (1981) *Nature* 292:128; Amann *et al.* (1985) *Gene* 40:183; Studier *et al.* (1986) *J. Mol. Biol.* 189:113; EPO Publ. Nos. 036 776, 136 829 and 136 907), *Streptococcus cremoris* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655); *Streptococcus lividans* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655), *Streptomyces lividans* (U.S. Patent 4,745,056).

Methods of introducing exogenous DNA into bacterial hosts are well-known in the art, and usually include either the transformation of bacteria treated with CaCl_2 or other agents, such as divalent cations and DMSO. DNA can also be introduced into bacterial cells by

electroporation. Transformation procedures usually vary with the bacterial species to be transformed. (See e.g., use of *Bacillus*: Masson *et al.* (1989) *FEMS Microbiol. Lett.* 60:273; Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541; use of *Campylobacter*: Miller *et al.* (1988) *Proc. Natl. Acad. Sci.* 85:856; and Wang *et al.* (1990) *J. Bacteriol.* 172:949; use of *Escherichia coli*: Cohen *et al.* (1973) *Proc. Natl. Acad. Sci.* 69:2110; Dower *et al.* (1988) *Nucleic Acids Res.* 16:6127; Kushner (1978) "An improved method for transformation of *Escherichia coli* with ColE1-derived plasmids. In *Genetic Engineering: Proceedings of the International Symposium on Genetic Engineering* (eds. H.W. Boyer and S. Nicosia); Mandel *et al.* (1970) *J. Mol. Biol.* 53:159; Taketo (1988) *Biochim. Biophys. Acta* 949:318; use of *Lactobacillus*: Chassy *et al.* (1987) *FEMS Microbiol. Lett.* 44:173; use of *Pseudomonas*: Fiedler *et al.* (1988) *Anal. Biochem* 170:38; use of *Staphylococcus*: Augustin *et al.* (1990) *FEMS Microbiol. Lett.* 66:203; use of *Streptococcus*: Barany *et al.* (1980) *J. Bacteriol.* 144:698; Harlander (1987) "Transformation of *Streptococcus lactis* by electroporation, in: *Streptococcal Genetics* (ed. J. Ferretti and R. Curtiss III); Perry *et al.* (1981) *Infect. Immun.* 32:1295; Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655; Somkuti *et al.* (1987) *Proc. 4th Evr. Cong. Biotechnology* 1:412.

v. Yeast Expression

Yeast expression systems are also known to one of ordinary skill in the art. A yeast promoter is any DNA sequence capable of binding yeast RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site (the "TATA Box") and a transcription initiation site. A yeast promoter may also have a second domain called an upstream activator sequence (UAS), which, if present, is usually distal to the structural gene. The UAS permits regulated (inducible) expression. Constitutive expression occurs in the absence of a UAS. Regulated expression may be either positive or negative, thereby either enhancing or reducing transcription.

Yeast is a fermenting organism with an active metabolic pathway, therefore sequences encoding enzymes in the metabolic pathway provide particularly useful promoter sequences.

Examples include alcohol dehydrogenase (ADH) (EPO Publ. No. 284 044), enolase, glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphate-dehydrogenase (GAP or GAPDH), hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, and pyruvate kinase (PyK) (EPO Publ. No. 329 203). The yeast *PHO5* gene, encoding acid phosphatase, also provides useful promoter sequences (Myanohara *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:1).

In addition, synthetic promoters which do not occur in nature also function as yeast promoters. For example, UAS sequences of one yeast promoter may be joined with the transcription activation region of another yeast promoter, creating a synthetic hybrid promoter. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region (U.S. Patent Nos. 4,876,197 and 4,880,734). Other examples of hybrid promoters include promoters which consist of the regulatory sequences of either the *ADH2*, *GAL4*, *GAL10*, OR *PHO5* genes, combined with the transcriptional activation region of a glycolytic enzyme gene such as GAP or PyK (EPO Publ. No. 164 556). Furthermore, a yeast promoter can include naturally occurring promoters of non-yeast origin that have the ability to bind yeast RNA polymerase and initiate transcription. Examples of such promoters include, *inter alia*, (Cohen *et al.* (1980) *Proc. Natl. Acad. Sci. USA* 77:1078; Henikoff *et al.* (1981) *Nature* 283:835; Hollenberg *et al.* (1981) *Curr. Topics Microbiol. Immunol.* 96:119; Hollenberg *et al.* (1979) "The Expression of Bacterial Antibiotic Resistance Genes in the Yeast *Saccharomyces cerevisiae*," in: *Plasmids of Medical, Environmental and Commercial Importance* (eds. K.N. Timmis and A. Puhler); Mercerau-Puigalon *et al.* (1980) *Gene* 11:163; Panthier *et al.* (1980) *Curr. Genet.* 2:109;).

A DNA molecule may be expressed intracellularly in yeast. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Fusion proteins provide an alternative for yeast expression systems, as well as in mammalian, plant, baculovirus, and bacterial expression systems. Usually, a DNA sequence encoding the N-terminal portion of an endogenous yeast protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the yeast or human

superoxide dismutase (SOD) gene, can be linked at the 5' terminus of a foreign gene and expressed in yeast. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. See e.g., EPO Publ. No. 196056. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin-specific processing protease) to cleave the ubiquitin from the foreign protein. Through this method, therefore, native foreign protein can be isolated (e.g., WO88/024066).

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provide for secretion in yeast of the foreign protein. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell.

DNA encoding suitable signal sequences can be derived from genes for secreted yeast proteins, such as the yeast invertase gene (EPO Publ. No. 012 873; JPO Publ. No. 62:096,086) and the A-factor gene (U.S. Patent 4,588,684). Alternatively, leaders of non-yeast origin, such as an interferon leader, exist that also provide for secretion in yeast (EPO Publ. No. 060 057).

A preferred class of secretion leaders are those that employ a fragment of the yeast alpha-factor gene, which contains both a "pre" signal sequence, and a "pro" region. The types of alpha-factor fragments that can be employed include the full-length pre-pro alpha factor leader (about 83 amino acid residues) as well as truncated alpha-factor leaders (usually about 25 to about 50 amino acid residues) (U.S. Patent Nos. 4,546,083 and 4,870,008; EPO Publ. No. 324 274). Additional leaders employing an alpha-factor leader fragment that provides for secretion include hybrid alpha-factor leaders made with a presequence of a first yeast, but a pro-region from a second yeast alpha factor. (See e.g., PCT Publ. No. WO 89/02463.)

Usually, transcription termination sequences recognized by yeast are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator

sequence and other yeast-recognized termination sequences, such as those coding for glycolytic enzymes.

Usually, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as yeast or bacteria. The replicon may have two replication systems, thus allowing it to be maintained, for example, in yeast for expression and in a prokaryotic host for cloning and amplification. Examples of such yeast-bacteria shuttle vectors include YEp24 (Botstein *et al.* (1979) *Gene* 8:17-24), pCI/1 (Brake *et al.* (1984) *Proc. Natl. Acad. Sci. USA* 81:4642-4646), and YRp17 (Stinchcomb *et al.* (1982) *J. Mol. Biol.* 158:157). In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably have at least about 10, and more preferably at least about 20. Enter a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host. See e.g., Brake *et al.*, *supra*.

Alternatively, the expression constructs can be integrated into the yeast genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to a yeast chromosome that allows the vector to integrate, and preferably contain two homologous sequences flanking the expression construct. Integrations appear to result from recombinations between homologous DNA in the vector and the yeast chromosome (Orr-Weaver *et al.* (1983) *Methods in Enzymol.* 101:228-245). An integrating vector may be directed to a specific locus in yeast by selecting the appropriate homologous sequence for inclusion in the vector. See Orr-Weaver *et al.*, *supra*. One or more expression construct may integrate, possibly affecting levels of recombinant protein produced (Rine *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:6750). The chromosomal sequences included in the vector can occur either as a single segment in the vector, which results in the integration of the entire vector, or two segments homologous to adjacent segments in the chromosome and flanking the expression construct in the vector, which can result in the stable integration of only the expression construct.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of yeast strains that have been transformed. Selectable markers may include biosynthetic genes that can be expressed in the yeast host, such as *ADE2*, *HIS4*, *LEU2*, *TRP1*, and *ALG7*, and the G418 resistance gene, which confer resistance in yeast cells to tunicamycin and G418, respectively. In addition, a suitable selectable marker may also provide yeast with the ability to grow in the presence of toxic compounds, such as metal. For example, the presence of *CUP1* allows yeast to grow in the presence of copper ions (Butt *et al.* (1987) *Microbiol. Rev.* 51:351).

Alternatively, some of the above described components can be put together into transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extrachromosomal replicons or integrating vectors, have been developed for transformation into many yeasts. For example, expression vectors and methods of introducing exogenous DNA into yeast hosts have been developed for, *inter alia*, the following yeasts: *Candida albicans* (Kurtz, *et al.* (1986) *Mol. Cell. Biol.* 6:142); *Candida maltosa* (Kunze, *et al.* (1985) *J. Basic Microbiol.* 25:141); *Hansenula polymorpha* (Gleeson, *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302); *Kluyveromyces fragilis* (Das, *et al.* (1984) *J. Bacteriol.* 158:1165); *Kluyveromyces lactis* (De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:737; Van den Berg *et al.* (1990) *Bio/Technology* 8:135); *Pichia guillermondii* (Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141); *Pichia pastoris* (Cregg, *et al.* (1985) *Mol. Cell. Biol.* 5:3376; U.S. Patent Nos. 4,837,148 and 4,929,555); *Saccharomyces cerevisiae* (Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163); *Schizosaccharomyces pombe* (Beach and Nurse (1981) *Nature* 300:706); and *Yarrowia lipolytica* (Davidow, *et al.* (1985) *Curr. Genet.* 10:380471 Gaillardin, *et al.* (1985) *Curr. Genet.* 10:49).

Methods of introducing exogenous DNA into yeast hosts are well-known in the art, and usually include either the transformation of spheroplasts or of intact yeast cells treated with alkali cations. Transformation procedures usually vary with the yeast species to be transformed. See e.g., [Kurtz *et al.* (1986) *Mol. Cell. Biol.* 6:142; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; *Candida*]; [Gleeson *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302; *Hansenula*]; [Das *et al.* (1984) *J.*

Bacteriol. 158:1165; De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:1165; Van den Berg *et al.* (1990) *Bio/Technology* 8:135; Kluyveromyces]; [Cregg *et al.* (1985) *Mol. Cell. Biol.* 5:3376; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; U.S. Patent Nos. 4,837,148 and 4,929,555; Pichia]; [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163 Saccharomyces]; [Beach and Nurse (1981) *Nature* 300:706; Schizosaccharomyces]; [Davidow *et al.* (1985) *Curr. Genet.* 10:39; Gaillardin *et al.* (1985) *Curr. Genet.* 10:49; Yarrowia].

Definitions

A composition containing X is "substantially free of" Y when at least 85% by weight of the total X+Y in the composition is X. Preferably, X comprises at least about 90% by weight of the total of X+Y in the composition, more preferably at least about 95% or even 99% by weight.

A "conserved" *Neisseria* amino acid fragment or protein is one that is present in a particular Neisserial protein in at least x% of *Neisseria*. The value of x may be 50% or more, e.g., 66%, 75%, 80%, 90%, 95% or even 100% (i.e. the amino acid is found in the protein in question in all *Neisseria*). In order to determine whether an amino acid is "conserved" in a particular Neisserial protein, it is necessary to compare that amino acid residue in the sequences of the protein in question from a plurality of different *Neisseria* (a reference population). The reference population may include a number of different *Neisseria* species or may include a single species. The reference population may include a number of different serogroups of a particular species or a single serogroup. A preferred reference population consists of the 5 most common *Neisseria* strains.

The term "heterologous" refers to two biological components that are not found together in nature. The components may be host cells, genes, or regulatory regions, such as promoters. Although the heterologous components are not found together in nature, they can function together, as when a promoter heterologous to a gene is operably linked to the gene. Another example is where a Neisserial sequence is heterologous to a mouse host cell.

"Epitope" means antigenic determinant, and may elicit a cellular and/or humoral response.

Conditions for "high stringency" are 65 degrees C in 0.1 xSSC 0.5% SDS solution.

An “origin of replication” is a polynucleotide sequence that initiates and regulates replication of polynucleotides, such as an expression vector. The origin of replication behaves as an autonomous unit of polynucleotide replication within a cell, capable of replication under its own control. An origin of replication may be needed for a vector to replicate in a particular host cell. With certain origins of replication, an expression vector can be reproduced at a high copy number in the presence of the appropriate proteins within the cell. Examples of origins are the autonomously replicating sequences, which are effective in yeast; and the viral T-antigen, effective in COS-7 cells.

A “mutant” sequence is defined as a DNA, RNA or amino acid sequence differing from but having homology with the native or disclosed sequence. Depending on the particular sequence, the degree of homology (sequence identity) between the native or disclosed sequence and the mutant sequence is preferably greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) which is calculated as described above. As used herein, an “allelic variant” of a nucleic acid molecule, or region, for which nucleic acid sequence is provided herein is a nucleic acid molecule, or region, that occurs at essentially the same locus in the genome of another or second isolate, and that, due to natural variation caused by, for example, mutation or recombination, has a similar but not identical nucleic acid sequence. A coding region allelic variant typically encodes a protein having similar activity to that of the protein encoded by the gene to which it is being compared. An allelic variant can also comprise an alteration in the 5' or 3' untranslated regions of the gene, such as in regulatory control regions. (see, for example, U.S. Patent 5,753,235).

Antibodies

As used herein, the term “antibody” refers to a polypeptide or group of polypeptides composed of at least one antibody combining site. An “antibody combining site” is the three-dimensional binding space with an internal surface shape and charge distribution complementary to the features of an epitope of an antigen, which allows a binding of the antibody with the antigen. “Antibody” includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, humanized antibodies, altered antibodies, univalent antibodies, Fab proteins, and single domain antibodies.

Antibodies against the proteins of the invention are useful for affinity chromatography, immunoassays, and distinguishing/identifying *Neisseria* menB proteins.

Antibodies elicited against the proteins of the present invention bind to antigenic polypeptides or proteins or protein fragments that are present and specifically associated with strains of *Neisseria meningitidis* menB. In some instances, these antigens may be associated with specific strains, such as those antigens specific for the menB strains. The antibodies of the invention may be immobilized to a matrix and utilized in an immunoassay or on an affinity chromatography column, to enable the detection and/or separation of polypeptides, proteins or protein fragments or cells comprising such polypeptides, proteins or protein fragments. Alternatively, such polypeptides, proteins or protein fragments may be immobilized so as to detect antibodies bindably specific thereto.

Antibodies to the proteins of the invention, both polyclonal and monoclonal, may be prepared by conventional methods. In general, the protein is first used to immunize a suitable animal, preferably a mouse, rat, rabbit or goat. Rabbits and goats are preferred for the preparation of polyclonal sera due to the volume of serum obtainable, and the availability of labeled anti-rabbit and anti-goat antibodies. Immunization is generally performed by mixing or emulsifying the protein in saline, preferably in an adjuvant such as Freund's complete adjuvant, and injecting the mixture or emulsion parenterally (generally subcutaneously or intramuscularly). A dose of 50-200 µg/injection is typically sufficient. Immunization is generally boosted 2-6 weeks later with one or more injections of the protein in saline, preferably using Freund's incomplete adjuvant. One may alternatively generate antibodies by *in vitro* immunization using methods known in the art, which for the purposes of this invention is considered equivalent to *in vivo* immunization. Polyclonal antisera is obtained by bleeding the immunized animal into a glass or plastic container, incubating the blood at 25°C for one hour, followed by incubating at 4°C for 2-18 hours. The serum is recovered by centrifugation (e.g., 1,000g for 10 minutes). About 20-50 ml per bleed may be obtained from rabbits.

Monoclonal antibodies are prepared using the standard method of Kohler & Milstein (*Nature* (1975) 256:495-96), or a modification thereof. Typically, a mouse or rat is immunized as described above. However, rather than bleeding the animal to extract serum, the spleen (and optionally several large lymph nodes) is removed and dissociated into single cells. If desired, the spleen cells may be screened (after removal of nonspecifically adherent cells) by applying a cell suspension to a plate or well coated with the protein antigen. B-cells that express membrane-bound immunoglobulin specific for the antigen bind to the plate, and

are not rinsed away with the rest of the suspension. Resulting B-cells, or all dissociated spleen cells, are then induced to fuse with myeloma cells to form hybridomas, and are cultured in a selective medium (e.g., hypoxanthine, aminopterin, thymidine medium, "HAT"). The resulting hybridomas are plated by limiting dilution, and are assayed for the production of antibodies which bind specifically to the immunizing antigen (and which do not bind to unrelated antigens). The selected MAb-secreting hybridomas are then cultured either *in vitro* (e.g., in tissue culture bottles or hollow fiber reactors), or *in vivo* (as ascites in mice).

If desired, the antibodies (whether polyclonal or monoclonal) may be labeled using conventional techniques. Suitable labels include fluorophores, chromophores, radioactive atoms (particularly ^{32}P and ^{125}I), electron-dense reagents, enzymes, and ligands having specific binding partners. Enzymes are typically detected by their activity. For example, horseradish peroxidase is usually detected by its ability to convert 3,3',5,5'-tetramethylbenzidine (TMB) to a blue pigment, quantifiable with a spectrophotometer. "Specific binding partner" refers to a protein capable of binding a ligand molecule with high specificity, as for example in the case of an antigen and a monoclonal antibody specific therefor. Other specific binding partners include biotin and avidin or streptavidin, IgG and protein A, and the numerous receptor-ligand couples known in the art. It should be understood that the above description is not meant to categorize the various labels into distinct classes, as the same label may serve in several different modes. For example, ^{125}I may serve as a radioactive label or as an electron-dense reagent. HRP may serve as enzyme or as antigen for a MAb. Further, one may combine various labels for desired effect. For example, MAbs and avidin also require labels in the practice of this invention: thus, one might label a MAb with biotin, and detect its presence with avidin labeled with ^{125}I , or with an anti-biotin MAb labeled with HRP. Other permutations and possibilities will be readily apparent to those of ordinary skill in the art, and are considered as equivalents within the scope of the instant invention.

Antigens, immunogens, polypeptides, proteins or protein fragments of the present invention elicit formation of specific binding partner antibodies. These antigens, immunogens, polypeptides, proteins or protein fragments of the present invention comprise immunogenic compositions of the present invention. Such immunogenic compositions may further comprise or include adjuvants, carriers, or other compositions that promote or enhance

or stabilize the antigens, polypeptides, proteins or protein fragments of the present invention. Such adjuvants and carriers will be readily apparent to those of ordinary skill in the art.

Pharmaceutical Compositions

Pharmaceutical compositions can comprise (include) either polypeptides, antibodies, or nucleic acid of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature, when given to a patient that is febrile. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgment of the clinician.

For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of

organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

Delivery Methods

Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals; in particular, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal and transcutaneous applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Vaccines

Vaccines according to the invention may either be prophylactic (i.e., to prevent infection) or therapeutic (i.e., to treat disease after infection).

Such vaccines comprise immunizing antigen(s) or immunogen(s), immunogenic polypeptide, protein(s) or protein fragments, or nucleic acids (e.g., ribonucleic acid or deoxyribonucleic acid), usually in combination with "pharmaceutically acceptable carriers," which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or

liposomes), and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the immunogen or antigen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, *H. pylori*, etc. pathogens.

Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59 (PCT Publ. No. WO 90/14837), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA), (b) SAF, containing 10% Squalene, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) RibiTM adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (DetoxTM); (3) saponin adjuvants, such as StimulonTM (Cambridge Bioscience, Worcester, MA) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (e.g., IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (e.g., gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc; (6) detoxified mutants of a bacterial ADP-ribosylating toxin such as a cholera toxin (CT), a pertussis toxin (PT), or an *E. coli* heat-labile toxin (LT), particularly LT-K63, LT-R72, CT-S109, PT-K9/G129; see, e.g., WO 93/13302 and WO 92/19265; and (7) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59 are preferred.

As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-*sn*-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), etc.

The vaccine compositions comprising immunogenic compositions (e.g., which may include the antigen, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Alternatively, vaccine compositions comprising immunogenic compositions may comprise an antigen, polypeptide, protein, protein fragment or nucleic acid in a pharmaceutically acceptable carrier.

More specifically, vaccines comprising immunogenic compositions comprise an immunologically effective amount of the immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By "immunologically effective amount", it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (e.g., nonhuman primate, primate, *etc.*), the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

Typically, the vaccine compositions or immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

The immunogenic compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Additional formulations suitable for other modes of administration include oral and pulmonary formulations, suppositories, and transdermal and transcutaneous applications. Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.

As an alternative to protein-based vaccines, DNA vaccination may be employed (e.g., Robinson & Torres (1997) *Seminars in Immunology* 9:271-283; Donnelly *et al.* (1997) *Annu Rev Immunol* 15:617-648).

Gene Delivery Vehicles

Gene therapy vehicles for delivery of constructs, including a coding sequence of a therapeutic of the invention, to be delivered to the mammal for expression in the mammal, can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches in *in vivo* or *ex vivo* modality. Expression of such coding sequence can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence *in vivo* can be either constitutive or regulated.

The invention includes gene delivery vehicles capable of expressing the contemplated nucleic acid sequences. The gene delivery vehicle is preferably a viral vector and, more preferably, a retroviral, adenoviral, adeno-associated viral (AAV), herpes viral, or alphavirus vector. The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picornavirus, poxvirus, or togavirus viral vector. See generally, Jolly (1994) *Cancer Gene Therapy* 1:51-64; Kimura (1994) *Human Gene Therapy* 5:845-852; Connelly (1995) *Human Gene Therapy* 6:185-193; and Kaplitt (1994) *Nature Genetics* 6:148-153.

Retroviral vectors are well known in the art, including B, C and D type retroviruses, xenotropic retroviruses (for example, NZB-X1, NZB-X2 and NZB9-1 (see O'Neill (1985) *J. Virol.* 53:160) polytropic retroviruses e.g., MCF and MCF-MLV (see Kelly (1983) *J. Virol.* 45:291), spumaviruses and lentiviruses. See RNA Tumor Viruses, Second Edition, Cold Spring Harbor Laboratory, 1985.

Portions of the retroviral gene therapy vector may be derived from different retroviruses. For example, retrovector LTRs may be derived from a Murine Sarcoma Virus, a tRNA binding site from a Rous Sarcoma Virus, a packaging signal from a Murine Leukemia Virus, and an origin of second strand synthesis from an Avian Leukosis Virus.

These recombinant retroviral vectors may be used to generate transduction competent retroviral vector particles by introducing them into appropriate packaging cell lines (see US patent 5,591,624). Retrovirus vectors can be constructed for site-specific integration into host cell DNA by incorporation of a chimeric integrase enzyme into the retroviral particle (see WO96/37626). It is preferable that the recombinant viral vector is a replication defective recombinant virus.

Packaging cell lines suitable for use with the above-described retrovirus vectors are well known in the art, are readily prepared (see WO95/30763 and WO92/05266), and can be used to create producer cell lines (also termed vector cell lines or "VCLs") for the production of recombinant vector particles. Preferably, the packaging cell lines are made from human parent cells (e.g., HT1080 cells) or mink parent cell lines, which eliminates inactivation in human serum.

Preferred retroviruses for the construction of retroviral gene therapy vectors include Avian Leukosis Virus, Bovine Leukemia Virus, Murine Leukemia Virus, Mink-Cell Focus-Inducing Virus, Murine Sarcoma Virus, Reticuloendotheliosis Virus and Rous Sarcoma Virus. Particularly preferred Murine Leukemia Viruses include 4070A and 1504A (Hartley and Rowe (1976) *J Virol* 19:19-25), Abelson (ATCC No. VR-999), Friend (ATCC No. VR-245), Graffi, Gross (ATCC No. VR-590), Kirsten, Harvey Sarcoma Virus and Rauscher (ATCC No. VR-998) and Moloney Murine Leukemia Virus (ATCC No. VR-190). Such retroviruses may be obtained from depositories or collections such as the American Type Culture Collection ("ATCC") in Rockville, Maryland or isolated from known sources using commonly available techniques.

Exemplary known retroviral gene therapy vectors employable in this invention include those described in patent applications GB2200651, EP0415731, EP0345242, EP0334301, WO89/02468; WO89/05349, WO89/09271, WO90/02806, WO90/07936, WO94/03622, WO93/25698, WO93/25234, WO93/11230, WO93/10218, WO91/02805, WO91/02825, WO95/07994, US 5,219,740, US 4,405,712, US 4,861,719, US 4,980,289, US 4,777,127, US 5,591,624. See also Vile (1993) *Cancer Res* 53:3860-3864; Vile (1993) *Cancer Res* 53:962-967; Ram (1993) *Cancer Res* 53 (1993) 83-88; Takamiya (1992) *J Neurosci Res* 33:493-503; Baba (1993) *J Neurosurg* 79:729-735; Mann (1983) *Cell* 33:153; Cane (1984) *Proc Natl Acad Sci* 81:6349; and Miller (1990) *Human Gene Therapy* 1.

Human adenoviral gene therapy vectors are also known in the art and employable in this invention. See, for example, Berkner (1988) *Biotechniques* 6:616 and Rosenfeld (1991) *Science* 252:431, and WO93/07283, WO93/06223, and WO93/07282. Exemplary known adenoviral gene therapy vectors employable in this invention include those described in the above referenced documents and in WO94/12649, WO93/03769, WO93/19191, WO94/28938, WO95/11984, WO95/00655, WO95/27071, WO95/29993, WO95/34671, WO96/05320, WO94/08026, WO94/11506, WO93/06223, WO94/24299, WO95/14102,

WO95/24297, WO95/02697, WO94/28152, WO94/24299, WO95/09241, WO95/25807, WO95/05835, WO94/18922 and WO95/09654. Alternatively, administration of DNA linked to killed adenovirus as described in Curiel (1992) *Hum. Gene Ther.* 3:147-154 may be employed. The gene delivery vehicles of the invention also include adenovirus associated virus (AAV) vectors. Leading and preferred examples of such vectors for use in this invention are the AAV-2 based vectors disclosed in Srivastava, WO93/09239. Most preferred AAV vectors comprise the two AAV inverted terminal repeats in which the native D-sequences are modified by substitution of nucleotides, such that at least 5 native nucleotides and up to 18 native nucleotides, preferably at least 10 native nucleotides up to 18 native nucleotides, most preferably 10 native nucleotides are retained and the remaining nucleotides of the D-sequence are deleted or replaced with non-native nucleotides. The native D-sequences of the AAV inverted terminal repeats are sequences of 20 consecutive nucleotides in each AAV inverted terminal repeat (i.e., there is one sequence at each end) which are not involved in HP formation. The non-native replacement nucleotide may be any nucleotide other than the nucleotide found in the native D-sequence in the same position. Other employable exemplary AAV vectors are pWP-19, pWN-1, both of which are disclosed in Nahreini (1993) *Gene* 124:257-262. Another example of such an AAV vector is psub201 (see Samulski (1987) *J. Virol.* 61:3096). Another exemplary AAV vector is the Double-D ITR vector. Construction of the Double-D ITR vector is disclosed in US Patent 5,478,745. Still other vectors are those disclosed in Carter US Patent 4,797,368 and Muzyczka US Patent 5,139,941, Chartejee US Patent 5,474,935, and Kotin WO94/288157. Yet a further example of an AAV vector employable in this invention is SSV9AFABTKneo, which contains the AFP enhancer and albumin promoter and directs expression predominantly in the liver. Its structure and construction are disclosed in Su (1996) *Human Gene Therapy* 7:463-470. Additional AAV gene therapy vectors are described in US 5,354,678, US 5,173,414, US 5,139,941, and US 5,252,479.

The gene therapy vectors comprising sequences of the invention also include herpes vectors. Leading and preferred examples are herpes simplex virus vectors containing a sequence encoding a thymidine kinase polypeptide such as those disclosed in US 5,288,641 and EP0176170 (Roizman). Additional exemplary herpes simplex virus vectors include HFEM/ICP6-LacZ disclosed in WO95/04139 (Wistar Institute), pHSVlac described in Geller (1988) *Science* 241:1667-1669 and in WO90/09441 and WO92/07945, HSV Us3::pgC-lacZ

described in Fink (1992) *Human Gene Therapy* 3:11-19 and HSV 7134, 2 RH 105 and GAL4 described in EP 0453242 (Breakefield), and those deposited with the ATCC as accession numbers ATCC VR-977 and ATCC VR-260.

Also contemplated are alpha virus gene therapy vectors that can be employed in this invention. Preferred alpha virus vectors are Sindbis viruses vectors. Togaviruses, Semliki Forest virus (ATCC VR-67; ATCC VR-1247), Middleberg virus (ATCC VR-370), Ross River virus (ATCC VR-373; ATCC VR-1246), Venezuelan equine encephalitis virus (ATCC VR923; ATCC VR-1250; ATCC VR-1249; ATCC VR-532), and those described in US patents 5,091,309, 5,217,879, and WO92/10578. More particularly, those alpha virus vectors described in U.S. Serial No. 08/405,627, filed March 15, 1995, WO94/21792, WO92/10578, WO95/07994, US 5,091,309 and US 5,217,879 are employable. Such alpha viruses may be obtained from depositories or collections such as the ATCC in Rockville, Maryland or isolated from known sources using commonly available techniques. Preferably, alphavirus vectors with reduced cytotoxicity are used (see USSN 08/679640).

DNA vector systems such as eukaryotic layered expression systems are also useful for expressing the nucleic acids of the invention. See WO95/07994 for a detailed description of eukaryotic layered expression systems. Preferably, the eukaryotic layered expression systems of the invention are derived from alphavirus vectors and most preferably from Sindbis viral vectors.

Other viral vectors suitable for use in the present invention include those derived from poliovirus, for example ATCC VR-58 and those described in Evans, *Nature* 339 (1989) 385 and Sabin (1973) *J. Biol. Standardization* 1:115; rhinovirus, for example ATCC VR-1110 and those described in Arnold (1990) *J Cell Biochem* L401; pox viruses such as canary pox virus or vaccinia virus, for example ATCC VR-111 and ATCC VR-2010 and those described in Fisher-Hoch (1989) *Proc Natl Acad Sci* 86:317; Flexner (1989) *Ann NY Acad Sci* 569:86, Flexner (1990) *Vaccine* 8:17; in US 4,603,112 and US 4,769,330 and WO89/01973; SV40 virus, for example ATCC VR-305 and those described in Mulligan (1979) *Nature* 277:108 and Madzak (1992) *J Gen Virol* 73:1533; influenza virus, for example ATCC VR-797 and recombinant influenza viruses made employing reverse genetics techniques as described in US 5,166,057 and in Enami (1990) *Proc Natl Acad Sci* 87:3802-3805; Enami & Palese (1991) *J Virol* 65:2711-2713 and Luytjes (1989) *Cell* 59:110, (see also McMichael (1983) *NEJ Med* 309:13, and Yap (1978) *Nature* 273:238 and *Nature* (1979) 277:108); human

immunodeficiency virus as described in EP-0386882 and in Buchschacher (1992) *J. Virol.* 66:2731; measles virus, for example ATCC VR-67 and VR-1247 and those described in EP-0440219; Aura virus, for example ATCC VR-368; Bebaru virus, for example ATCC VR-600 and ATCC VR-1240; Cabassou virus, for example ATCC VR-922; Chikungunya virus, for example ATCC VR-64 and ATCC VR-1241; Fort Morgan Virus, for example ATCC VR-924; Getah virus, for example ATCC VR-369 and ATCC VR-1243; Kyzylagach virus, for example ATCC VR-927; Mayaro virus, for example ATCC VR-66; Mucambo virus, for example ATCC VR-580 and ATCC VR-1244; Ndumu virus, for example ATCC VR-371; Pixuna virus, for example ATCC VR-372 and ATCC VR-1245; Tonate virus, for example ATCC VR-925; Trinita virus, for example ATCC VR-469; Una virus, for example ATCC VR-374; Whataroa virus, for example ATCC VR-926; Y-62-33 virus, for example ATCC VR-375; O'Nyong virus, Eastern encephalitis virus, for example ATCC VR-65 and ATCC VR-1242; Western encephalitis virus, for example ATCC VR-70, ATCC VR-1251, ATCC VR-622 and ATCC VR-1252; and coronavirus, for example ATCC VR-740 and those described in Hamre (1966) *Proc Soc Exp Biol Med* 121:190.

Delivery of the compositions of this invention into cells is not limited to the above mentioned viral vectors. Other delivery methods and media may be employed such as, for example, nucleic acid expression vectors, polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example see US Serial No. 08/366,787, filed December 30, 1994 and Curiel (1992) *Hum Gene Ther* 3:147-154 ligand linked DNA, for example see Wu (1989) *J Biol Chem* 264:16985-16987, eucaryotic cell delivery vehicles cells, for example see US Serial No.08/240,030, filed May 9, 1994, and US Serial No. 08/404,796, deposition of photopolymerized hydrogel materials, hand-held gene transfer particle gun, as described in US Patent 5,149,655, ionizing radiation as described in US5,206,152 and in WO92/11033, nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip (1994) *Mol Cell Biol* 14:2411-2418 and in Woffendin (1994) *Proc Natl Acad Sci* 91:1581-1585.

Particle mediated gene transfer may be employed, for example see US Serial No. 60/023,867. Briefly, the sequence can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, as described in Wu &

Wu (1987) *J. Biol. Chem.* 262:4429-4432, insulin as described in Hucked (1990) *Biochem Pharmacol* 40:253-263, galactose as described in Plank (1992) *Bioconjugate Chem* 3:533-539, lactose or transferrin.

Naked DNA may also be employed to transform a host cell. Exemplary naked DNA introduction methods are described in WO 90/11092 and US 5,580,859. Uptake efficiency may be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method may be improved further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm.

Liposomes that can act as gene delivery vehicles are described in U.S. 5,422,120, WO95/13796, WO94/23697, WO91/14445 and EP-524,968. As described in USSN. 60/023,867, on non-viral delivery, the nucleic acid sequences encoding a polypeptide can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then be incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, insulin, galactose, lactose, or transferrin. Other delivery systems include the use of liposomes to encapsulate DNA comprising the gene under the control of a variety of tissue-specific or ubiquitously-active promoters. Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al* (1994) *Proc. Natl. Acad. Sci. USA* 91(24):11581-11585. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in U.S. 5,149,655; use of ionizing radiation for activating transferred gene, as described in U.S. 5,206,152 and WO92/11033.

Exemplary liposome and polycationic gene delivery vehicles are those described in US 5,422,120 and 4,762,915; in WO 95/13796; WO94/23697; and WO91/14445; in EP-0524968; and in Stryer, *Biochemistry*, pages 236-240 (1975) W.H. Freeman, San Francisco; Szoka (1980) *Biochem Biophys Acta* 600:1; Bayer (1979) *Biochem Biophys Acta* 550:464; Rivnay (1987) *Meth Enzymol* 149:119; Wang (1987) *Proc Natl Acad Sci* 84:7851; Plant (1989) *Anal Biochem* 176:420.

A polynucleotide composition can comprises therapeutically effective amount of a gene therapy vehicle, as the term is defined above. For purposes of the present invention, an effective dose will be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

Delivery Methods

Once formulated, the polynucleotide compositions of the invention can be administered (1) directly to the subject; (2) delivered *ex vivo*, to cells derived from the subject; or (3) *in vitro* for expression of recombinant proteins. The subjects to be treated can be mammals or birds. Also, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a tumor or lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in *eg.* WO93/14778. Examples of cells useful in *ex vivo* applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells.

Generally, delivery of nucleic acids for both *ex vivo* and *in vitro* applications can be accomplished by the following procedures, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Polynucleotide and polypeptide pharmaceutical compositions

In addition to the pharmaceutically acceptable carriers and salts described above, the following additional agents can be used with polynucleotide and/or polypeptide compositions.

A. Polypeptides

One example are polypeptides which include, without limitation: asioloorosomucoid (ASOR); transferrin; asialoglycoproteins; antibodies; antibody fragments; ferritin; interleukins; interferons, granulocyte, macrophage colony stimulating factor (GM-CSF),

granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), stem cell factor and erythropoietin. Viral antigens, such as envelope proteins, can also be used. Also, proteins from other invasive organisms, such as the 17 amino acid peptide from the circumsporozoite protein of plasmodium falciparum known as RII.

B.Hormones, Vitamins, Etc.

Other groups that can be included are, for example: hormones, steroids, androgens, estrogens, thyroid hormone, or vitamins, folic acid.

C.Polyalkylenes, Polysaccharides, etc.

Also, polyalkylene glycol can be included with the desired polynucleotides or polypeptides. In a preferred embodiment, the polyalkylene glycol is polyethylene glycol. In addition, mono-, di-, or polysaccharides can be included. In a preferred embodiment of this aspect, the polysaccharide is dextran or DEAE-dextran. Also, chitosan and poly(lactide-co-glycolide)

D.Lipids, and Liposomes

The desired polynucleotide or polypeptide can also be encapsulated in lipids or packaged in liposomes prior to delivery to the subject or to cells derived therefrom.

Lipid encapsulation is generally accomplished using liposomes which are able to stably bind or entrap and retain nucleic acid. The ratio of condensed polynucleotide or polypeptide to lipid preparation can vary but will generally be around 1:1 (mg DNA:micromoles lipid), or more of lipid. For a review of the use of liposomes as carriers for delivery of nucleic acids, see, Hug and Sleight (1991) *Biochim. Biophys. Acta.* 1097:1-17; Straubinger (1983) *Meth. Enzymol.* 101:512-527.

Liposomal preparations for use in the present invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner (1987) *Proc. Natl. Acad. Sci. USA* 84:7413-7416); mRNA (Malone (1989) *Proc. Natl. Acad. Sci. USA* 86:6077-6081); and purified transcription factors (Debs (1990) *J. Biol. Chem.* 265:10189-10192), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, NY. (See, also, Felgner *supra*). Other commercially available liposomes include transfectace (DDAB/DOPE) and

DOTAP/DOPE (Boehringer). Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, *eg.* Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; WO90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, AL), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art. See *eg.* Straubinger (1983) *Meth. Immunol.* 101:512-527; Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; Papahadjopoulos (1975) *Biochim. Biophys. Acta* 394:483; Wilson (1979) *Cell* 17:77; Deamer & Bangham (1976) *Biochim. Biophys. Acta* 443:629; Ostro (1977) *Biochem. Biophys. Res. Commun.* 76:836; Fraley (1979) *Proc. Natl. Acad. Sci. USA* 76:3348; Enoch & Strittmatter (1979) *Proc. Natl. Acad. Sci. USA* 76:145; Fraley (1980) *J. Biol. Chem.* (1980) 255:10431; Szoka & Papahadjopoulos (1978) *Proc. Natl. Acad. Sci. USA* 75:145; and Schaefer-Ridder (1982) *Science* 215:166.

E. Lipoproteins

In addition, lipoproteins can be included with the polynucleotide or polypeptide to be delivered. Examples of lipoproteins to be utilized include: chylomicrons, HDL, IDL, LDL, and VLDL. Mutants, fragments, or fusions of these proteins can also be used. Also, modifications of naturally occurring lipoproteins can be used, such as acetylated LDL. These lipoproteins can target the delivery of polynucleotides to cells expressing lipoprotein receptors. Preferably, if lipoproteins are including with the polynucleotide to be delivered, no other targeting ligand is included in the composition.

Naturally occurring lipoproteins comprise a lipid and a protein portion. The protein portion are known as apoproteins. At the present, apoproteins A, B, C, D, and E have been

isolated and identified. At least two of these contain several proteins, designated by Roman numerals, AI, AII, AIV; CI, CII, CIII.

A lipoprotein can comprise more than one apoprotein. For example, naturally occurring chylomicrons comprises of A, B, C, and E, over time these lipoproteins lose A and acquire C and E apoproteins. VLDL comprises A, B, C, and E apoproteins, LDL comprises apoprotein B; and HDL comprises apoproteins A, C, and E.

The amino acid of these apoproteins are known and are described in, for example, Breslow (1985) *Annu Rev. Biochem* 54:699; Law (1986) *Adv. Exp Med. Biol.* 151:162; Chen (1986) *J Biol Chem* 261:12918; Kane (1980) *Proc Natl Acad Sci USA* 77:2465; and Utermann (1984) *Hum Genet* 65:232.

Lipoproteins contain a variety of lipids including, triglycerides, cholesterol (free and esters), and phospholipids. The composition of the lipids varies in naturally occurring lipoproteins. For example, chylomicrons comprise mainly triglycerides. A more detailed description of the lipid content of naturally occurring lipoproteins can be found, for example, in *Meth. Enzymol.* 128 (1986). The composition of the lipids are chosen to aid in conformation of the apoprotein for receptor binding activity. The composition of lipids can also be chosen to facilitate hydrophobic interaction and association with the polynucleotide binding molecule.

Naturally occurring lipoproteins can be isolated from serum by ultracentrifugation, for instance. Such methods are described in *Meth. Enzymol.* (*supra*); Pitas (1980) *J. Biochem.* 255:5454-5460 and Mahey (1979) *J Clin. Invest* 64:743-750.

Lipoproteins can also be produced by *in vitro* or recombinant methods by expression of the apoprotein genes in a desired host cell. See, for example, Atkinson (1986) *Annu Rev Biophys Chem* 15:403 and Radding (1958) *Biochim Biophys Acta* 30: 443.

Lipoproteins can also be purchased from commercial suppliers, such as Biomedical Technologies, Inc., Stoughton, Massachusetts, USA.

Further description of lipoproteins can be found in Zuckermann et al., PCT. Appln. No. US97/14465.

F.Polycationic Agents

Polycationic agents can be included, with or without lipoprotein, in a composition with the desired polynucleotide or polypeptide to be delivered.

Polycationic agents, typically, exhibit a net positive charge at physiological relevant pH and are capable of neutralizing the electrical charge of nucleic acids to facilitate delivery to a desired location. These agents have both in vitro, ex vivo, and in vivo applications. Polycationic agents can be used to deliver nucleic acids to a living subject either intramuscularly, subcutaneously, etc.

The following are examples of useful polypeptides as polycationic agents: polylysine, polyarginine, polyornithine, and protamine. Other examples include histones, protamines, human serum albumin, DNA binding proteins, non-histone chromosomal proteins, coat proteins from DNA viruses, such as (X174, transcriptional factors also contain domains that bind DNA and therefore may be useful as nucleic acid condensing agents. Briefly, transcriptional factors such as C/CEBP, c-jun, c-fos, AP-1, AP-2, AP-3, CPF, Prot-1, Sp-1, Oct-1, Oct-2, CREP, and TFIID contain basic domains that bind DNA sequences.

Organic polycationic agents include: spermine, spermidine, and putrescine.

The dimensions and of the physical properties of a polycationic agent can be extrapolated from the list above, to construct other polypeptide polycationic agents or to produce synthetic polycationic agents.

Synthetic Polycationic Agents

Synthetic polycationic agents which are useful include, for example, DEAE-dextran, polybrene. Lipofectin[®], and lipofectAMINE[®] are monomers that form polycationic complexes when combined with polynucleotides or polypeptides.

Immunodiagnostic Assays

Neisserial antigens of the invention can be used in immunoassays to detect antibody levels (or, conversely, anti-Neisserial antibodies can be used to detect antigen levels). Immunoassays based on well defined, recombinant antigens can be developed to replace invasive diagnostics methods. Antibodies to Neisserial proteins within biological samples, including for example, blood or serum samples, can be detected. Design of the immunoassays is subject to a great deal of variation, and a variety of these are known in the art. Protocols for the immunoassay may be based, for example, upon competition, or direct reaction, or sandwich type assays. Protocols may also, for example, use solid supports, or may be by immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the labels may be, for example, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays which amplify the signals from the probe are also known; examples of which are

assays which utilize biotin and avidin, and enzyme-labeled and mediated immunoassays, such as ELISA assays.

Kits suitable for immunodiagnosis and containing the appropriate labeled reagents are constructed by packaging the appropriate materials, including the compositions of the invention, in suitable containers, along with the remaining reagents and materials (for example, suitable buffers, salt solutions, *etc.*) required for the conduct of the assay, as well as suitable set of assay instructions.

Nucleic Acid Hybridisation

“Hybridization” refers to the association of two nucleic acid sequences to one another by hydrogen bonding. Typically, one sequence will be fixed to a solid support and the other will be free in solution. Then, the two sequences will be placed in contact with one another under conditions that favor hydrogen bonding. Factors that affect this bonding include: the type and volume of solvent; reaction temperature; time of hybridization; agitation; agents to block the non-specific attachment of the liquid phase sequence to the solid support (Denhardt's reagent or BLOTTO); concentration of the sequences; use of compounds to increase the rate of association of sequences (dextran sulfate or polyethylene glycol); and the stringency of the washing conditions following hybridization. See Sambrook *et al.* [*supra*] Volume 2, chapter 9, pages 9.47 to 9.57.

“Stringency” refers to conditions in a hybridization reaction that favor association of very similar sequences over sequences that differ. For example, the combination of temperature and salt concentration should be chosen that is approximately 120 to 200°C below the calculated T_m of the hybrid under study. The temperature and salt conditions can often be determined empirically in preliminary experiments in which samples of genomic DNA immobilized on filters are hybridized to the sequence of interest and then washed under conditions of different stringencies. See Sambrook *et al.* at page 9.50.

Variables to consider when performing, for example, a Southern blot are (1) the complexity of the DNA being blotted and (2) the homology between the probe and the sequences being detected. The total amount of the fragment(s) to be studied can vary a magnitude of 10, from 0.1 to 1 µg for a plasmid or phage digest to 10^{-9} to 10^{-8} g for a single copy gene in a highly complex eukaryotic genome. For lower complexity polynucleotides, substantially shorter blotting, hybridization, and exposure times, a smaller amount of starting polynucleotides, and lower specific activity of probes can be used. For example, a single-copy

yeast gene can be detected with an exposure time of only 1 hour starting with 1 μg of yeast DNA, blotting for two hours, and hybridizing for 4-8 hours with a probe of 10^8 cpm/ μg . For a single-copy mammalian gene a conservative approach would start with 10 μg of DNA, blot overnight, and hybridize overnight in the presence of 10% dextran sulfate using a probe of greater than 10^8 cpm/ μg , resulting in an exposure time of ~24 hours.

Several factors can affect the melting temperature (T_m) of a DNA-DNA hybrid between the probe and the fragment of interest, and consequently, the appropriate conditions for hybridization and washing. In many cases the probe is not 100% homologous to the fragment. Other commonly encountered variables include the length and total G+C content of the hybridizing sequences and the ionic strength and formamide content of the hybridization buffer. The effects of all of these factors can be approximated by a single equation:

$$T_m = 81 + 16.6(\log_{10} C_i) + 0.4\%[(G + C)] - 0.6(\% \text{formamide}) - 600/n - 1.5(\% \text{mismatch}).$$

where C_i is the salt concentration (monovalent ions) and n is the length of the hybrid in base pairs (slightly modified from Meinkoth & Wahl (1984) *Anal. Biochem.* 138: 267-284).

In designing a hybridization experiment, some factors affecting nucleic acid hybridization can be conveniently altered. The temperature of the hybridization and washes and the salt concentration during the washes are the simplest to adjust. As the temperature of the hybridization increases (*ie.* stringency), it becomes less likely for hybridization to occur between strands that are nonhomologous, and as a result, background decreases. If the radiolabeled probe is not completely homologous with the immobilized fragment (as is frequently the case in gene family and interspecies hybridization experiments), the hybridization temperature must be reduced, and background will increase. The temperature of the washes affects the intensity of the hybridizing band and the degree of background in a similar manner. The stringency of the washes is also increased with decreasing salt concentrations.

In general, convenient hybridization temperatures in the presence of 50% formamide are 42°C for a probe with is 95% to 100% homologous to the target fragment, 37°C for 90% to 95% homology, and 32°C for 85% to 90% homology. For lower homologies, formamide content should be lowered and temperature adjusted accordingly, using the equation above. If the homology between the probe and the target fragment are not known, the simplest approach is to start with both hybridization and wash conditions which are nonstringent. If non-specific bands or high background are observed after autoradiography, the filter can be

washed at high stringency and reexposed. If the time required for exposure makes this approach impractical, several hybridization and/or washing stringencies should be tested in parallel.

Nucleic Acid Probe Assays

Methods such as PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes according to the invention can determine the presence of cDNA or mRNA. A probe is said to "hybridize" with a sequence of the invention if it can form a duplex or double stranded complex, which is stable enough to be detected.

The nucleic acid probes will hybridize to the Neisserial nucleotide sequences of the invention (including both sense and antisense strands). Though many different nucleotide sequences will encode the amino acid sequence, the native Neisserial sequence is preferred because it is the actual sequence present in cells. mRNA represents a coding sequence and so a probe should be complementary to the coding sequence; single-stranded cDNA is complementary to mRNA, and so a cDNA probe should be complementary to the non-coding sequence.

The probe sequence need not be identical to the Neisserial sequence (or its complement) — some variation in the sequence and length can lead to increased assay sensitivity if the nucleic acid probe can form a duplex with target nucleotides, which can be detected. Also, the nucleic acid probe can include additional nucleotides to stabilize the formed duplex. Additional Neisserial sequence may also be helpful as a label to detect the formed duplex. For example, a non-complementary nucleotide sequence may be attached to the 5' end of the probe, with the remainder of the probe sequence being complementary to a Neisserial sequence. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the a Neisserial sequence in order to hybridize therewith and thereby form a duplex which can be detected.

The exact length and sequence of the probe will depend on the hybridization conditions, such as temperature, salt condition and the like. For example, for diagnostic applications, depending on the complexity of the analyte sequence, the nucleic acid probe typically contains at least 10-20 nucleotides, preferably 15-25, and more preferably at least 30 nucleotides, although it may be shorter than this. Short primers generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

Probes may be produced by synthetic procedures, such as the triester method of Matteucci *et al.* [*J. Am. Chem. Soc.* (1981) 103:3185], or according to Urdea *et al.* [*Proc. Natl. Acad. Sci. USA* (1983) 80: 7461], or using commercially available automated oligonucleotide synthesizers.

The chemical nature of the probe can be selected according to preference. For certain applications, DNA or RNA are appropriate. For other applications, modifications may be incorporated *eg.* backbone modifications, such as phosphorothioates or methylphosphonates, can be used to increase *in vivo* half-life, alter RNA affinity, increase nuclease resistance *etc.* [*eg.* see Agrawal & Iyer (1995) *Curr Opin Biotechnol* 6:12-19; Agrawal (1996) *TIBTECH* 14:376-387]; analogues such as peptide nucleic acids may also be used [*eg.* see Corey (1997) *TIBTECH* 15:224-229; Buchardt *et al.* (1993) *TIBTECH* 11:384-386].

One example of a nucleotide hybridization assay is described by Urdea *et al.* in international patent application WO92/02526 [see also US patent 5,124,246].

Alternatively, the polymerase chain reaction (PCR) is another well-known means for detecting small amounts of target nucleic acids. The assay is described in: Mullis *et al.* [*Meth. Enzymol.* (1987) 155: 335-350]; US patent 4,683,195; and US patent 4,683,202. Two "primer" nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers can comprise sequence that does not hybridize to the sequence of the amplification target (or its complement) to aid with duplex stability or, for example, to incorporate a convenient restriction site. Typically, such sequence will flank the desired Neisserial sequence.

A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a threshold amount of target nucleic acids are generated by the polymerase, they can be detected by more traditional methods, such as Southern blots. When using the Southern blot method, the labelled probe will hybridize to the Neisserial sequence (or its complement).

Also, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al* [*supra*]. mRNA, or cDNA generated from mRNA using a polymerase enzyme, can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labelled probe and then washed to remove any unhybridized probe. Next, the duplexes

containing the labeled probe are detected. Typically, the probe is labelled with a radioactive moiety.

EXAMPLES

The examples describe nucleic acid sequences which have been identified in *N. meningitidis*, and *N. gonorrhoeae* along with their respective and putative translation products. Not all of the nucleic acid sequences are complete *ie.* they encode less than the full-length wild-type protein.

The examples are generally in the following format:

- a nucleotide sequence which has been identified in *N. meningitidis*
- the putative translation product of said *N. meningitidis* sequence
- a computer analysis of said translation product based on database comparisons
- a corresponding nucleotide sequence identified from *N. gonorrhoeae*
- the putative translation product of said *N. gonorrhoeae* sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a corresponding nucleotide sequence identified from strain A of *N. meningitidis*
- the putative translation product of said *N. meningitidis* strain A sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a description of the characteristics of the protein which indicates that it might be suitably antigenic or immunogenic.

Sequence comparisons were performed at NCBI (<http://www.ncbi.nlm.nih.gov>) using the algorithms BLAST, BLAST2, BLASTn, BLASTp, tBLASTn, BLASTx, & tBLASTx [*eg.* see also Altschul *et al.* (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research* 25:2289-3402]. Searches were performed against the following databases: non-redundant GenBank+EMBL+DDBJ+PDB sequences and non-redundant GenBank CDS translations+PDB+SwissProt+SPupdate+PIR sequences.

Dots within nucleotide sequences represent nucleotides which have been arbitrarily introduced in order to maintain a reading frame. In the same way, double-underlined nucleotides were removed. Lower case letters represent ambiguities which arose during

alignment of independent sequencing reactions (some of the nucleotide sequences in the examples are derived from combining the results of two or more experiments).

Nucleotide sequences were scanned in all six reading frames to predict the presence of hydrophobic domains using an algorithm based on the statistical studies of Esposti *et al.* [Critical evaluation of the hydropathy of membrane proteins (1990) *Eur J Biochem* 190:207-219]. These domains represent potential transmembrane regions or hydrophobic leader sequences.

Open reading frames were predicted from fragmented nucleotide sequences using the program ORFFINDER (NCBI).

Underlined amino acid sequences indicate possible transmembrane domains or leader sequences in the ORFs, as predicted by the PSORT algorithm (<http://www.psort.nibb.ac.jp>). Functional domains were also predicted using the MOTIFS program (GCG Wisconsin & PROSITE).

For each of the following examples: based on the presence of a putative leader sequence and/or several putative transmembrane domains (single-underlined) in the gonococcal protein, it is predicted that the proteins from *N. meningitidis* and *N. gonorrhoeae*, and their respective epitopes, could be useful antigens or immunogenic compositions for vaccines or diagnostics.

The standard techniques and procedures which may be employed in order to perform the invention (*e.g.* to utilize the disclosed sequences for vaccination or diagnostic purposes) were summarized above. This summary is not a limitation on the invention but, rather, gives examples that may be used, but are not required.

In particular, the following methods were used to express, purify and biochemically characterize the proteins of the invention.

Chromosomal DNA Preparation

N.meningitidis strain 2996 was grown to exponential phase in 100ml of GC medium, harvested by centrifugation, and resuspended in 5ml buffer (20%(w/v) Sucrose, 50mM Tris-HCl, 50mM EDTA, pH8). After 10 minutes incubation on ice, the bacteria were lysed by adding 10ml of lysis solution (50mM NaCl, 1% Na-Sarkosyl, 50µg/ml Proteinase K), and the suspension incubated at 37°C for 2 hours. Two phenol extractions (equilibrated to pH 8) and one CHCl₃/isoamylalcohol (24:1) extraction were performed. DNA was precipitated by addition of 0.3M sodium acetate and 2 volumes of ethanol, and collected by centrifugation.

The pellet was washed once with 70%(v/v) ethanol and redissolved in 4.0ml TE buffer (10mM Tris-HCl, 1mM EDTA, pH 8.0). The DNA concentration was measured by reading the OD at 260 nm.

Oligonucleotide design

Synthetic oligonucleotide primers were designed on the basis of the coding sequence of each ORF, using (a) the meningococcus B sequence when available, or (b) the gonococcus/meningococcus A sequence, adapted to the codon preference usage of meningococcus as necessary. Any predicted signal peptides were omitted, by designing the 5' primers to sequence immediately downstream from the predicted leader sequence.

For most ORFs, the 5' primers included two restriction enzyme recognition sites (*Bam*HI-*Nde*I, *Bam*HI-*Nhe*I, *Eco*RI-*Nde*I or *Eco*RI-*Nhe*I), depending on the restriction pattern of the gene of interest. The 3' primers included a *Xho*I or a *Hind*III restriction site (table 1). This procedure was established in order to direct the cloning of each amplification product (corresponding to each ORF) into two different expression systems: pGEX-KG (using *Bam*HI-*Xho*I, *Bam*HI-*Hind*III, *Eco*RI-*Xho*I or *Eco*RI-*Hind*III), and pET21b+ (using *Nde*I-*Xho*I, *Nhe*I-*Xho*I, *Nde*I-*Hind*III or *Nhe*I-*Hind*III).

5'-end primer tail:	<u>CGCGGATCCCATATG</u>	(<i>Bam</i> HI- <i>Nde</i> I)
	<u>CGCGGATCCGCTAGC</u>	(<i>Bam</i> HI- <i>Nhe</i> I)
	<u>CCGGAATTCTACATATG</u>	(<i>Eco</i> RI- <i>Nde</i> I)
	<u>CCGGAATTCTAGCTAGC</u>	(<i>Eco</i> RI- <i>Nhe</i> I)
3'-end primer tail:	<u>CCCGCTCGAG</u>	(<i>Xho</i> I)
	<u>CCCGCTCGAG</u>	(<i>Hind</i> III)

For cloning ORFs into the pGEX-His vector, the 5' and 3' primers contained only one restriction enzyme site (*Eco*RI, *Kpn*I or *Sal*I for the 5' primers and *Pst*I, *Xba*I, *Sph*I or *Sal*I for the 3' primers). Again restriction sites were chosen according to the particular restriction pattern of the gene (table 1).

5'-end primer tail:	(AAA) <u>AAAGAATTC</u>	(<i>Eco</i> RI)
	(AAA) <u>AAAGGTACC</u>	(<i>Kpn</i> I)
3'-end primer tail:	(AAA) <u>AAACTGCAG</u>	(<i>Pst</i> I)
	(AAA) <u>AAATCTAGA</u>	(<i>Xba</i> I)

5' or 3'-end primer tail: AAAGCATGC (*Sph*I) AAAAAAGTCGAC (*Sal*I)

As well as containing the restriction enzyme recognition sequences, the primers included nucleotides which hybridized to the sequence to be amplified. The melting temperature depended on the number and type of hybridising nucleotides in the whole primer, and was determined for each primer using the formulae:

$$T_m = 4 (G+C) + 2 (A+T) \quad (\text{tail excluded})$$

$$T_m = 64.9 + 0.41 (\% \text{ GC}) - 600/N \quad (\text{whole primer})$$

The melting temperatures of the selected oligonucleotides were usually 65-70°C for the whole oligo and 50-55°C for the hybridising region alone.

Table 1 shows the forward and reverse primers used for each amplification. In certain cases, the sequence of the primer does not exactly match the sequence of the predicted ORF. This is because when initial amplifications were performed, the complete 5' and/or 3' sequences for some meningococcal B ORFs were not known. However the corresponding sequences had been identified in *Gonococcus* or in *Meningococcus A*. Hence, when the *Meningococcus B* sequence was incomplete or uncertain, *Gonococcal* or *Meningococcal A* sequences were used as the basis for primer design. These sequences were altered to take account of codon preference. It can be appreciated that, once the complete sequence is identified, this approach will no longer be necessary.

Oligonucleotides were synthesized using a Perkin Elmer 394 DNA/RNA Synthesizer, eluted from the columns in 2.0ml NH₄OH, and deprotected by 5 hours incubation at 56°C. The oligos were precipitated by addition of 0.3M Na-Acetate and 2 volumes ethanol. The samples were centrifuged and the pellets resuspended in either 100µl or 1.0ml of water. The OD₂₆₀ was determined using a Perkin Elmer Lambda Bio spectrophotometer and the concentration adjusted to 2-10pmol/µl.

Amplification

The standard PCR protocol was as follows: 50-200ng of genomic DNA was used as a template in the presence of 20-40µM of each oligonucleotide primer, 400-800µM dNTPs solution, 1x PCR buffer (including 1.5mM MgCl₂), 2.5 units *TaqI* DNA polymerase (using

Perkin-Elmer AmpliTaq, GIBCO Platinum, Pwo DNA polymerase, or Tahara Shuzo Taq polymerase). In some cases, PCR was optimised by the addition of 10µl DMSO or 50µl 2M Betaine.

After a hot start (adding the polymerase during a preliminary 3 minute incubation of the whole mix at 95°C), each sample underwent a two-step amplification. The first 5 cycles were performed using the hybridization temperature that excluded the restriction enzyme tail of the primer (see above). This was followed by 30 cycles using the hybridization temperature calculated for the whole length oligos. The cycles were completed with a 10 minute extension step at 72°C. The standard cycles were as follows:

	Denaturation	Hybridisation	Elongation
First 5 cycles	30 seconds 95°C	30 seconds 50-55°C	30-60 seconds 72°C
Last 30 cycles	30 seconds 95°C	30 seconds 65-70°C	30-60 seconds 72°C

Elongation times varied according to the length of the ORF to be amplified. Amplifications were performed using either a 9600 or a 2400 Perkin Elmer GeneAmp PCR System. To check the results, 1/10 of the amplification volume was loaded onto a 1-1.5% (w/v) agarose gel and the size of each amplified fragment compared with a DNA molecular weight marker.

The amplified DNA was either loaded directly on a 1% agarose gel or first precipitated with ethanol and resuspended in a volume suitable to be loaded on a 1.0% agarose gel. The DNA fragment corresponding to the band of correct size was purified using the Qiagen Gel Extraction Kit, following the manufacturer's protocol. DNA fragments were eluted in a volume of 30µl or 50µl with either H₂O or 10mM Tris, pH 8.5.

Digestion of PCR fragments

The purified DNA corresponding to the amplified fragment was doubly-digested with the appropriate restriction enzymes for; cloning into pET-21b+ and expressing the protein as a C-terminus His-tagged fusion, for cloning into pGEX-KG and expressing the protein as a N-

terminus GST-fusion, and for cloning into pGEX-His and expressing the protein as a N-terminus GST-His tagged fusion.

Each purified DNA fragment was incubated at 37°C for 3 hours to overnight with 20 units of appropriate restriction enzyme (New England Biolabs) in a volume of either 30 or 40µl in the presence of suitable digestion buffer. Digested fragments were purified using the QIAquick PCR purification kit (following the manufacturer's instructions) and eluted in a volume of 30µl or 50µl with either H₂O or 10mM Tris, pH 8.5. The DNA concentration was determined by quantitative agarose gel electrophoresis (1.0% gel) in the presence of a titrated molecular weight marker.

Digestion of the cloning vectors (pET22B, pGEX-KG, pTRC-His A, pET21b+, pGEX-KG, and pGEX-His)

The vector pGEX-His is a modified pGEX-2T vector carrying a region encoding six histidine residues upstream of the thrombin cleavage site and containing the multiple cloning site of the vector pTRC99 (Pharmacia). 10 µg plasmid was double-digested with 50 units of each restriction enzyme in 200 µl reaction volume in the presence of appropriate buffer by overnight incubation at 37°C. After loading the whole digestion on a 1% agarose gel, the band corresponding to the digested vector was purified from the gel using the Qiagen QIAquick Gel Extraction Kit and the DNA was eluted in 50 µl of 10 mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD₂₆₀ of the sample, and adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

10µg of plasmid vector was doubly-digested with 50 units of each restriction enzyme in a volume of 200µl with the appropriate buffer overnight at 37°C. The digest was loaded onto a 1.0% agarose gel and the band corresponding to the digested vector purified using the Qiagen QIAquick Gel Extraction Kit. DNA was eluted in 50µl of 10mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD_{260nm} and the concentration adjusted to 50µg/µl. 1µl of plasmid was used for each cloning procedure.

Cloning

For some ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated in both pET22b and pGEX-KG. In a final volume of 20 µl, a molar

ratio of 3:1 fragment/vector was ligated using 0.5 μ l of NEB T4 DNA ligase (400 units/ μ l), in the presence of the buffer supplied by the manufacturer. The reaction was incubated at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit", following the manufacturer's instructions.

In order to introduce the recombinant plasmid in a suitable strain, 100 μ l *E. coli* DH5 competent cells were incubated with the ligase reaction solution for 40 minutes on ice, then at 37°C for 3 minutes, then, after adding 800 μ l LB broth, again at 37°C for 20 minutes. The cells were then centrifuged at maximum speed in an Eppendorf microfuge and resuspended in approximately 200 μ l of the supernatant. The suspension was then plated on LB ampicillin (100 mg/ml).

The screening of the recombinant clones was performed by growing 5 randomly-chosen colonies overnight at 37 °C in either 2 ml (pGEX or pTC clones) or 5ml (pET clones) LB broth + 100 μ g/ml ampicillin. The cells were then pelleted and the DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions, to a final volume of 30 μ l. 5 μ l of each individual miniprep (approximately 1g) were digested with either *NdeI/XhoI* or *BamHI/XhoI* and the whole digestion loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1Kb DNA Ladder, GIBCO). The screening of the positive clones was made on the base of the correct insert size.

For other ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated into both pET21b+ and pGEX-KG. A molar ratio of of 3:1 fragment/vector was used in a final volume of 20 μ l, that included 0.5 μ l T4 DNA ligase (400 units/ μ l, NEB) and ligation buffer supplied by the manufacturer. The reaction was performed at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit" and the manufacturer's protocol.

Recombinant plasmid was transformed into 100 μ l of competent *E. coli* DH5 or HB101 by incubating the ligase reaction solution and bacteria for 40 minutes on ice then at 37°C for 3 minutes. This was followed by the addition of 800 μ l LB broth and incubation at 37°C for 20 minutes. The cells were centrifuged at maximum speed in an Eppendorf microfuge, resuspended in approximately 200 μ l of the supernatant and plated onto LB ampicillin (100mg/ml) agar.

Screening for recombinant clones was performed by growing 5 randomly selected colonies overnight at 37°C in either 2.0ml (pGEX-KG clones) or 5.0ml (pET clones) LB broth + 100µg/ml ampicillin. Cells were pelleted and plasmid DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions. Approximately 1µg of each individual miniprep was digested with the appropriate restriction enzymes and the digest loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1kb DNA Ladder, GIBCO). Positive clones were selected on the basis of the size of insert.

ORFs were cloned into PGEX-His, by doubly-digesting the PCR product and ligating into similarly digested vector. After cloning, recombinant plasmids were transformed into the *E.coli* host W3110. Individual clones were grown overnight at 37°C in LB broth with 50µg/ml ampicillin.

Certain ORFs may be cloned into the pGEX-HIS vector using *EcoRI-PstI* cloning sites, or *EcoRI-SalI*, or *SalI-PstI*. After cloning, the recombinant plasmids may be introduced in the *E.coli* host W3110.

Expression

Each ORF cloned into the expression vector may then be transformed into the strain suitable for expression of the recombinant protein product. 1 µl of each construct was used to transform 30 µl of *E.coli* BL21 (pGEX vector), *E.coli* TOP 10 (pTRC vector) or *E.coli* BL21-DE3 (pET vector), as described above. In the case of the pGEX-His vector, the same *E.coli* strain (W3110) was used for initial cloning and expression. Single recombinant colonies were inoculated into 2ml LB+Amp (100 µg/ml), incubated at 37°C overnight, then diluted 1:30 in 20 ml of LB+Amp (100 µg/ml) in 100 ml flasks, making sure that the OD₆₀₀ ranged between 0.1 and 0.15. The flasks were incubated at 30°C in gyratory water bath shakers until OD indicated exponential growth suitable for induction of expression (0.4-0.8 OD for pET and pTRC vectors; 0.8-1 OD for pGEX and pGEX-His vectors). For the pET, pTRC and pGEX-His vectors, the protein expression was induced by addition of 1mM IPTG, whereas in the case of pGEX system the final concentration of IPTG was 0.2 mM. After 3 hours incubation at 30°C, the final concentration of the sample was checked by OD. In order to check expression, 1ml of each sample was removed, centrifuged in a microfuge, the pellet

resuspended in PBS, and analysed by 12% SDS-PAGE with Coomassie Blue staining. The whole sample was centrifuged at 6000g and the pellet resuspended in PBS for further use.

GST-fusion proteins large-scale purification.

For some ORFs, a single colony was grown overnight at 37°C on LB+Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600 ml of fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD₅₅₀ 0.8-1. Protein expression was induced with 0.2mM IPTG followed by three hours incubation. The culture was centrifuged at 8000 rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml cold PBS. The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia) (previously washed with PBS) and incubated at room temperature for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold PBS for 10 minutes, resuspended in 1ml cold PBS, and loaded on a disposable column. The resin was washed twice with 2ml cold PBS until the flow-through reached OD₂₈₀ of 0.02-0.06. The GST-fusion protein was eluted by addition of 700µl cold Glutathione elution buffer 10mM reduced glutathione, 50mM Tris-HCl) and fractions collected until the OD₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel using either Biorad SDS-PAGE Molecular weight standard broad range (M1) (200, 116.25, 97.4, 66.2, 45, 31, 21.5, 14.4, 6.5 kDa) or Amersham Rainbow Marker (M'') (220, 66, 46, 30, 21.5, 14.3 kDa) as standards. As the MW of GST is 26kDa, this value must be added to the MW of each GST-fusion protein.

For other ORFs, for each clone to be purified as a GST-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp. (100µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD_{550nm} reached 0.6-0.8. Recombinant protein expression was induced by addition of IPTG (final concentration 0.2mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml cold PBS. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia), previously equilibrated with PBS, and incubated at room temperature with gentle agitation for 30 min. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batchwise) with 10ml cold PBS for 10 min, resuspended in 1ml cold PBS, and loaded onto a disposable column. The resin continued to be washed with cold PBS, until the OD_{280nm} of the flow-through reached 0.02-0.01. The GST-fusion protein was eluted by addition of 700µl cold glutathione elution buffer (10mM reduced glutathione, 50mM Tris-HCl pH 8.0) and fractions collected, until the OD_{280nm} of the eluate indicated all the recombinant protein was obtained. 20µl aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. The molecular mass of the purified proteins was determined using either the Bio-Rad broad range molecular weight standard (M1) (200, 116, 97.4, 66.2, 45.0, 31.0, 21.5, 14.4, 6.5 kDa) or the Amersham Rainbow Marker (M2) (220, 66.2, 46.0, 30.0, 21.5, 14.3 kDa). The molecular weights of GST-fusion proteins are a combination of the 26 kDa GST protein and its fusion partner. Protein concentrations were estimated using the Bradford assay.

His-fusion soluble proteins large-scale purification.

For some ORFs, a single colony was grown overnight at 37°C on a LB + Amp agar plate. The bacteria were inoculated into 20ml of LB+Amp liquid culture and incubated overnight in a water bath shaker. Bacteria were diluted 1:30 into 600ml fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD₅₅₀ 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000 rpm at 4°C, the supernatant was discarded and the bacterial pellet was resuspended in 7.5ml cold 10mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 10 mM imidazole, pH 8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Ni²⁺-resin (Pharmacia) (previously washed with 10mM imidazole buffer) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold 10mM imidazole buffer for 10 minutes,

resuspended in 1ml cold 10mM imidazole buffer and loaded on a disposable column. The resin was washed at 4°C with 2ml cold 10mM imidazole buffer until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The resin was washed with 2ml cold 20mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 20 mM imidazole, pH 8) until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl cold 250mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 250 mM imidazole, pH 8) and fractions collected until the O.D₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

His-fusion insoluble proteins large-scale purification.

A single colony was grown overnight at 37 °C on a LB + Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600ml fresh medium and let to grow at the optimal temperature (37°C) to O.D₅₅₀ 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml buffer B (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed twice and centrifuged again. The supernatant was stored at -20°C, while the pellets were resuspended in 2 ml guanidine buffer (6M guanidine hydrochloride, 100mM phosphate buffer, 10 mM Tris-HCl, pH 7.5) and treated in a homogenizer for 10 cycles. The product was centrifuged at 13000 rpm for 40 minutes. The supernatant was mixed with 150µl Ni²⁺-resin (Pharmacia) (previously washed with buffer B) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700 g for 5 minutes at 4°C. The resin was washed twice with 10 ml buffer B for 10 minutes, resuspended in 1ml buffer B, and loaded on a disposable column. The resin was washed at room temperature with 2ml buffer B until the flow-through reached the OD₂₈₀ of 0.02-0.06. The resin was washed with 2ml buffer C (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl elution buffer (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions collected until the OD₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

Purification of His-fusion proteins.

For each clone to be purified as a His-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp (100 µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100 µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD_{550nm} reached 0.6-0.8. Expression of recombinant protein was induced by addition of IPTG (final concentration 1.0mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml of either (i) cold buffer A (300mM NaCl, 50mM phosphate buffer, 10mM imidazole, pH 8.0) for soluble proteins or (ii) buffer B (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8) for insoluble proteins. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. For insoluble proteins, pellets were resuspended in 2.0 ml buffer C (6M guanidine hydrochloride, 100mM phosphate buffer, 10mM Tris-HCl, pH 7.5) and treated with a Dounce homogenizer for 10 cycles. The homogenate was centrifuged at 13 000xg for 40 min and the supernatant retained.

Supernatants for both soluble and insoluble preparations were mixed with 150µl Ni²⁺-resin (previously equilibrated with either buffer A or buffer B, as appropriate) and incubated at room temperature with gentle agitation for 30 min. The resin was Chelating Sepharose Fast Flow (Pharmacia), prepared according to manufacturers protocol. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batch-wise) with 10ml buffer A or B for 10 min, resuspended in 1.0 ml buffer A or B and loaded onto a disposable column. The resin continued to be washed with either (i) buffer A at 4°C or (ii) buffer B at room temperature, until the OD_{280nm} of the flow-through reached 0.02-0.01. The resin was further washed with either (i) cold buffer C (300mM NaCl, 50mM phosphate buffer, 20mM imidazole, pH 8.0) or (ii) buffer D (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the the OD_{280nm} of the flow-through reached 0.02-0.01. The His-fusion protein was eluted by addition of 700µl of either (i) cold elution buffer A (300mM NaCl, 50mM phosphate buffer, 250mM imidazole, pH 8.0) or (ii) elution buffer B (8 M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions

collected until the OD_{280nm} indicated all the recombinant protein was obtained. 20 μ l aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. Protein concentrations were estimated using the Bradford assay.

His-fusion proteins renaturation

In the cases where denaturation was required to solubilize proteins, a renaturation step was employed prior to immunization. Glycerol was added to the denatured fractions obtained above to give a final concentration of 10%(v/v). The proteins were diluted to 200 μ g/ml using dialysis buffer I (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, 2.0M urea, pH 8.8) and dialysed against the same buffer for 12-14 hours at 4°C. Further dialysis was performed with buffer II (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Alternatively, 10% glycerol was added to the denatured proteins. The proteins were then diluted to 20 μ g/ml using dialysis buffer I (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, 2M urea, pH 8.8) and dialysed against the same buffer at 4°C for 12-14 hours. The protein was further dialysed against dialysis buffer II (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Protein concentration was evaluated using the formula:

$$\text{Protein (mg/ml)} = (1.55 \times OD_{280}) - (0.76 \times OD_{260})$$

Purification of proteins

To analyse the solubility, pellets obtained from 3.0ml cultures were resuspended in 500 μ l buffer M1 (PBS pH 7.2). 25 μ l of lysozyme (10mg/ml) was added and the bacteria incubated for 15 min at 4°C. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and the pellet resuspended in buffer M2 [8M urea, 0.5M NaCl, 20mM imidazole and 0.1M NaH_2PO_4] and incubated for 3 to 4 hours at 4°C. After centrifugation, the supernatant was collected and the pellet resuspended in buffer M3 [6M guanidinium-HCl, 0.5M NaCl, 20mM imidazole and 0.1M NaH_2PO_4] overnight at 4°C. The

supernatants from all steps were analysed by SDS-PAGE. Some proteins were found to be soluble in PBS, others need urea or guanidium-HCl for solubilization.

For preparative scale purifications, 500ml cultures were induced and fusion proteins solubilized in either buffer M1, M2 or M3 using the procedure described above. Crude extracts were loaded onto a Ni-NTA superflow column (Quiagen) equilibrated with buffer M1, M2 or M3 depending on the solubilization buffer employed. Unbound material was eluted by washing the column with the same buffer. The recombinant fusion protein was eluted with the corresponding buffer containing 500mM imidazole then dialysed against the same buffer in the absence of imidazole.

Mice immunisations

20µg of each purified protein are used to immunise mice intraperitoneally. In the case of some ORFs, Balb-C mice were immunised with Al(OH)₃ as adjuvant on days 1, 21 and 42, and immune response was monitored in samples taken on day 56. For other ORFs, CD1 mice could be immunised using the same protocol. For ORFs 25 and 40, CD1 mice were immunised using Freund's adjuvant, and the same immunisation protocol was used, except that the immune response was measured on day 42, rather than 56. Similarly, for still other ORFs, CD1 mice were immunised with Freund's adjuvant, but the immune response was measured on day 49. Alternatively, 20µg of each purified protein was mixed with Freund's adjuvant and used to immunise CD1 mice intraperitoneally. For many of the proteins, the immunization was performed on days 1, 21 and 35, and immune response was monitored in samples taken on days 34 and 49. For some proteins, the third immunization was performed on day 28, rather than 35, and the immune response was measured on days 20 and 42, rather than 34 and 49.

ELISA assay (sera analysis)

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 7ml of Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10000 rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated

for 2 hours at room temperature and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200 µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200 µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN₃ in PBS) were added to each well and the plates incubated for 90 minutes at 37°C. Wells were washed three times with PBT. 100 µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100 µl of substrate buffer for HRP (25 ml of citrate buffer pH5, 10 mg of O-phenildiamine and 10 µl of H₂O) were added to each well and the plates were left at room temperature for 20 minutes. 100 µl H₂SO₄ was added to each well and OD₄₉₀ was followed. The ELISA was considered positive when OD490 was 2.5 times the respective pre-immune sera.

Alternatively, The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10 000rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated for 1 hour at 37°C and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN₃ in PBS) were added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 100µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100µl of substrate buffer for HRP (25ml of citrate buffer pH5, 10mg of O-

phenildiamine and 10 μ l of H₂O₂) were added to each well and the plates were left at room temperature for 20 minutes. 100 μ l of 12.5% H₂SO₄ was added to each well and OD₄₉₀ was followed. The ELISA titers were calculated arbitrarily as the dilution of sera which gave an OD₄₉₀ value of 0.4 above the level of preimmune sera. The ELISA was considered positive when the dilution of sera with OD₄₉₀ of 0.4 was higher than 1:400.

FACScan bacteria Binding Assay procedure.

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 4 tubes containing 8ml each Mueller-Hinton Broth (Difco) containing 0.25% glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.35-0.5. The culture was centrifuged for 10 minutes at 4000rpm. The supernatant was discarded and the pellet was resuspended in blocking buffer (1% BSA in PBS, 0.4% NaN₃) and centrifuged for 5 minutes at 4000rpm. Cells were resuspended in blocking buffer to reach OD₆₂₀ of 0.07. 100 μ l bacterial cells were added to each well of a Costar 96 well plate. 100 μ l of diluted (1:100, 1:200, 1:400) sera (in blocking buffer) were added to each well and plates incubated for 2 hours at 4°C. Cells were centrifuged for 5 minutes at 4000rpm, the supernatant aspirated and cells washed by addition of 200 μ l/well of blocking buffer in each well. 100 μ l of R-Phicoerytrin conjugated F(ab)₂ goat anti-mouse, diluted 1:100, was added to each well and plates incubated for 1 hour at 4°C. Cells were spun down by centrifugation at 4000rpm for 5 minutes and washed by addition of 200 μ l/well of blocking buffer. The supernatant was aspirated and cells resuspended in 200 μ l/well of PBS, 0.25% formaldehyde. Samples were transferred to FACScan tubes and read. The condition for FACScan (Laser Power 15mW) setting were: FL2 on; FSC-H threshold:92; FSC PMT Voltage: E 01; SSC PMT: 474; Amp. Gains 6.1; FL-2 PMT: 586; compensation values: 0.

OMV preparations

Bacteria were grown overnight on 5 GC plates, harvested with a loop and resuspended in 10 ml 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30 minutes and the bacteria disrupted by sonication for 10' on ice (50% duty cycle, 50% output). Unbroken cells were removed by centrifugation at 5000g for 10 minutes and the total cell envelope

fraction recovered by centrifugation at 50000g at 4°C for 75 minutes. To extract cytoplasmic membrane proteins from the crude outer membranes, the whole fraction was resuspended in 2% sarkosyl (Sigma) and incubated at room temperature for 20 minutes. The suspension was centrifuged at 10000g for 10 minutes to remove aggregates, and the supernatant further ultracentrifuged at 50000g for 75 minutes to pellet the outer membranes. The outer membranes were resuspended in 10mM Tris-HCl, pH8 and the protein concentration measured by the Bio-Rad Protein assay, using BSA as a standard.

Whole Extracts preparation

Bacteria were grown overnight on a GC plate, harvested with a loop and resuspended in 1ml of 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30' minutes.

Western blotting

Purified proteins (500ng/lane), outer membrane vesicles (5µg) and total cell extracts (25µg) derived from MenB strain 2996 were loaded onto a 12% SDS-polyacrylamide gel and transferred to a nitrocellulose membrane. The transfer was performed for 2 hours at 150mA at 4°C, using transfer buffer (0.3 % Tris base, 1.44 % glycine, 20% (v/v) methanol). The membrane was saturated by overnight incubation at 4°C in saturation buffer (10% skimmed milk, 0.1% Triton X100 in PBS). The membrane was washed twice with washing buffer (3% skimmed milk, 0.1% Triton X100 in PBS) and incubated for 2 hours at 37°C with mice sera diluted 1:200 in washing buffer. The membrane was washed twice and incubated for 90 minutes with a 1:2000 dilution of horseradish peroxidase labelled anti-mouse Ig. The membrane was washed twice with 0.1% Triton X100 in PBS and developed with the Opti-4CN Substrate Kit (Bio-Rad). The reaction was stopped by adding water.

Bactericidal assay

MC58 and 2996 strains were grown overnight at 37°C on chocolate agar plates. 5-7 colonies were collected and used to inoculate 7ml Mueller-Hinton broth. The suspension was incubated at 37°C on a nutator and let to grow until OD₆₂₀ was in between 0.5-0.8. The culture was aliquoted into sterile 1.5ml Eppendorf tubes and centrifuged for 20 minutes at maximum speed in a microfuge. The pellet was washed once in Gey's buffer (Gibco) and resuspended in the same buffer to an OD₆₂₀ of 0.5, diluted 1:20000 in Gey's buffer and stored at 25°C.

50µl of Gey's buffer/1% BSA was added to each well of a 96-well tissue culture plate. 25µl of diluted (1:100) mice sera (dilution buffer: Gey's buffer/0.2% BSA) were added to each well and the plate incubated at 4°C. 25µl of the previously described bacterial suspension were added to each well. 25µl of either heat-inactivated (56°C waterbath for 30 minutes) or normal baby rabbit complement were added to each well. Immediately after the addition of the baby rabbit complement, 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 0). The 96-well plate was incubated for 1 hour at 37°C with rotation and then 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 1). After overnight incubation the colonies corresponding to time 0 and time 1h were counted.

Gene Variability

The *ORF4* and *919* genes were amplified by PCR on chromosomal DNA extracted from various *Neisseria* strains (see list of strains). The following oligonucleotides used as PCR primers were designed in the upstream and downstream regions of the genes:

orf 4.1	(forward)	CGAATCCGGACGGCAGGACTC
orf 4.3	(reverse)	GGCAGGGAATGGCGGATTAAAG
919.1	(forward)	AAAATGCCTCTCCACGGCTG or CTGCGCCCTGTGTTAAAATCCCCT
919.6	(reverse)	CAAATAAGAAAGGAATTTTG or GGTATCGCAAACTTCGCCTTAATGCG

The PCR cycling conditions were:

1 cycle	2 min. at 94°
30 cycles	30 sec. at 94°
	30 sec. at ~ 54° or ~ 60° (in according to T _m of the primers)
	40 sec. at 72°
1 cycle	7 min. at 72°

The PCR products were purified from 1 % agarose gel and sequenced using the following primers:

orf 4.1 (forward)	CGAATCCGGACGGCAGGACTC
orf 4.2 (forward)	CGACCGCGCCTTTGGGACTG
orf 4.3 (reverse)	GGCAGGGAATGGCGGATTAAAG
orf 4.4 (reverse)	TCTTTGAGTTTGATCCAACC

- 919.1 (forward) AAAATGCCTCTCCACGGCTG or
CTGCGCCCTGTGTAAATCCCCT
- 919.2 (forward) ATCCTTCCGCCTCGGCTGCG
- 919.3 (forward) AAAACAGCGGCACAATCGAC
- 919.4 (forward) ATAAGGGCTACCTCAAATC
- 919.5 (forward) GCGCGTGGATTATTTTGGG
- 919.6 (reverse) CAAATAAGAAAGGAATTTTG or
GGTATCGCAAACTTCGCCTTAATGCG
- 919.7 (reverse) CCCAAGGTAATGTAGTGCCG
- 919.8 (reverse) TAAAAAAAGTTCGACAGGG
- 919.9 (reverse) CCGTCCGCCTGTCGTCGCC
- 919.10 (reverse) TCGTTCCGGCGGGGTCGGG

All documents cited herein are incorporated by reference in their entireties.

The following Examples are presented to illustrate, not limit, the invention

EXAMPLE 1

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

Table 1: Oligonucleotides used for PCR for Examples 2-10

ORF	Primer	Sequence	Restriction sites
279	Forward	CGCGGATCCCATATG-TTGCCTGCAATCACGATT <SEQ ID 3021>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTAGAAGCGGGCGGCAA <SEQ ID 3022>	XhoI
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA <SEQ ID 3023>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC <SEQ ID 3024>	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT <SEQ ID 3025>	BamHI-NdeI
	Reverse	CCCGCTCGAG-ATTTACTTTTTTGATGTCGAC <SEQ ID 3026>	XhoI
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC <SEQ ID 3027>	BamHI-NdeI
	Reverse	CCCGCTCGAG-CGGGCGGTATTCGGG <SEQ ID 3028>	XhoI
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT <SEQ ID 3029>	BamHI-NdeI

128	Reverse	CCCGCTCGAG-ATAATAATATCCCGCGCCC <SEQ ID 3030>	XhoI
	Forward	CGCGGATCCCATATG-ACTGACAACGCACT <SEQ ID 3031>	BamHI-NdeI
206	Reverse	CCCGCTCGAG-GACCGCGTTGTCGAAA <SEQ ID 3032>	XhoI
	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA <SEQ ID 3033>	BamHI-NdeI
287	Reverse	CCCGCTCGAG-TTCTGTAAAAAAGTATGTGC <SEQ ID 3034>	XhoI
	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG <SEQ ID 3035>	EcoRI-NheI
406	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTGTGCC <SEQ ID 3036>	XhoI
	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG <SEQ ID 3037>	BamHI-NdeI
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG <SEQ ID 3038>	XhoI

Localization of the ORFs

The following DNA and amino acid sequences are identified by titles of the following form: [g, m, or a] [#].[seq or pep], where "g" means a sequence from *N. gonorrhoeae*, "m" means a sequence from *N. meningitidis B*, and "a" means a sequence from *N. meningitidis A*; "#" means the number of the sequence; "seq" means a DNA sequence, and "pep" means an amino acid sequence. For example, "g001.seq" refers to an *N. gonorrhoeae* DNA sequence, number 1. The presence of the suffix "-1" to these sequences indicates an additional sequence found for the same ORF, thus, data for an ORF having both an unsuffixed and a suffixed sequence designation applies to both such designated sequences. Further, open reading frames are identified as ORF #, where "#" means the number of the ORF, corresponding to the number of the sequence which encodes the ORF, and the ORF designations may be suffixed with ".ng" or ".a", indicating that the ORF corresponds to a *N. gonorrhoeae* sequence or a *N. meningitidis A* sequence, respectively. The word "partial" before a sequence indicates that the sequence may be a partial or a complete ORF. Computer analysis was performed for the comparisons that follow between "g", "m", and "a" peptide sequences; and therein the "pep" suffix is implied where not expressly stated. Further, in the event of a conflict between the text immediately preceding and describing which sequences are being compared, and the

designated sequences being compared, the designated sequence controls and is the actual sequence being compared.

ORF: contig:

279 gnm4.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3039>:

m279.seq

```

1   ATAACGCGGA TTTGCGGCTG CTTGATTTCA ACGGTTTTCA GGGCTTCGGC
51  AAGTTTGTCT GCGGCGGGTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CGGGCAGCGG CAGGGCGCGT TTGGCACCGG CTTCTTTGGC GGCAGCCATG
151 GCGCGTCCGA CGGCGGCGGC GTTGCCCTGCA ATCACGATTT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCACTTCGCT TTGGGCGGCT TCGGCACAAA
251 TGGCTTTAAC CTGCTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA GGCGCACGAG
351 TTTGACCGCG TCGGCAAAAT TCAATGCGCC GCGGCAACG AGTGCGGTGT
401 ATTCGCCGAG GCTGTGTCCG GCAACGGCGG CAGGCGTTT GCCGCCCGCT
451 TCTAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 3040; ORF 279>:

m279.pep

```

1   ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTTSLWAA SAQMALTCSS SKPRIAAIAP
101 TPCGTADCIS SARRRTSLTA SAKFNAPAAT SAVYSPRLCP ATAAGVLPPE
151 SK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3041>:

g279.seq

```

1   atgacgcgga tttgcggctg cttgatttca acggttttga gtgtttcggc
51  aagtttgtcg gcggcggtt tcatacaggct gcaatgggaa ggaacggata
101 ccggcagcgg cagggcgcggt ttggctccgg cttctttggc ggcagccatg
151 gtgcgtccga cggcggcggc gttgcctgca atcacgactt gtccggcgga
201 gttgaagttg acggcttcga ccacttcgcc ctgtgcggat tcggcacaaa
251 tctgcctgac ctgttcatct tccaaaccca aaatggccgc cattgcgcct
301 acgccttgcg gtacggcgga ctgcatcagt tcggcgcgca ggcggacgag
351 tttgacggca tcggcaaaat ccaatgcttc ggcgcgaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgttt gccgccact
451 tccaaatag

```

This corresponds to the amino acid sequence <SEQ ID 3042; ORF 279.ng>:

g279.pep

```

1   MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTCSS SKPKMAAIAP
101 TPCGTADCIS SARRRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
	: : : : : : : :					
g279	MTRICGLISTVLSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA					
	10	20	30	40	50	60

	70	80	90	100	110	120
m279.pep	ITICPGELKLTASTTSLWAASQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA					
g279	ITTCPGELKLTASTTSPCADSAQICLTCSSSKPKMAAIAPTPCGTADCISSARRRTSLTA					
	70	80	90	100	110	120
	130	140	150			
m279.pep	SAKFNAPAATSAVYSPRLCPATAAGVLPASKX					
g279	SAKSNASAATSAVYSPRLCPATAAGVLPPTSKX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3043>:

```
a279.seq
1  ATGACNCNGA TTTGCGGCTG CTTGATTTC ACGGTTTNN GGGCTTCGGC
51  GAGTTTGTG GCGGCGGGTT TCATGAGGCT GCAATGGGA GGTACNGACA
101 CNGGCAGCG CAGGCGCGCT TTGGCGCCG CTCTTTGGC GGCAAGCATA
151 GCGCGCTCGA CGGCGGCGG ATTCCTGCA ATCACGACT GTCCGGGCGA
201 GTTGAAGTTG ACGGCTTCAA CCACTTCAT CTGTGCGGAT TCGGCGCAAA
251 TTTGTTTAC CTGTTTCAT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAG TCGGCGCGCA NGCGCACGAG
351 TTTGACGCG TCGGCAAAT CCAATGCGC GCGGCAACN AGTGC GTGT
401 ATTCGCCGAN GCTGTGTCCG GCAACGGCG CAGGCGTTT GCCGCCCGT
451 TCCGAATAG
```

This corresponds to the amino acid sequence <SEQ ID 3044; ORF 279.a>:

```
a279.pep
1  MTXICGCLIS TVXRASASLS AAGFMRLQWE GTDTGSGRAR LAPASLAASI
51  ARSTAAALPA ITTCPGELKL TASTTSSCAD SAQICFTCSS SKPRIAATAP
101 TPCGTADCIS SARXRTSLTA SAKSNAPAAT SAVYSPXLCP ATAAGVLPAP
151 SE*
```

m279/a279 ORFs 279 and 279.a showed a 88.2% identity in 152 aa overlap

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
a279	MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRARLAPASLAASIARSTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m279.pep	ITICPGELKLTASTTSLWAASQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA					
a279	ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTPCGTADCISSARXRTSLTA					
	70	80	90	100	110	120
	130	140	150			
m279.pep	SAKFNAPAATSAVYSPRLCPATAAGVLPASKX					
a279	SAKSNAPAATSAVYSPXLCPATAAGVLPASEX					
	130	140	150			

519 and 519-1 gnm7.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3045>:

```
m519.seq (partial)
1  ..TCCGTTATCG GCGGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
51  AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGgCTTgGG
101 GTGTGAAGGT TTTGCGTTAT GAGATTAAAG ACTTGTTCC GCCGCAAGAA
151 ATCCTTCGCT CAATGCAGGC GCAAATACT GCCGAACGCG AAAAACGCGC
201 CCGTATCGCC GAATCCGAAG GTCGTAAAAT CGAACAAATC AACCTTGCCA
```

```

251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
351 AGGTGAAGCG GAATCCTTGC GCCTTGTTGC CGAAGCCAAT GCCGAAGCCA
401 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTTGCCGAC ATCGGCAGCC
551 TGATTTCTGC CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

```

This corresponds to the amino acid sequence <SEQ ID 3046; ORF 519>:

```

m519.pep (partial)
1 ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
51 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLAGQREAE IQQSEGEAQA
101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLISAGMK IIDSSKTAK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3047>:

```

g519.seq
1 atggaatttt tcattatctt gttggcagcc gtcgccgttt tcggcttcaa
51 atcctttgtc gtcattcccc agcaggaagt ccacgttgtc gaaaggctcg
101 ggcgtttcca tcgcgccttg acggcgggtt tgaatatatt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta tttccaagta accgatccca aactcgccct atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgtcggttc
351 cggtatcggg cgtatggagt tggacaaaac gttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgcgag ggcttggggg
451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
501 ctttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg acaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg cttaggctgc
651 ggtcaatgcg tccaatgccc agaaaatcgc ccgcatcaac cgcgccaaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgcccgcct tcaaacccaa agcggggcgg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggattaag cccgccaaag ttgccgaaat cgggaaccct
901 aattttcggc ggcatgaaaa attttcgcca gaagcaaaaa cggccaaata
951 a

```

This corresponds to the amino acid sequence <SEQ ID 3048; ORF 519.ng>:

```

g519.pep
1 MEFFIILLAA VAVFGFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEN
251 RQIAAALQTQ SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP
301 NFRHEKFSP EAKTAK*

```

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

```

m519/g519
m519.pep
10 20 30
SVIGRMELDKTFEERDEINSTVVAALDEAA
|||||
g519 YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
90 100 110 120 130 140
40 50 60 70 80 90
m519.pep GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLAGQREAE

```

```

g519      |||||:|||||
          150      160      170      180      190      200
          GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRKIEQINLASGQREAE

m519.pep      100      110      120      130      140      150
          IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
g519      |||||:|||||
          210      220      230      240      250      260
          IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQSGADAV

m519.pep      160      170      180      190      200
          NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTAK
g519      |||||:|||||
          270      280      290      300      310
          NLKIAGQYVTAFAKLNKAKEDNTRIKPAKVAEIGNPNFRRHEKFSPEAKTAK

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3049>:

```

a519.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGC GTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAG
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAAATA

```

This corresponds to the amino acid sequence <SEQ ID 3050; ORF 519.a>:

```

a519.pep
1  MEFFIILLAA VVVFGEKFSV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEGRKIEQINLAS
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519/a519 ORFs 519 and 519.a showed a 99.5% identity in 199 aa overlap

```

m519.pep      10      20      30
          SVIGRMELDKTFEERDEINSTVVVAALDEAA
a519      |||||:|||||
          90      100      110      120      130      140
          YFQVTDPKLASYGSSNYIMAITQLAQTTLRVIGRMELDKTFEERDEINSTVVSALDEAA

m519.pep      40      50      60      70      80      90
          GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
a519      |||||:|||||
          150      160      170      180      190      200
          GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE

          100      110      120      130      140      150

```

```

m519.pep      IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a519          IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
                210      220      230      240      250      260

                160      170      180      190      200
m519.pep      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a519          NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                270      280      290      300      310

```

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3051>:

```

m519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
101 GCGGTTTCCA TCGCGCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGGACAA TACGCAGCTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC TGTTGTTGCG GCTTGGACG AGGCGGCCGG GGCTTGGGGT
451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCATATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3052; ORF 519-1>:

```

m519-1.
1  MEFFIILLVA VAVFGFSFV VIPOQEVHVV ERLGRFHRAL TAGLNILIPF
51 IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGAEQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3053>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51 ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCATATGCG TCCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGGGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG

```


851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAAACCG CCAATATA

This corresponds to the amino acid sequence <SEQ ID 3054; ORF 519-1.ng>:

g519-1.pep
1 MEFFIILLAA VAVFGFKSFV VIPQQEVHV V ERLGRFHRAL TAGLNILIPF
51 IDR VAYRHS L KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

m519-1/g519-1 ORFs 519-1 and 519-1.ng showed a 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHS L					
m519-1	MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHS L					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep	LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
m519-1	LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
	250	260	270	280	290	300
g519-1.pep	LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
m519-1	LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
	250	260	270	280	290	300
g519-1.pep	ISAGMKIIDSSKTAKX					
m519-1	ISAGMKIIDSSKTAKX					
	310					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3055>:

a519-1.seq
1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GGCGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTC
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA

```

401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGC GTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGT CAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3056; ORF 519-1.a>:

a519-1.pep.

```

1  MEFFIILLAA VVVFQFKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
51  IDR VAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPK LASYGS
101 SNYIMAITQL AQTTLR SVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLR YEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EG EAQAVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 ORFs 519-1 and 519-1.a showed a 99.0% identity in 315 aa overlap

a519-1.pep	MEFFIILLAAVVVFQFKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
m519-1	MEFFIILLVAVAVFGFKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
	10 20 30 40 50 60
a519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLR SVIG
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLR SVIG
	70 80 90 100 110 120
a519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
	130 140 150 160 170 180
a519-1.pep	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAVNASNAEKIARINRAKGEAESLR
m519-1	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAVNASNAEKIARINRAKGEAESLR
	190 200 210 220 230 240
a519-1.pep	LVAEANA EAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
m519-1	LVAEANA EAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
	250 260 270 280 290 300
a519-1.pep	ISAGMKIIDSSKTAKX
m519-1	ISAGMKIIDSSKTAKX
	310

576 and 576-1 gnm22.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3057>:

```
m576.seq.. (partial)
1  ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
51  GCAAAATGAAG GAACAGGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101 CCAATGCAGGC AGTGTATGAC GGCAAAAGAA TCAAAATGAC CGAAGAGCAG
151 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGAGCCGT
201 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCGGGC
301 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401 TCGACAGCAG CAAAGCCAAAC GCGCGCCCGG TCACCTTCCC TTTGAGCCAA
451 GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
501 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551 GCGACAAAAA CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
601 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651 CATCAAAAAA GTAAATTAA
```

This corresponds to the amino acid sequence <SEQ ID 3058; ORF 576>:

```
m576.pcp.. (partial)
  1  ..MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
 51  AQEVMMKFLQ  EQQAKAVEKH KADAKANKEK GEAFLENAA  KDGVKTTASG
101  LQYKITQGE  GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151  VIPGWTEGVQ  LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
201  KIGAPENAPA  KQPAQVDIKK VN*
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3059>:

g576.seq.. (partial)

1	..atgggcggtgg	acatcggacg	ctccctgaaa	caaatgaagg	aacaggggcgc
51	ggaaatcgat	ttgaaagtct	ttaccgatgc	catgcaggca	gtgtatgacg
101	gcaaagaat	caaaatgacc	gaagagcagg	cccaggaagt	gatgtgaaa
151	ttcctgcagg	agcagcaggc	taaagccgta	gaaaaacaca	aggcggatgc
201	gaaggccaac	aaagaaaaag	gcgaagcctt	cctgaaggaa	aatgccgcgcg
251	aagacggcgt	gaagaccact	gcttcgcgtc	tgcagtacaa	aatcaccaaa
301	cagggtgaag	gcaaacagcc	gacaaaagac	gacatcgta	ccgtggaata
351	cgaaggccgc	ctgattgacg	gtaccgtatt	gcacagcagc	aaagccaacg
401	gcggcccggc	caccttccct	ttgagccaag	tgattccggg	ttggaccgaa
451	ggcgtagcgg	ttctgaaaga	aggcggcgaa	gccacgttct	acatcccgtc
501	caaccttgcc	taccgcgaac	agggtgcggg	cgaaaaaatc	ggtccgaacg
551	ccactttgg	atttgacgtg	aaactgtgtc	aaatcggcgc	accggaaaac
601	gcgcccgcga	agcagccgga	tcaagtcgac	atcaaaaaag	taaattaa

This corresponds to the amino acid sequence <SEQ ID 3060; ORF 576.ng>:

g576.pep.. (partial)

1	..MGVDIGRSLK	QMKEQGAEID	LKVFTDAMQA	VYDGKEIKMT	EEQAQEVMMK
51	FLQEQQAKAV	EKHKADAKAN	KEKGEAFLKE	NAAEDGVKTT	ASGLQYKITK
101	QGEGKQPTKD	DIVTVEYEGR	LIDGTVFDSS	KANGGPATFP	LSQVIPGWTE
151	GVRLLKEGGE	ATFYIPSNLA	YREQGAGEKI	GP NATLVFDV	KLVKIGAPEN
201	APAKOPDOVD	IKKVN*			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 ORFs 576 and 576.ng showed a 97.2% identity in 215 aa overlap

m576.pep 10 20 30 40 50 60
 MQQASYAMGVDIGRSLKQMKEQGAIEDLKVFTEAMQAVYDGKEIKMTEEQAQEVMMKFLQ
 |||||

```

g576      MGVDIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLQ
              10      20      30      40      50

              70      80      90      100     110     120
m576.pep  EQQAKAVEKHKADAKANKEKGEAFLKENAAKDGVKTTASGLQYKITKQEGGKOPTKDDIV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g576      EQQAKAVEKHKADAKANKEKGEAFLKENAAEDGVKTTASGLQYKITKQEGGKOPTKDDIV
              60      70      80      90      100     110

              130     140     150     160     170     180
m576.pep  TVEYEGRLIDGTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYRE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g576      TVEYEGRLIDGTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYRE
              120     130     140     150     160     170

              190     200     210     220
m576.pep  QGAGDKIGPNATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN*
              ||||:|||||:|||||:|||||:|||||:|||||:|||||
g576      QGAGEKIGPNATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN*
              180     190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3061>:

```

a576.seq
1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGC GGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGCGC CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTGG TATTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 3062; ORF 576.a>:

```

a576.pep
1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGKTTASG
151 LQYKITKQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

m576/a576 ORFs 576 and 576.a showed a 99.5% identity in 222 aa overlap

```

              10      20      30
m576.pep      MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||
a576          CGKKEAAPAS ASEPAASSA QGDTSSIGSTM MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
              30      40      50      60      70      80

              40      50      60      70      80      90
m576.pep      FTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKHKADAKANKEKGEAFLKENAA
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a576          FTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKHKADAKANKEKGEAFLKENAA
              90      100     110     120     130     140

```

	100	110	120	130	140	150
m576.pep	KDGVKTTASGLQYKITKQEGEKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ					
a576	KDGVKTTASGLQYKITKQEGEKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ					
	150	160	170	180	190	200
	160	170	180	190	200	210
m576.pep	VIPGWTEGVQLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFVDVKLVKIGAPENAPA					
a576	VILGWTEGVQLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFVDVKLVKIGAPENAPA					
	210	220	230	240	250	260
	220					
m576.pep	KQPAQVDIKKVN					
a576	KQPAQVDIKKVN					
	270					

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3063>:

```

m576-1.seq
1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCGG CCGCTTTGGC
51  ACTTTCCGCC TCGGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 CCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 3064; ORF 576-1>:

```

m576-1.pep
1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLQOMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3065>:

```

g576-1.seq
1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCGG CCGCTTTGGC
51  ACTTTCCGCC TCGGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTGCCGCG CAGGGCGACA CCTCTTCAAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
201 ACAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGATG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCCCAGGAAG TGATGATGAA ATTCCTGCAG GAGCAGCAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
401 TCCTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT
451 CTGCAATACA AAATCACCAA ACAGGGTGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG CCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG

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701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3066; ORF 576-1.ng>:

g576-1.pep

1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKOMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
 151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ
 201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV
 251 KIGAPENAPA KQPDQVDIKK VN*

g576-1/m576-1 ORFs 576-1 and 576-1.ng showed a 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASAAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASAAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
g576-1.pep	DIGRSLKOMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKOMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
g576-1.pep	DIGRSLKOMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKOMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
g576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
g576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
g576-1.pep	GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLKEGGEATFYIPSNLAYREQGAGEKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVIPGWTEGVQLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
g576-1.pep	GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLKEGGEATFYIPSNLAYREQGAGEKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVIPGWTEGVQLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
g576-1.pep	ATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3067>:

a576-1.seq

1 ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTCCG CCGCTTTGGC
 51 ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
 101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
 151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
 201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTGAAAGTC TTTACCGAAG
 251 CCATGCAGGC AGTGTATGAC GGCAAGAAA TCAAATGAC CGAAGAGCAG
 301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
 351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
 401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
 451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
 501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
 551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
 601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
 651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG

701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3068; ORF 576-1.a>:

a576-1.pep
 1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
 151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
 201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
 251 KIGAPENAPA KQPAQVDIKK VN*

a576-1/m576-1 ORFs 576-1 and 576-1.a showed a 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a576-1.pep	DIGRSLKQMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
	130	140	150	160	170	180
a576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITQGEKGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITQGEKGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
	250	260	270			
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

919 gnm43.seq

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3069>:

m919.seq
 1 ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TACGGCATCG CCGCCGCCAT
 51 CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
 101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC
 151 GGAACGACGG TCGGCGCGCG CGGGGCCGTC TATACCGTTG TACCGCACCT
 201 GTCCCTGCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT
 251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
 301 TGCGCCCAAG CCTTTCAAAC CCCCCTCCAT TCCTTTCAGG CAAAACAGTT
 351 TTTTGAACGC TATTTACGCG CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
 401 CCGGTACGGT TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGACAGG

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451 CGGACGGCAC AAGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATAACGCGC ACCTCTCCcG ATTCCCCATC ACCGCGCGCA CAACAGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTACGCC
751 GAAGACCCTG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCyTA CGTTTCCATC GGACGCTATA TGGCGGATAA GGGCTACCTC
901 AAATCGGAC AAACCTCCAT GCAGGGCATT AAGTCTTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC
1051 ACGCCGCTGA TGGGGGAATA TGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTGGGTGCG CCCTTATTG TCGCCACCGC CCATCCGGT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTC CTACCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3070; ORF 919>:

```

m919.pep
1 MKKYLFRAL YGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51 GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSRFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KSYMQRNPQR LAEVLGQNPS YIFFRELAGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 3071>:

```

g919.seq
1 ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccAT
51 CctcgCGGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATTT TGCCAAAAGC CTGCAATCCT
251 TCCGCCCTCG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGatGTG
301 TCGCCCCAAG CCTTTCAAAC CCCCCTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGC cgtGGCaggt tgcaggcaAC GGAAGcCTTG
401 CaggtaaggT TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATAACGCGC ACCTCTCCCG ATTCCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCgcgcTT GACGGCAAag cccCATCCT CggttacgC
751 GAagaccCcg tcgaacttTT TTTCATGCAC AtccaaggCT CGGGCCGCCT
801 GAAAACCCcg tccggcaaat acatCCGCat cggatagcc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctaTA TGGCGGACAA AGGTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcata aaagcTATA TCGCGCAAAA
951 TCCGCAACGC CTCGCCAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCGTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGGT ACCCGCAAAG
1151 CCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```


This corresponds to the amino acid sequence <SEQ ID 3072; ORF 919.ng>:

```

g919.pep
  1 MKKHLLRSAL YGIAAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
 51 GTTVAGGGAV YTVVPHLSMP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTERARFPIY GIPDDFISVP LPAGLRGGKN LVRIRQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS GNEGPVGALG
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF 919.ng) from *N. gonorrhoeae*:

m919/g919

m919.pep	10	20	30	40	50	60
	MKKYLFRALYGI AAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
g919	MKKHLLRSALYGI AAAAILAACQSRSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV					
	10	20	30	40	50	60
m919.pep	70	80	90	100	110	120
	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSFQAKQFFER					
g919	YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSFQAKRFFER					
	70	80	90	100	110	120
m919.pep	130	140	150	160	170	180
	YFTPQVAGNGSLAGTVTGYIEPVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA					
g919	YFTPQVAGNGSLAGTVTGYIEPVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRGGKN					
	130	140	150	160	170	180
m919.pep	190	200	210	220	230	240
	LVRIRQTGKNSGTIDNTGGTHTADLSRFPI TARTTAIKGRFEGRSFLPYHTRNQINGGAL					
g919	LVRIRQTGKNSGTIDNAGGHTADLSRFPI TARTTAIKGRFEGRSFLPYHTRNQINGGAL					
	190	200	210	220	230	240
m919.pep	250	260	270	280	290	300
	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL					
g919	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL					
	250	260	270	280	290	300
m919.pep	310	320	330	340	350	360
	KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYI FFRELAYSNDGPVGALGTPLMGEYAGA					
g919	KLGQTSMQGIKAYMRNPQRLAEVLGQNPSYI FFRELAYSNDGPVGALGTPLMGEYAGA					
	310	320	330	340	350	360
m919.pep	370	380	390	400	410	420
	VDRHYITLGAPLFVATAHPVTRKALNRLIM AQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
g919	IDRHYITLGAPLFVATAHPVTRKALNRLIM AQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
	370	380	390	400	410	420

	430	440
m919.pep	QKTTGYVWQLLPNGMKPEYRPX	
g919	QKTTGYVWQLLPNGMKPEYRPX	
	430	440

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3073>:

```

a919.seq
1  ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TCGGCGCATCG CCGCCGCCAT
51 CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCGCC
151 GGAACGACGG TCGGCGCGCG CGGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAACCC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CTTTCAAAC CCCCCTCCAT TCCGTTCAGG CAAAACAGTT
351 TTTTGAACGC TATTTACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 TCCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACGCGCG ACCTCTCCA ATTCCCATC ACTGCGGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTTACGCC
751 GAAGACCCCG TCGAACTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCGG CGCAGTGGGC
1051 ACGCCGCTGA TGGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCGACGAAG CCGGCGAAT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3074; ORF 919.a>:

```

a919.pep
1  MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDFA
51 GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSQFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGSRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMQQNPR LAEVLGQNPS YIFFRELTGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

m919/a919 ORFs 919 and 919.a showed a 98.6% identity in 441 aa overlap

	10	20	30	40	50	60
m919.pep	MKKYLFRALYGLIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
a919	MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER					
a919	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER					
	70	80	90	100	110	120

	130	140	150	160	170	180
m919.pep	YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRRTAQARFPIYGIPDDFISVPLPAGLRSGKA					
a919	YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRRTAQARFPIYGIPDDFISVPLPAGLRSGKA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m919.pep	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
a919	LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m919.pep	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
a919	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m919.pep	KLQGTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA					
a919	KLQGTSMQGIKAYMQQNPRQRLAEVLGQNPSYIFFRELGTSSNDGPVGALGTPLMGEYAGA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m919.pep	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK					
a919	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK					
	370	380	390	400	410	420
	430	440				
m919.pep	QKTTGYVWQLLPNGMKPEYRPX					
a919	QKTTGYVWQLLPNGMKPEYRPX					
	430	440				

121 and 121-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3075>:

m121.seq

```

1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCAGCG CTTTACCCCC TACCCCGGCA GGTTACGCCG CCAATTGCTG
151 GATTTCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATAACAGC TTGCCGATTT
351 GCCGCTGCTG GCGxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
401 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
451 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
501 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
551 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
601 xxxxxxCAGC TTCCTTACGA CAAAACGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCGG TATTTTCGCAC
701 AACGCCACCC TAAAGCACG GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGGACCGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA

```

1051 GCAACCGGCG CATCCAAACC GTGTATTCTG AnCGCGGGAT ATTATTATTG
1101 A

This corresponds to the amino acid sequence <SEQ ID 3076; ORF 121>:

m121.pep

```

1 METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRQLL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL AXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX
151 XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX
201 xxQLPYDKNG AKSAQGNILP QLLDRLLAHP YFAQRHPKST GRELFAINWL
251 ETYLDGGENR YDVLRTLRSF TAQTVCDAYS HAAADARQMY ICDGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3077>:

g121.seq

```

1 ATGGAAACAC AGCTTTACAT CGGCATTATG TCGGGAACCA GTATGGACGG
51 GGCGGATGCC GTGCTGGTAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCT TACCCCTGACC GGTTCGCGCC CAAATTGCTG
151 GATTTGCAGG ACACAGGCAC AGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCTCCGTGC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTtac AGCATAACG TTGCCGATTT
351 GCCGCTGCTG GCGGAACTGa cgcggatttt TACCGTCggc gacttcCGCA
401 GCCGCGACCT TGCTGCCGGC GGacaAGGTG CGCCGCTCGT CCCCgcCTTT
451 CACGAAGCCC TGTTCCGCGA TGACAGGGAA ACACGCGTGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCgGCGCA CCCCgcTTTCG
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGAcgcgtg gacgcaggca
601 cacTGGcagc TGCCTTACGA CAAAaaccgt gcAAAGgcgg cacAAGGCAA
651 catatTGCcg cAACTGCTCG gcaggctGCT CGCCcaccCG TATTTCTCAC
701 AACCCcacc aaAAAGCACG GGgcGCGaac Tgtttgccct AAattggctc
751 gaaacctAcc ttgacggcgg cgaaaaccga tacgacgtat tgcggacgct
801 ttcccgattc accgcgcaaa ccgTttggga cgcggtctca CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCTCAATG GGTGGAGGCG gccgCATttg
1001 cgtggttggc GGCGTGTTGG ATTAACGCA TTCCCGGTAG TCCGCACAAA
1051 GCGACCGCG CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3078; ORF 121.ng>:

g121.pep

```

1 METQLYIGIM SGTSMGADA VLVRMDGGKW LGAEGHAFTP YPDRLLRRKLL
51 DLQDTGTDEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPC DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL AELTRIFTVG DFRSRDLAAG GQGAPLVPAP
151 HEALFRDDRE TRVVLNIGGI ANISVLPPGA PAFGFDTPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLGRLLAHP YFSQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLRSF TAQTVWDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWLAACW INRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

ORF 121 shows 73.5% identity over a 366 aa overlap with a predicted ORF (ORF121.ng) from *N. gonorrhoeae*:

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL					
	: : : : :					
g121	METQLYIGIMSGTSMGADAVLVRMDGGKWLGAEGHAFTPYPDRLLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
	: : : : :					

```

g121      HRSRMLSQELSRLYAQTAELLCSQNLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL
           70      80      90      100      110      120
           130      140      150      160      170      180
m121.pep  AXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
           | : : : : :
g121      AELTRIFTVGDFRSRDLAAGGQGAPLVPAPFHEALFRDDRETRVVLNIGGIANISVLPPGA
           130      140      150      160      170      180
           190      200      210      220      230      240
m121.pep  XXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST
           : : : |||||:||||| |||||:| ||||
g121      PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST
           190      200      210      220      230      240
           250      260      270      280      290      300
m121.pep  GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADARQMYICDGGIRNPV
           |||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
g121      GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDVSHAAADARQMYICGGGIRNPV
           250      260      270      280      290      300
           310      320      330      340      350      360
m121.pep  LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL
           |||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
g121      LMADLAECFGTRVSLHSTAE LNLDPOWVEAAAFWLAACWINRIPGSPHKATGASKPCIL
           310      320      330      340      350      360

m121.pep  XAGYYYY
           |||||
g121      GAGYYYY

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3079>:

```

a121.seq
1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTACGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCGGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGCGCCGGC GGACAAGGCG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCGCCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACCCACCC TAAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGGCAGCCT
801 TTCCCGATT CCGCGCAAA CCGTTTTCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCG
1001 CATGGATGGC GGCGTGTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG GGCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3080; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGDGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPEHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAP
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV

```

301 LMADLAECFG TRVSLHSTAE LNLDPOWVEA AAFAWMAACW VNRI PGSPHK
 351 ATGASKPCIL GAGYYY*

m121/a121 ORFs 121 and 121.a showed a 74.0% identity in 366 aa overlap

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMDGADAVLIRMDGGKWLGAEGHAFTYPYGRLLRQLLDLQDTGADEL					
a121	METQLYIGIMSGTSMDGADAVLIRMDGGKWLGAEGHAFTYPYGRLLRQLLDLQDTGADEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
a121	HRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAPEHYSYVQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121.pep	XX					
a121	AERTQIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121.pep	XXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
a121	PAFGFDTGPGNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADARQMYICDGGIRNPV					
a121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m121.pep	LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRI PGSPHKATGASKPCIL					
a121	LMADLAECFGTRVSLHSTAE LNLDPOWVEA AAFAWMAACWVNRI PGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYYX					
a121	GAGYYYYX					

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3081>:

m121-1.seq

```

1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCCG CCAATTGCTG
151 GATTTGCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCCTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATT
351 GCCGCTGCTG GCGGAACGGA CGCGGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGCGCCGCG GGACAAGGCG CGCCACTCGT CCCCCTTTT
451 CACGAAGCCC TGTTCCGCGA CAACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCGGACGCA CCCGCTTCG
551 GCTTCGACAC AGGCGCGGCG AATATGCTGA TGGACGCGTG GACGACGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCG TATTTCGCAC
701 AAAAAACCCC TAAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGCGCG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCGA CGCCGCTCTCA CACGACGCGG

```

```

851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGNATTG
1001 CGTGGTTGGC GCGGTGTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG ANCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3082; ORF 121-1>:

```

m121-1.pep
  1 METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRQLL
  51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
 101 TVRHAPHEGY SIQLADLPLL AERTRIFTVG DFRSRDLAAG GQGAPLVPAP
 151 HEALFRDNRE TRAVLNIGGI ANISVLPPDA PAFGFDTPGPG NMLMDAWTQA
 201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
 251 ETYLDGGENR YDVLRTLSRF TAQTVCAVS HAAADARQMY ICGGGIRNPV
 301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
 351 ATGASKPCIL XAGYYY*

```

m121-1/g121 ORFs 121-1 and 121.ng showed a 95.6% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEHGAFTPPYPGRLLRRQLLDLQDTGADEL					
	: : : : :					
g121	METQLYIGIMSGTSMGDADAVLVRMDGGKWLGAEHGAFTPPYDRLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPHEGYISQLADLPLL					
	: : : : :					
g121	HRSRMLSQELSRLYAQTAAELLCSQNLAPCDITALGCHGQTVRHAPHEGYISQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121-1.pep	AERTRIFTVGDFRSRDLAAGGQGAPLVPAPFHEALFRDNRETRAVLNIGGIANISVLPPDA					
	: : : : :					
g121	AELTRIFTVGDFRSRDLAAGGQGAPLVPAPFHEALFRDDRETRVVLNIGGIANISVLPPGA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121-1.pep	PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	: : : : :					
g121	PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121-1.pep	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCAVSHAAADARQMYICGGGIRNPV					
	: : : : :					
g121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDAVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m121-1.pep	LMADLAECFGTRVSLHSTADLNLDPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
	: : : : :					
g121	LMADLAECFGTRVSLHSTAE LNLDPQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
	XAGYYYYX					
m121-1.pep						
g121	GAGYYYYX					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3083>:

```

a121-1.seq
  1 ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG

```

```

51  GCGGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCCG CAAATTGCTG
151 GATTTGCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGCGCCGGC GGACAAGGCG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCCGCCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGACGGCA
601 CACTGCGAGC TTCCTTACGA CAAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTGCGAC
701 AACCCACCCC TAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGCGACGCT
801 TTCCCATTTC ACCGCGCAAA CCGTTTTTCA CGCCGTCTCA CACGACGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTTC
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3084; ORF 121-1.a>:

```

a121-1.pep
  1  METQLYIGIM SGTSMDGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPESY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AFAWMAACW VNRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

m121-1/a121-1 ORFs 121-1 and 121-1.a showed a 96.4% identity in 366 aa overlap

```

              10      20      30      40      50      60
m121-1.pep  METQLYIGIMSGTSMDGADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRQLLDLQDTGADEL
a121-1      METQLYIGIMSGTSMDGADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRQLLDLQDTGADEL
              10      20      30      40      50      60

              70      80      90      100     110     120
m121-1.pep  HRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL
a121-1      HRSRMLSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAPESYSVQLADLPLL
              70      80      90      100     110     120

              130     140     150     160     170     180
m121-1.pep  AERTRIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDNRETRAVLNIGGIANISVLPPDA
a121-1      AERTQIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDDRETRAVLNIGGIANISVLPPDA
              130     140     150     160     170     180

              190     200     210     220     230     240
m121-1.pep  PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST
a121-1      PAFGFDTPGPNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST
              190     200     210     220     230     240

              250     260     270     280     290     300
m121-1.pep  GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDVASHAAADARQMYICGGGIRNPV
a121-1      GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFDAVSHAAADARQMYICGGGIRNPV
              250     260     270     280     290     300

```


	310	320	330	340	350	360
m121-1.pep	LMADLAECFGTRVSLHSTADLNLD	PQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL				
a121	LMADLAECFGTRVSLHSTAE	NLDLPQWVEAAFAWMAACWVNRIPGSPHKATGASKPCIL				
	310	320	330	340	350	360

m121-1.pep	XAGYYYY
a121	GAGYYYY

128 and 128-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3085>:

```
m128.seq (partial)
1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTG
201 GGGCGTGGTG TCGCACTCA ACTGCGTCGC CGACACGCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAA AACCAAATC AACCAC
1  TACGCCAGCG AAAAACTGCG CGAAGCCAAA TACGCGTTCA GCGAAACCGA
51  wGTCAAAAAA TAYTTCCcyG TCGGCAAwGT ATTAAACGGA CTGTTCGCCC
101 AAmTCAAAAA ACTmTACGGC ATCGGATTTA CCGAAAAAAC yGTCCCGTC
151 TGGCACAAAG ACGTGCCTA TTKtGAATTG CAACAAAACG GCGAAmCCAT
201 AGGCGGCGTT TATATGGATT TGTACGCACG CGAAGGCAAA CGCGGCGGCG
251 CGTGGATGAA CGACTACAAA GGCCGCCGCC GTTTTTCAGA CGGCACGCTG
301 CAAYTGCCCA CCGCCTACCT CGTCTGCAAC TTCGCCCCAC CCGTCGGCGG
351 CAGGGAAGCC CGCyTGAGCC ACGACGAAAT CCTCATCCTC TTCCACGAAA
401 CCGGACACGG GCTGCACCAC CTGCTTACCC AAGTGGACGA ACTGGGCGTA
451 TCCGGCATCA ACGGCGTAKA ATGGGACGCG GTCGAACTGC CCAGCCAGTT
501 TATGGAATAA TTCGTTTGGG AATACAATGT CTTGGCACAA mTGTCAGCCC
551 ACGAAGAAAC CGGcgTTCCC yTGCCGAAAG AACTCTTsGA CAAAwTGCTC
601 GCCGCCAAAA ACTTCCAAsG CGGCATGTTC yTsGTCCGGC AAwTGGAGTT
651 CGCCCTCTTT GATATGATGA TTTACAGCGA AGACGACGAA GGCCGTCTGA
701 AAAACTGGCA ACAGGTTTTA GACAGCGTGC GCAAAAAAGT CGCCGTCATC
751 CAGCCGCCCG AATACAACCG CTTGCGCTTG AGCTTCGGCC ACATCTTCGC
801 AGGCGGCTAT TCCGCGCTn ATTACAGCTA CGCGTGGGCG GAAGTATTGA
851 GCGCGGACGC ATACGCCGCC TTTGAAGAAA GCGACGATGT CGCCGCCACA
901 GGCAAACGCT TTTGGCAGGA AATCCTCGCC GTCGGGGnAT CGCGCAGCGG
951 nGCAGAATCC TTCAAAGCCT TCCGCGGCCG CGAACCAGC ATAGACGCAC
1001 TCTTGCGCCA CAGCGGTTTC GACAACGCGG TCTGA
```

This corresponds to the amino acid sequence <SEQ ID 3086; ORF 128>:

```
m128.pep (partial)
1  MTDNALHLHG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51  NTVEPLTGIT ERVGRWGVV SHLNCVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NH

//
1  YASEKLREAK YAFSETXVKK YFPVGXVLNG LFAQXKKLYG IGFTEKTPVP
51  WHKDVRyxEL QONGEXIGGV YMDLYAREGK RGGAWMNDYK GRRRFSdGTL
101 QLPTAYLVCN FAPPVGGREA RLSHDEILIL FHETGHGLHH LLTQVDELGV
151 SGINGVxWDA VELPSQFMEN FVWEYNVLAQ XSAHEETGVP LPKELXDKXL
201 AAKNFQxGMF XVRQXEFALF DMmIYSEDDE GRLKNWQQVL DSVRKKVAVI
251 QPPEYNRFAL SFGHIFAGGY SAAXYSYAWA EVLSADAYAA FEESDDVAAT
301 GKRFWQEILA VGXSRSgAES FKAFRGREPS IDALLRHSGF DNAV*
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3087>:

```

g128.seq
1  atgattgaca acgCActgct ccacttgggc gaagaaccCC GTTTTaatca
51  aatccaaacc gaagACAtca AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTGT
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTGCA ACGCTTCCCC CCGCACAAAA AACCAAGCTC GATCAGGACC
401 TGCGCGATTT CGTATTGAGC GGCGCGGAAC TGCCGCCCGA ACGGCAAGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 CCCGCGCAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTATCC AATACGCCGG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGcctaa cTGCTCGGCT TTAATAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACGCCC GAACAGGTTT TAAACTTCCT GCACGACCTC
901 GCGCGCCGCG CCAAACCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 TCTCGCCCGG GAACACCTCG GTCTCGCCGA CCCGAGCCG TGGGACTTGA
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTTCTGGCAG GCCTGTTGCG
1101 CCAAATCAAA AAATCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGGCACA AGACGTGCGC TATTTGAAT TGCAACAAA CGGCAAAACC
1201 ATCGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGActaca AAGGCCGCCG CCGCTTTGCC GACGgcacGC
1301 TGCAACTGCC CACCGCCTAC CTCTCTGCA ACTTCGCCCC GCCCTCGGC
1351 GGCAAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACCC TCTTCCACGA
1401 AacCGGCCAC GGAATGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCCGGCAT CAACggcgtA GAATGGGACG CGGTGGAAT GCCCAGCCAG
1501 TTTATGGAAG ACTTCGTTTG GGAATACAAT GTATTGGCAC AAATGTCCGC
1551 CCACGAAGAA AccgGCGAGC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TcgCGCCAA AAATCTCCAG CGCGGTATGT TCCTCGTCCG GCAAAATGAG
1651 TTCGCCCTCT TCGATATGAT GATTACAGT GAAAGCGACG AATGCCGTCT
1701 GAAAACTGG CAGCAGGTTT TAGACAGCGT GCGCAAAGAA GTcGCCGTCA
1751 TCCAACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCacatctTC
1801 GCcgcgGCT ATTCGCGAGG CTATTACAGC TACGCATGGG CCGAAGTCct
1851 CAGCACCGAT GCCTACGCCG CCTTTGAAGA AAGcGACGac gtcGCCGCCA
1901 CAGGCAAACG CTTCTGGCAA GAAAtccttg ccgtcgscgg ctCCCGCAGC
1951 gcgCGGAAT CTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTGCTGCGC CAaagcggtT TCGACAACGC gGcttgA

```

This corresponds to the amino acid sequence <SEQ ID 3088; ORF 128.ng>:

```

g128.pep
1  MIDNALLHLG EEPRFNQIQT EDIKPAVQTA IAEARGQIAA VKAQHTGWA
51  NTVERLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAG
201 AAQSEGKTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASLSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNFIHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDSL YAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDVR YFELQQNGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTQLQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGEPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS ESDECR LKNW QQVLDSVRKE VAVIQPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSTD AYAAFEESDD VAATGKRWFQ EILAVGGSRs

```

651 AAESFKAFRG REPSIDALLR QSGFDNAA*

ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng)
from *N. gonorrhoeae*:

m128/g128

	10	20	30	40	50	60
g128.pep	MIDNALLHLGEEPRFNQIQTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT					
m128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g128.pep	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
m128	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130	140	150	160	170	180
g128.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128	TLSPAQKTKLNH					
	130					
	//					
				340	350	360
g128.pep	YAGEKLREAKYAFSETEVKKYFPVGKVLG					
m128	YASEKLREAKYAFSETXVKKYFPVGXVLNG					
				10	20	30
	370	380	390	400	410	420
g128.pep	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWMNDYK					
m128	LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
	430	440	450	460	470	480
g128.pep	GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHLHLLTQVDELGV					
m128	GRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHLHLLTQVDELGV					
	100	110	120	130	140	150
	490	500	510	520	530	540
g128.pep	SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQXGMF					
m128	SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQXGMF					
	160	170	180	190	200	210
	550	560	570	580	590	600
g128.pep	LVRQMEFALFDMMIYSEDEGRKLNWQQVLDVSRKEVAVIQPPEYNRFANSFGHIFAGGY					
m128	XVRQXEFALFDMMIYSEDEGRKLNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIFAGGY					
	220	230	240	250	260	270
	610	620	630	640	650	660
g128.pep	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRGREPS					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRGREPS					
	280	290	300	310	320	330

```

          670      679
g128.pep  IDALLRQSGFDNAAX
          |||||:|||||:
m128      IDALLRHSGFDNAVX
          340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3089>:

```

a128.seq
1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTAC CGACACGCC GAACTGCGCG
251 CCGCCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACCCAGATC
401 TGCGCGATTT CGTCCTCAGC GGCGCGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACGCT TGCCGCGATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTATCC AATACGCCGA CAACGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTTCG
1101 CCAAATCAAA AACTCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAGAAG CCCGTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAA ATTTCTGTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAATTTCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAAACG CTTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTTCAAAGC CTTCGCGGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3090; ORF 128.a>:

```

a128.pep
1  MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51  NTVEPLTGIT ERVGRIWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNLGFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTQLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME

```

551 FALFDMMIYS EDDEGR LKNW QQVLD S VRKE VAVVRPPEYN RFANSFGHIF
 601 AGGYSAGYYS YAWAEVLSAD AYA AFEESDD VAATGKRWFQ EILAVGGSRS
 651 AAESFKA FRG REPSIDALLR HSGFDNAA*

m128/a128 ORFs 128 and 128.a showed a 66.0% identity in 677 aa overlap

m128.pep	10	20	30	40	50	60
	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQTHTGWANTVEPLTGIT					
a128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQTHTGWANTVEPLTGIT					
	10	20	30	40	50	60
m128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
a128	ERVGRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
m128.pep	130					
	TLSPAQKTKLNH-----					
a128	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
m128.pep	-----					
a128	FDDAAPLAGIPEDALAMFAAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
	190	200	210	220	230	240
m128.pep	-----					
a128	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMDTPEQVLNFLHDL					
	250	260	270	280	290	300
m128.pep						140
						YASEKLREAKYAFSETXVKKYFPVGX
a128						ARRAKPYAEKDLAEVKAFARESLGLADLPWDLGYAGEKLREAKYAFSETEVKKYFPVGK
	310	320	330	340	350	360
m128.pep	160	170	180	190	200	210
	VLNGLFAQXKKLYGIGFTEKTVPVVHKDVRYXELQQNGEXIGGVYMDLYAREGKRGGAWM					
a128	VLNGLFAQIKKLYGIGFTEKTVPVVHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
m128.pep	220	230	240	250	260	270
	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD					
a128	NDYKGRRRFSDGTLQLPTAYLVCNFTPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
	430	440	450	460	470	480
m128.pep	280	290	300	310	320	330
	ELGVSGINGVXWD AVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLA AKNFQ					
a128	ELGVSGINGVEWD AVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLA AKNFQ					
	490	500	510	520	530	540
m128.pep	340	350	360	370	380	390
	XGMFXVRQXEFALFDMMIYSEDDEGR LKNWQQVLD S VRKKVAVIQPPEYNRFALSFGHIF					
a128	RGMFLVRQMEFALFDMMIYSEDDEGR LKNWQQVLD S VRKEVAVVRPPEYNRFANSFGHIF					
	550	560	570	580	590	600

```

          400      410      420      430      440      450
m128.pep  AGGYSAA XSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRG
          |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
          610      620      630      640      650      660

          460      470
m128.pep  REPSIDALLRHSGFDNAVX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      REPSIDALLRHSGFDNAAX
          670

```

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3091>:

```

m128-1.seq
1  ATGACTGACA ACGCACTGCT CCATTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACC CGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTGC AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTGCG CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTCGAC ACCCTCTCCC CCGCACAAAA AACCAAATC AACCACGATC
401 TGC CGGATT CGTCCTCAGC GGCGCGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAAA GCGAAAGCAA AACAGGCTAC AAAATCGGCT TGCAGATTCC
651 ACACTACCTC GCCGTATCC AATACGCCGA CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAACTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGCAA ACGCCCTGCA
801 AACC GCCAAA CTGCTCGGCT TCAAAACTA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACGCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCGCGCGCG CCAAACCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCGCCCCG GAAAGCCTGA ACCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCAG CGAAAACTG CGCGAAGCCA AATACGCGTT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTTCG
1101 CCAAAATCAA AAATCTTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGCGGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC ACCCGTCGGC
1351 GGCAGGGAAG CCCGCCTGAG CCACGACGAA ATCCTCATCC TCTTCCACGA
1401 AACC GGACAC GGGCTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CGGTGGAAT GCCAGCCAG
1501 TTTATGGAAA ATTTCTGTTG GGAATACAAT GTCTTGGCAC AAATGTCAGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAATTTCAA CGCGGCATGT TCCTCGTCCG GCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAAAA GTCGCCGTCA
1751 TCCAGCCGCC CGAATACAAC CGCTTCGCC TGAAGCTTCG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCGAG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAAACG CTTTGGGAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTCCAAAGC CTTCCGCGGC CGCGAACCGA GCATAGACGC
2001 ACTTTGCGC CACAGCGGTT TCGACAACGC GGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 3092; ORF 128-1>:

```

m128-1.pep.
1  MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51  NTVEPLTGIT ERVGRIWGVV SHLNSVADTP ELRAVYNELM PEITVFFTEI

```

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101  GDIELYNRF  KTIKNSPEFD  TLSPAQKTKL  NHDLRDFVLS  GAELPPEQQA
151  ELAKLQTEGA  QLSAKFSQNV  LDATDAFGIY  FDDAAPLAGI  PEDALAMFAA
201  AAQSESKTGY  KIGLQIPHYL  AVIQYADNRE  LREQIYRAYV  TRASELSDDG
251  KFDNTANIDR  TLANALQTAK  LLGFKNYAEL  SLATKMADTP  EQVLNFLHDL
301  ARRAKPYAEK  DLAEVKAFAR  ESLNLADLQF  WDLGYASEKL  REAKYAFSET
351  EVKKYFPVGK  VLNGLFAQIK  KLYGIGFTEK  TVPVVHKDVR  YFELQQNGET
401  IGGVYMDLYA  REGKRGGAWM  NDYKGRRRFS  DGTLLQLPTAY  LVCNFAPPVG
451  GREARLSHDE  ILILFHETGH  GLHLLLTQVD  ELGVSGINGV  EWDAVEGPSQ
501  FMENFVWEYN  VLAQMSAHEE  TGVPLPKELF  DKMLAAKNFQ  RGMFLVRQME
551  FALFDDMIYS  EDDEGRLLKNW  QQVLDSVRKK  VAVIQPPEYN  RFALSFGHIF
601  AGGYSAGYYS  YAWAEVLSAD  AYAAFEESDD  VAATGKRWFQ  EILAVGGSRS
651  AAESFKAFRG  REPSIDALLR  HSGFDNAV*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3093>:

g128-1.seq (partial)

```

1  ATGATTGACA  ACGCACTGCT  CCACTTGGGC  GAAGAACCCC  GTTTTAATCA
51  AATCAAAACC  GAAGACATCA  AACCCTGGCT  CCAAACCGCC  ATCGCCGAAG
101 CGCGCGGACA  AATCGCCGCC  GTCAAAGCGC  AAACGCACAC  CGGCTGGGCG
151 AACACCGTCG  AGCGTCTGAC  CGGCATCACC  GAACGCGTCG  GCAGGATTGT
201 GGGCGTCGTG  TCCCATCTCA  ACTCCGTCGT  CGACACGCCC  GAACTGCGCG
251 CCGTCTATAA  CGAACTGATG  CCTGAAATCA  CCGTCTTCTT  CACCGAAATC
301 GGACAAGACA  TCGAACTGTA  CAACCGCTTC  AAAACCATCA  AAAATTCCCC
351 CGAATTGCA  ACGCTTTCCC  CCGCACAAAA  AACCAAGCTC  GATCACGACC
401 TGCAGCATTT  CGTATTGAGC  GCGCGGAAC  TGCCGCCCGA  ACGGCAGGCA
451 GAACTGGCAA  AACTGCAAAC  CGAAGGCGCG  CAACTTTCCG  CCAAATCTCT
501 CCAAACGTC  CTAGACGCGA  CCGACGCGTT  CGGCATTAC  TTTGACGATG
551 CCGCACCGCT  TGCCGGCATT  CCCGAAGACG  CGCTCGCCAT  GTTTGCCGCC
601 GCGCGGCAAA  GCGAAGGCAA  AACAGGTTAC  AAAATCGGCT  TGCAGATTCC
651 GCACTACCTT  GCCGTTATCC  AATACGCGCG  CAACCGCGAA  CTGCGCGAAC
701 AAATCTACCG  CGCCTACGTT  ACCCGTGCCA  GCGAACTTTC  AAACGACGGC
751 AAATTCGACA  ACACCGCCAA  CATCGACCGC  ACGCTCGAAA  ACGCATTGAA
801 AACCGCCAAA  CTGCTCGGCT  TTAATAATTA  CGCCGAATTG  TCGCTGGCAA
851 CCAAATGGC  GGACACGCCC  GAACAGGTTT  TAAACTTCCT  GCACGACCTC
901 GCGCGCGCG  CCAAACCTTA  CGCCGAAAAA  GACCTCGCCG  AAGTCAAAGC
951 CTTCGCCCCG  GAACACCTCG  GTCTCGCCGA  CCCGCAGCCG  TGGGACTTGA
1001 GCTACGCCG  CGAAAACTG  CGCGAAGCCA  AATACGCATT  CAGCGAAACC
1051 GAAGTCAAAA  AATACTTCCC  CGTCGCGAAA  GTTCTGGCAG  GCCTGTTCGC
1101 CCAAATCAAA  AAATCTACG  GCATCGGATT  CGCCGAAAAA  ACCGTTCCCG
1151 TCTGGCACAA  AGACGTGCGC  TATTTTGAAT  TGCAACAAAA  CGGCAAAACC
1201 ATCGGCGGCG  TTTATATGGA  TTTGTACGCA  CGCGAAGGCA  AACGCGGCGG
1251 CGCGTGGATG  AACGACTACA  AAGCGCGCCG  CCGCTTTGCC  GACGGCACGC
1301 TGCAACTGCC  CACCGCTTAC  CTCGTCTGCA  ACTTCGCCCC  GCCGTCGGC
1351 GGCAAGAAG  CGCGTTTAAG  CCACGACGAA  ATCCTCACCC  TCTTCCACGA
1401 AACCGCCAC  GGAATGCACC  ACCTGCTTAC  CCAAGTGGAC  GAACTGGGCG
1451 TGTCCGGCAT  CAACGGCGTA  AAA

```

This corresponds to the amino acid sequence <SEQ ID 3094; ORF 128-1.ng>:

g128-1.pep (partial)

```

1  MIDNALLHLG  EEPRFNQIKT  EDIKPAVQTA  IAEARGQIAA  VKAQHTGWA
51  NTVERTLGIT  ERVGRIWGVV  SHLNSVVDTP  ELRAVYNELM  PEITVFTEI
101  GDIELYNRF  KTIKNSPEFA  TLSPAQKTKL  DHDLRDFVLS  GAELPPERQA
151  ELAKLQTEGA  QLSAKFSQNV  LDATDAFGIY  FDDAAPLAGI  PEDALAMFAA
201  AAQSEGKTGY  KIGLQIPHYL  AVIQYAGNRE  LREQIYRAYV  TRASELSNDG
251  KFDNTANIDR  TLENALKTAK  LLGFKNYAEL  SLATKMADTP  EQVLNFLHDL
301  ARRAKPYAEK  DLAEVKAFAR  EHLGLADPQP  WDLSYAGEKL  REAKYAFSET
351  EVKKYFPVGK  VLAGLFAQIK  KLYGIGFAEK  TVPVVHKDVR  YFELQQNGKT
401  IGGVYMDLYA  REGKRGGAWM  NDYKGRRRFA  DGTLLQLPTAY  LVCNFAPPVG
451  GKEARLSHDE  ILTLFHETGH  GLHLLLTQVD  ELGVSGINGV  K

```

m128-1/g128-1 ORFs 128-1 and 128-1.ng showed a 94.5% identity in 491 aa overlap

10 20 30 40 50 60

100

g128-1.pep	MIDNALLHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQHTGTWANTVERLTGIT
m128-1	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGTWANTVEPLTGIT
	10 20 30 40 50 60
g128-1.pep	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA
m128-1	ERVGRIWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
	70 80 90 100 110 120
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
g128-1.pep	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV
	190 200 210 220 230 240
g128-1.pep	TRASELSNDGKFDNTANIDRTLLENALKTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
	250 260 270 280 290 300
g128-1.pep	ARRAKPYAEKDLAEVKAFAREHLGLADQPWDLGYASEKLREAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLPWDLGYASEKLREAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQQNGKTIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD
	430 440 450 460 470 480
g128-1.pep	ELGVSGINGVK
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
	490 500 510 520 530 540

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3095>:

a128-1.seq

```

1  ATGACTGACA ACGCACTGCT CCATTGGGCG GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACTCA ACTCCGTCAC CGACACGCCC GAACTGCGCG
251 CCGCCTACAA TGAATTAATG CCGGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACACGATC
401 TGC GCGATT CGTCCTCAGC GCGCGGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC

```



```

501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCCTG TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTCATCC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAATA CTGCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTATTAAACG GACTGTTCCG
1101 CCAAATCAAA AAACCTCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCAGTCAG
1501 TTTATGAAAA ATTTCTGTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAACCTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCCGCTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCGCCA
1901 CAGGCAAACG CTTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3096; ORF 128-1.a>:

a128-1.pep

```

1 MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGW
51 NTVEPLTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMATDP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKRRRFS DGTQLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDVAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRKKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRWFQ EILAVGGSR
651 AAESFKAERG REPSIDALLR HSGFDNAA*

```

m128-1/a128-1 ORFs 128-1 and 128-1.a showed a 97.8% identity in 677 aa overlap

```

          10      20      30      40      50      60
a128-1.pep MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT
          |||
m128-1      MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT
          10      20      30      40      50      60

          70      80      90      100     110     120
a128-1.pep ERVGRWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          |||
m128-1      ERVGRWGVVSHLNSVADTPELRVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          70      80      90      100     110     120

          130     140     150     160     170     180

```

a128-1.pep	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
a128-1.pep	190 200 210 220 230 240
	FDDAAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAQSESKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
	190 200 210 220 230 240
a128-1.pep	250 260 270 280 290 300
	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
m128-1	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
	250 260 270 280 290 300
a128-1.pep	310 320 330 340 350 360
	ARRAKPYAEKDLAEVKAFARESGLADLQPWDLGAGEKLREAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESGLADLQPWDLGAGEKLREAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
a128-1.pep	370 380 390 400 410 420
	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
a128-1.pep	430 440 450 460 470 480
	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
	430 440 450 460 470 480
a128-1.pep	490 500 510 520 530 540
	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
	490 500 510 520 530 540
a128-1.pep	550 560 570 580 590 600
	RGMFLVRQMEFALFDMMIYSEDDEGRLLKNWQQVLDSVRKEVAVVRPPEYNRFANSFGHIF
m128-1	RGMFLVRQMEFALFDMMIYSEDDEGRLLKNWQQVLDSVRKKVAVIQPPEYNRFALSFGHIF
	550 560 570 580 590 600
a128-1.pep	610 620 630 640 650 660
	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
m128-1	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
	610 620 630 640 650 660
a128-1.pep	670 679
	REPSIDALLRHSGFDNAAX
m128-1	REPSIDALLRHSGFDNAVX
	670

206

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3097>:
m206.seq

```

1 ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51 CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GGCAGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAr AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCGCGCGACA TGGCGGCGGC AAGCCGsAAA ATCCCCGAcA GCCGcyTCAA
351 GGCCGGCGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGTACTCAC
401 ACGTCGGACT CTACATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TTTTACAGA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 3098; ORF 206>:

m206.pep..

```

1 MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRP
101 ARDMAAASRK IPDSRXKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3099>:

g206.seq

```

1 atgttttccc ccgacaaaac ccttttcctc tgtctcggcg cactgctcct
51 cgccctcatgc ggcacgacct ccggcaaaaca ccgccaaccg aaacccaaac
101 agacagtccg gcaaatccaa gccgtccgca tcagccacat cggccgcaca
151 caaggctcgc aggaactcat gctccacagc ctcggactca tcggcacgcc
201 ctacaaatgg ggcggcagca gcaccgcaac cggccttcgac tgcagcggca
251 tgattcaatt ggtttataaaa aacgccctca acgtcaagct gccgcgcacc
301 gcccgcgaca tggcggcggc aagccgcaaa atccccgaca gccgcctcaa
351 ggccggcgac atcgtattct tcaacaccgg cggcgcacac cgctactcac
401 acgtcggact ctacatcggc aacggcgaat tcattccatgc ccccggcagc
451 ggcaaaacca tcaaaaccga aaaactctcc acaccgtttt acgccaaaaa
501 ctaccttgga gcgcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 3100; ORF 206.ng>:

g206.pep

```

1 MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT
51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPRP
101 ARDMAAASRK IPDSRLKAGD IVFFNTGGAH RYSHVGLYIG NGEFIHAPGS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

```

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	:					
g206	MFSPDKTLFLCLGALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYKNALNVKLPRPTARDMAAASRKIPDSRXKAGD					
	:					
g206	LGLIGTPYKWGGSSTATGFD CSGMIQLVYKNALNVKLPRPTARDMAAASRKIPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
	: :					
g206	IVFFNTGGAHRYSHVGLYIGNGEFIHAPSGKTIKTEKLSTPFYAKNYLGAHTFFTE					

130 140 150 160 170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3101>:

```
a206.seq
1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GCGGCGAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCCCGCGACA TGGCGGCGGC AAGCCGCAAA ATCCCCGACA GCCGCCTTAA
351 GGCCGGCGAC CTGCTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TCTTTACAGA ATGA
```

This corresponds to the amino acid sequence <SEQ ID 3102; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRP
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 ORFs 206 and 206.a showed a 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
a206	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRP TARDMAAASRK IPDSRLKAGD					
a206	LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRP TARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS GKTIKTEKLS TPFYAKNYLGAHTFFTEX					
a206	LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS GKTIKTEKLS TPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	

287

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3103>:

```
m287.seq
1  ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTTC CCCTTTCAGC
51  CTGCGGGGGC GGCGGTGGCG GATCGCCCGA TGTCAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCCCT GTTGTCTCTG AAAAAGAGAC AGAGGCAAAG
151 GAAGATGCGC CACAGGCAGG TTCTCAAGGA CAGGGCGCGC CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CCGTTTCGGA AGAAAATACA GGCAATGGCG
251 GTGCGGTAAC AGCGGATAAT CCCAAAATG AAGACGAGGT GGCACAAAAT
301 GATATGCCGC AAAATGCCGC CGGTACAGAT AGTTCGACAC CGAATCACAC
351 CCCGGATCCG AATATGCTTG CCGGAAATAT GGAAAATCAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCCG GCAAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGGACGA TCCGTCGGCA GGCGGGCAAA ATGCCGGCAA
501 TACGGCTGCC CAAGGTGCAA ATCAAGCCGG AAACAATCAA GCCCGCGGTT
551 CTTCAGATCC CATCCCCGCG TCAAACCCTG CACCTGCGAA TGGCGGTAGC
```

```

601 AATTTTGGAA GGGTTGATT GGCTAATGGC GTTTTGATTG ACGGGCCGTC
651 GCAAAATATA ACGTTGACCC ACTGTAAAGG CGATTCTTGT AGTGGCAATA
701 ATTTCTTGGA TGAAGAAGTA CAGCTAAAAT CAGAATTTGA AAAATTAAGT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 TGTCGGTTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTTA TAAACCTAAA CCCACTTCAT TTGCGCGATT TAGGCGTTCT
901 GCACGGTCGA GCGGTCGCT TCCGGCCGAG ATGCCGCTGA TTCCCCTCAA
951 TCAGGCGGAT ACGCTGATTG TCGATGGGGA AGCGGTCAGC CTGACGGGGC
1001 ATTCGGGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCGG CGGATCGTAT GCCCTTCGTG TTCAAGGCCA
1101 ACCGGCAAAA GCGGAAATGC TTGCGGGCGC GGCCGTGTAC AACGGCGAAG
1151 TACTGCATTT CCATACGGAA AACGGCCGTC CGTACCCGAC CAGGGGCAGG
1201 TTTGCCGCAA AAGTCGATTT CGGCAGCAA TCTGTGGACG GCATTATCGA
1251 CAGCGGCGAT GATTTGCATA TGGGTACGCA AAAATTCAA GCCGCCATCG
1301 ATGGAACCGG CTTTAAGGGG ACTTGGACGG AAAATGGCAG CGGGGATGTT
1351 TCCGGAAGT TTTACGGCCC GGCCGGCGAG GAAGTGGCGG GAAAATACAG
1401 CTATCGCCCG ACAGATGCGG AAAAGGCGG ATTCGGCGTG TTTGCCGCA
1451 AAAAAGAGCA GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 3104; ORF 287>:

m287. pep

```

1 MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSKPAAP VVSEKETEAK
51 EDAPQAGSQG QGAPSAQGSQ DMAAVSEENT GNGGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTPNHTPDP NMLAGNMENQ ATDAGESSQP ANQPDMANAA
151 DGMQGDPSA GGQNAAGNTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
201 NFRGRVDLANG VLIDGPSQNI TLTHCKGDSC SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFVGL VADSVQMKGI NQYIIFYKPK PTSFARFRRS
301 ARSRRSLPAE MPLIPVNOAD TLIVDGEAVS LTGHSGNIFA PEGNYRYLTY
351 GAEKLPGGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDFGSK SVDGIIDSGD DLHMGTKQFK AAIDGNNGFKG TWTENGSGDV
451 SGKFYGPAGE EVAGKYSYRP TDAEKGGFGV FAGKKEQD*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3105>:

g287. seq

```

1 atgttttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51 ctgtgggggc ggcggtggcg gatcgcccga tgtcaagtcg gcgacacgc
101 cgtcaaaaacc ggccgcccc gttgttgctg aaaatgccgg ggaagggtg
151 ctgccgaaag aaaagaaaga tgaggaggca gcgggcggtg cgccgcaagc
201 cgatacgag gacgcaaccg ccggagaagg cagccaagat atggcgagc
251 tttcggcaga aaatacaggc aatggcggtg cggcaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaa atgccgccga
351 atccgcaaat caaacaggga acaaccaacc cgccggttct tcagattccg
401 cccccgcgtc aaacctgccc cctgcgaatg gcggtagcga ttttgaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgtcgc aaaataaac
501 gttgaccac tgtaaaggcg attcttgtaa tgggtgataa ttattggatg
551 aagaagcacc gtcaaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attaagcgat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tgctgacagg gtaaaaaagg atggaactaa caaatatata atcttctata
701 cggacaaaacc acctactcgt tctgcacggt cgaggaggtc gttccggcc
751 gagattccgc tgattcccgat caatcaggcc gatacgtgta ttgtggatg
801 ggaagcggtc agcctgacgg ggcattccgg caatatcttc gcgccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcgatcg
901 tatgccctcc gtgtgcaagg cgaaccggca aaaggcgaaa tgcttgttg
951 cacggccgtg tacaacggcg aagtgtgtgca tttccatatg gaaaacggcc
1001 gtccgtaccc gtccggaggc aggtttgccg caaaagtcga tttcggcagc
1051 aaatctgtgg acggcattat cgacagcggc gatgatttgc atatgggtac
1101 gcaaaaattc aaagccgcca tcgatgaaa cggctttaag gggacttga
1151 cggaaaaatg cggcgggat gtttccgga ggttttacgg cccggccggc
1201 gggaagtgg cgggaaaata cagctatcgc ccgacagatg ctgaaaagg
1251 cggattcggc gtgtttgccg gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 3106; ORF 287.ng>:

g287. pep

```

1 MFKRSVIAMA CIFPLSACGG GGGGSPDVKS ADTPSKPAAP VVAENAGEGV

```

[illegible]

g287 PTDAEKGGFGVFAGKKDRDX
420 430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3107>:

```

a287.seq
1   ATGTTTAAAC  GCAGTGTGAT  TGCAATGGCT  TGTATTGTTG  CCCTTTCAGC
51  CTGTGGGGGC  GCGGTGGCG  GATCGCCGCA  GTTTAAGTCG  CGCGACACGC
101 TGTCAAACCC  TGCCGCCCTT  GTTGTTACTG  AAGATGTCGG  GGAAGAGGTG
151 CTGCCGAAAG  AAAAGAAAGA  TGAGGAGGCG  GTGAGTGGTG  CGCCGCAAGC
201 CGATACGCAG  GACGCACCG  CCGGAAAAGG  CGGTCAAGAT  ATGGCGGCAG
251 TTTCCGCGCA  AAATACAGGC  AATGGCGGTG  CGGCAACAAC  GGATAATCCC
301 GAAAATAAAG  ACGAGGACCC  GCAAAATGAT  ATGCCGCAAA  ATGCCGCCGA
351 TACAGATAGT  TCGACACCGA  ATCACACCCC  TGCACCGAAT  ATGCCAACCA
401 GAGATATGGG  AAACCAAGCA  CCGGATGCCG  GGAATCGGC  ACAACCGGCA
451 AACCAACCGG  ATATGGCAAA  TGCGCGCGAC  GGAATGCAGG  GGGACGATCC
501 CTCGGCACGG  GAAATGCCG  GCAATACGGC  AGATCAAGCT  GCAAAATCAAG
551 CTGAAAACAA  TCAAGTCGCG  GGCTCTCAAA  ATCTGCCTC  TTCAACCAAT
601 CCTAACGCCA  CGAATGGCGG  CAGCGATTTT  GGAAGGATAA  ATGTAGCTAA
651 TGGCATCAAG  CTTGACAGCG  GTTCGGAATA  TGTAACGTTG  ACACATTGTA
701 AAGACAAAGT  ATGCGATAGA  GATTTCCTAG  ATGAAGAAGC  ACCACAAAAA
751 TCAGAATTGT  AAAAATTAA  TGATGAAGAA  AAAATTAAAT  AATATAAAAA
801 AGACGAGCAA  CGAGAGAATT  TTGTCGGTTT  GTTTGCTGAC  AGGGTAGAAA
851 AGAATGGAAC  TAACAAATAT  GTCATCATTT  ATAAAGACAA  GTCCGCTTCA
901 TCTTCATCTG  CGCGATTACG  GCGTCTCGCA  CGGTTCGAGG  GGTTCGCTTC
951 GGCCGAGATG  CCGCTGATT  CCGTCAATCA  CGCGGATACG  CTGATTGTCT
1001 ATGGGGAAGC  GGTCAGCCGT  ACGGGGCATT  GCGGCAATAT  CTTCGCGCCC
1051 GAAGGGAATT  ACCGGTATCT  GACTTACGGG  GCGGAAAAAT  TGTCCGGCGG
1101 ATCGTATGCC  CTCAGTGTGC  AAGGCGAACC  GGCAAAAGGC  GAAATGCTTG
1151 CGGGCACCGG  CGTGTAACA  GGCGAAGTGC  TGCATTTCCA  TATGGAAAAA
1201 GGCCGTCTGT  CCCCCTCCG  AGCAGGTTT  GCGCAAAAAG  TCGATTTCGG
1251 CAGCAAATCT  GTGGACGGCA  TTATCGACAG  CGCGCATGAT  TTGCATATGG
1301 GTACGCAAAA  ATTCAAAGCC  GTTATCGATG  GAAACGGCTT  TAAGGGGACT
1351 TGGACGGAAA  ATGGCGCGCG  GGATGTTTTT  GGAAGGTTTT  ACGGCCCGGC
1401 CGGCGAAGAA  GTGGCGGGAA  AATACAGTCA  TCGCCCGACA  GATGCGGAAA
1451 AGGGCGGATT  CGGCCTGTTT  CCGGCGAAAA  AAGAGCAGGA  TTGA

```

This corresponds to the amino acid sequence <SEQ ID 3108; ORF 287.a>:

a287.pep

1	<u>MFKRSVIAMA</u>	<u>CIVALSACGG</u>	GGGGSPDVKS	ADTLSPAAP	VVTEDVGEEV
51	LPKEKKDEEA	VSGAPQADTQ	DATAGKGGQD	MAAVSAENTG	NGGAATTDNP
101	ENKDEGPND	MPQNAADTDS	STPNHTPAPN	MPTRDMGNQA	PDAGESAQPA
151	NPQDMAAAD	GMQGDPSAG	ENAGNTADQA	ANQAENNQVG	GSQNFPASSTN
201	PNATNGGSDF	GRINVANGIK	LDSGSENVTL	THCKDKVCDR	DFLDEEAPPK
251	SEFEKLSDEE	KINKYKKDEQ	RENFVGLVAD	RVEKNGTNKY	VIIYKDKSAS
301	SSSARFRSA	RSRRSLPAEM	PLIPVNQADT	LIVDGEAVSL	TGHSGNIFAP
351	EGNYRYLTYG	AEKLSGGSYA	LSVQGEPAKG	EMLAGTAVYN	GEVLHFHFMK
401	GRPSPSGGRF	AAKVDFGSKS	VGGIIDS added	LHMGTQKFKA	VIDNGNFKGT
451	WTENGGGDVS	GRFYGPAGEE	VAGKYSRPT	DAEKGKGFV	AGKKEOD*

m287/a287 ORFs 287 and 287.a showed a 77.2% identity in 501 aa overlap

```

              10      20      30      40      49
m287.pep      MFKRSVIAMACIFALSACGGGGGSPDVKSAADTLSPAAPVVS-----KETEA
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287           MFKRSVIAMACIVALSACGGGGGSPDVKSAADTLSPAAPVVTEDEVGEEVLPKEKKDEEA
              10      20      30      40      50      60

              50      60      70      80      90      100     109
m287.pep      KEDAPQAGSQGQGPSAQGSQDMAAVSEENTGNNGAVTADNPKNEDEVAQNMPQNAAGT
              ||| :| | :||| ||||| ||||| ||||| ||||| ||||| |||||
a287           VSGAPQADTQ--DATAGKGGQDMAAVSAENTGNNGAATTNPFENKDEGPQNDMPQNAADT
              70      80      90      100     110

```

	110	120	130	140	150	160	169
m287.pep	DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADGMQGDPSAGGQNAGNTA						
a287	DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAADGMQGDPSAG-ENAGNTA						
	120	130	140	150	160	170	
	170	180	190	200	210	220	229
m287.pep	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFGVRDLANGVLIDGPSQNTLTHCKGDS						
a287	DQAANQAENNQVGGSQNPASSTNPATNGGSDFGRLNVANGIKLDSGSENVTLTHCKDKV						
	180	190	200	210	220	230	
	230	240	250	260	270	280	289
m287.pep	CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGNDFVGLVADSVQMKGINQYIIFYKP						
a287	CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKVIYKD						
	240	250	260	270	280	290	
	290	300	310	320	330	340	
m287.pep	KP--TSFARFRRSARSRRLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRY						
a287	KSASSSARFRRSARSRRLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRY						
	300	310	320	330	340	350	
	350	360	370	380	390	400	
m287.pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF						
a287	LTYGAEKLGGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRFSPSGGRFAAKVDF						
	360	370	380	390	400	410	
	410	420	430	440	450	460	
m287.pep	GSKSVDDGIIDSGDDLHMGTKQKFAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYS						
a287	GSKSVDDGIIDSGDDLHMGTKQKFAVIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYS						
	420	430	440	450	460	470	
	470	480	489				
m287.pep	YRPTDAEKGFGVFAGKKEQDX						
a287	YRPTDAEKGFGVFAGKKEQDX						
	480	490					

406

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3109>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGCCTTAAAT
451 ATTGCGGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAA
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTC GCAGTAGACA

```



```

701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACGGAAG GATTAATGGT CGATTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3110; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGLTG LTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGP *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3111>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAAC
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGCGGC GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGCT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3112; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGLTG LTSLSTLNA PALSRTQSDG SGSRSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFS DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGP *

```

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAAVKMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAAVKMDLQALHGR					

	10	20	30	40	50	60
	70	80	90	100	110	120
g406 . pep	KVALYIATMGDQGSGLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
m406	KVALYIATMGDQGSGLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
	130	140	150	160	170	180
g406 . pep	LTTSLSLTLNAPALSRTQSDGSGSRSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF					
m406	LTTSLSLTLNAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF					
	190	200	210	220	230	240
g406 . pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	250	260	270	280	290	300
g406 . pep	IKPKTNAFEAAYKENYALWMGPYKVSKGIKPTEGLMVDPSDIQPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAYKENYALWMGPYKVSKGIKPTEGLMVDPSDIRPYGNHTGNSAPSVEADN					
	310	320				
g406 . pep	SHEGYGYSDEAVRQHRQGQPX					
m406	SHEGYGYSDEVVRQHRQGQPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3113>:

```

a406 . seq
1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACACTGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TC CGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGCGGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTCTCTC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCGAC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3114; ORF 406.a>:

```

a406 . pep
1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFQVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQGSGLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGLTGG LTTSLSLTLN PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA

```

251 AYKENYALWM GPYKVSKGIK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN
 301 SHEGYGYSDE AVRRHRQGQP *

m406/a406 ORFs 406 and 406.a showed a 98.8% identity in 320 aa overlap

	10	20	30	40	50	60
m406.pep	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARAQVDMQALHGR					
a406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARAQVDMQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m406.pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG					
a406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m406.pep	LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
a406	LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m406.pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
a406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m406.pep	IKPKTNAFEAAAYKENYALWMPYKVSKGIKPTGLMVDFS DIRPYGNHTGNSAPSVEADN					
a406	IKPKTNAFEAAAYKENYALWMPYKVSKGIKPTGLMVDFS DIQPYGNHMGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
m406.pep	SHEGYGYSDEVVRQHRQGQPX					
a406	SHEGYGYSDEAVRRHRQGQPX					
	310	320				

EXAMPLE 2

Expression of ORF 919

The primer described in Table 1 for ORF 919 was used to locate and clone ORF 919. The predicted gene 919 was cloned in pET vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 919-His fusion protein purification. Mice were immunized with the purified 919-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; PP, purified protein, TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm

that 919 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 919 are provided in Figure 10. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 3

Expression of ORF 279

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 11. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 4

Expression of ORF 576 and 576-1

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera

were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 576 are provided in Figure 12. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 5

Expression of ORF 519 and 519-1

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. The predicted gene 519 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 13. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 6

Expression of ORF 121 and 121-1

The primer described in Table 1 for ORF 121 was used to locate and clone ORF 121. The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 121 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 121 are provided in Figure 14. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 121 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 7

Expression of ORF 128 and 128-1

The primer described in Table 1 for ORF 128 was used to locate and clone ORF 128. The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 128 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 128 are provided in Figure 15. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J.*

Immunol 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 128 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 8

Expression of ORF 206

The primer described in Table 1 for ORF 206 was used to locate and clone ORF 206. The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worth noting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a reactive band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 206 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 16. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 206 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 9

Expression of ORF 287

The primer described in Table 1 for ORF 287 was used to locate and clone ORF 287. The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A). These experiments confirm that 287 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 287 are provided in Figure 17. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 287 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 10

Expression of ORF 406

The primer described in Table 1 for ORF 406 was used to locate and clone ORF 406. The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 406 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 406 are provided in Figure 18. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 406 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 11

Table 2 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 225 among different strains.

Table 2

225 gene variability: List of used *Neisseria* strains

Identification Strains number	Source / reference
Group B	
zo01_225 NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo02_225 BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zo03_225 NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo04_225 297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zo05_225 1000	R. Moxon / Seiler <i>et al.</i> , 1996
zo06_225 BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zo07_225 BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zo08_225 528	R. Moxon / Seiler <i>et al.</i> , 1996
zo09_225 NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zo10_225 BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zo11_225 NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zo12_225 NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zo13_225 NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zo14_225 NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zo15_225 SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zo16_225 NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zo17_225 NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zo18_225 BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zo19_225 BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zo20_225 44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zo21_225 MC58	R. Moxon
zo96_225 2996	Our collection
Group A	
zo22_225 205900	R. Moxon
zo23_225 F6124	R. Moxon
z2491 Z2491	R. Moxon / Maiden <i>et al.</i> , 1998
Group C	
zo24_225 90/18311	R. Moxon
zo25_225 93/4286	R. Moxon

Others

zo26_225 A22 (group W) R. Moxon / Maiden *et al.*, 1998
 zo27_225 E26 (group X) R. Moxon / Maiden *et al.*, 1998
 zo28_225 860800 (group Y) R. Moxon / Maiden *et al.*, 1998
 zo29_225 E32 (group Z) R. Moxon / Maiden *et al.*, 1998

Gonococcus

zo32_225 Ng F62 R. Moxon / Maiden *et al.*, 1998
 zo33_225 Ng SN4 R. Moxon

fa1090 FA1090 R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

>FA1090 <SEQ ID 3115>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
 NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS
 GFMQHIFKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
 RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Z2491 <SEQ ID 3116>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRVPARRAGNA
 DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF
 MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Z001_225 <SEQ ID 3117>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDPSRFLN*

Z002_225 <SEQ ID 3118>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDPSRFLN*

Z003_225 <SEQ ID 3119>

MDSFFKPAVWAVLWLMFAVRLALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDPSRFLN*

Z004_225 <SEQ ID 3120>
MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z005_225 <SEQ ID 3121>
MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z006_225 <SEQ ID 3122>
MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z007_225 <SEQ ID 3123>
MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z008_225 <SEQ ID 3124>
MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z009_225 <SEQ ID 3125>
MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z010_225 <SEQ ID 3126>
MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z011_225 <SEQ ID 3127>
MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRFI
HAPRTGKNIEITSLSHKYWSGKYAFARRVKKN DPSRFLN*

Z012_225 <SEQ ID 3128>
MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z013_225 <SEQ ID 3129>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFIQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z014_225 <SEQ ID 3130>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z015_225 <SEQ ID 3131>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCS
GFMQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKN DPSRFLN*

Z016_225 <SEQ ID 3132>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z017_225 <SEQ ID 3133>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z018_225 <SEQ ID 3134>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z019_225 <SEQ ID 3135>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
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DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z020_225 <SEQ ID 3136>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPINRAPARRAGNADELIGSAMGLNEQPVLPVNRVPARRAGNA
DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKN DPSRFLN*

Z021_225 <SEQ ID 3137>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

Z022_225 <SEQ ID 3138>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR

SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z023_225 <SEQ ID 3139>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z024_225 <SEQ ID 3140>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z025_225 <SEQ ID 3141>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z026_225 <SEQ ID 3142>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z027_225 <SEQ ID 3143>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z028_225 <SEQ ID 3144>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z029_225 <SEQ ID 3145>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z032_225 <SEQ ID 3146>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PVNRAPARRAG
NADELIGSAMGLNEQPVL PVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS
GFMQHI FKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN*

Z033_225 <SEQ ID 3147>

MDSFFKPAVWAVLWLMFAVRSALADELTNLLSSREQILRQFAEDEQPVL PVNRAPARRAG
NADELIGSAMGLNEQPVL PVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS
GFMQHI FKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN*

Z096_225 <SEQ ID 3148>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDPSRFLN*

Figure 19 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 225, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 12

Table 3 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 235 among different strains.

Table 3

235 gene variability: List of used *Neisseria* strains

Identification Strains number	Reference
Group B	
gnmzq01 NG6/88	Seiler <i>et al.</i> , 1996
gnmzq02 BZ198	Seiler <i>et al.</i> , 1996
gnmzq03 NG3/88	Seiler <i>et al.</i> , 1996
gnmzq04 1000	Seiler <i>et al.</i> , 1996
gnmzq05 1000	Seiler <i>et al.</i> , 1996
gnmzq07 BZ169	Seiler <i>et al.</i> , 1996
gnmzq08 528	Seiler <i>et al.</i> , 1996
gnmzq09 NGP165	Seiler <i>et al.</i> , 1996
gnmzq10 BZ133	Seiler <i>et al.</i> , 1996
gnmzq11 NGE31	Seiler <i>et al.</i> , 1996
gnmzq13 NGE28	Seiler <i>et al.</i> , 1996
gnmzq14 NGH38	Seiler <i>et al.</i> , 1996
gnmzq15 SWZ107	Seiler <i>et al.</i> , 1996
gnmzq16 NGH15	Seiler <i>et al.</i> , 1996
gnmzq17 NGH36	Seiler <i>et al.</i> , 1996
gnmzq18 BZ232	Seiler <i>et al.</i> , 1996
gnmzq19 BZ83	Seiler <i>et al.</i> , 1996
gnmzq21 MC58	Virji <i>et al.</i> , 1992
Group A	
gnmzq22 205900	Our collection

gnmzq23	F6124	Our collection
z2491	Z2491	Maiden <i>et al.</i> , 1998

Group C

gnmzq24	90/18311	Our collection
gnmzq25	93/4286	Our collection

Others

gnmzq26	A22	(group W) Maiden <i>et al.</i> , 1998
gnmzq27	E26	(group X) Maiden <i>et al.</i> , 1998
gnmzq28	860800	(group Y) Maiden <i>et al.</i> , 1998
gnmzq29	E32	(group Z) Maiden <i>et al.</i> , 1998
gnmzq31	<i>N. lactamica</i>	Our collection

Gonococcus

gnmzq32	Ng F62	Maiden <i>et al.</i> , 1998
gnmzq33	Ng SN4	Our collection

fa1090	FA1090	Dempsey <i>et al.</i> 1991
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References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.
 Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279
 Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3149>
 MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGT
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

GNMZQ01 <SEQ ID 3150>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGT
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANNT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ02 <SEQ ID 3151>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGT
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ03 <SEQ ID 3152>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST

AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSIT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ04 <SEQ ID 3153>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSIT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ05 <SEQ ID 3154>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANNLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ07 <SEQ ID 3155>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSIT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ08 <SEQ ID 3156>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANNLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ09 <SEQ ID 3157>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSIT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ10 <SEQ ID 3158>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSIT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ11 <SEQ ID 3159>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSIT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ13 <SEQ ID 3160>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSIT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ14 <SEQ ID 3161>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSIT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ15 <SEQ ID 3162>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSIT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ16 <SEQ ID 3163>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ17 <SEQ ID 3164>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ18 <SEQ ID 3165>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ19 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ21 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ22 <SEQ ID 3167>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ23 <SEQ ID 3168>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ24 <SEQ ID 3169>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ25 <SEQ ID 3170>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ26 <SEQ ID 3171>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ27 <SEQ ID 3172>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ28 <SEQ ID 3173>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ29 <SEQ ID 3174>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ31 <SEQ ID 3175>
 MKPLILGLAAVLALSACQVQKAPDFDYTAFKESKPASILVVPPLNESPDVNGTWGMLAST
 AEPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITITEYGTS
 YQILDSVTTVSARARLVDSRNGKVLWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
 DRGYQVSKAAAYDLLSPYSHNGILKGPRFVEEQPK*

GNMZQ32 <SEQ ID 3176>
 MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

GNMZQ33 <SEQ ID 3177>
 MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

Z2491 <SEQ ID 3178>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

Figure 20 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 235, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 13

Table 4 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 287 among different strains.

Table 4

287 gene variability: List of used *Neisseria* strains

Identification Strains number	Reference
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Group B

287_2	BZ198	Seiler <i>et al.</i> , 1996
287_9	NGP165	Seiler <i>et al.</i> , 1996
287_14	NGH38	Seiler <i>et al.</i> , 1996
287_21	MC58	Virji <i>et al.</i> , 1992

Group A

z2491	Z2491	Maiden <i>et al.</i> , 1998
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Gonococcus

fa1090	FA1090	Dempsey <i>et al.</i> 1991
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References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.
 Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279
 Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

287_14 <SEQ ID 3179>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
 QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNMPQNAADTDSLTPNHTPAS
 NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNQ
 TAGSQNPASSTNPSATNSGGDFGRNTVGNVVIDGPSQNTLTHCKGDS CSGNNFLDEEV
 QLKSEFEKLSADAKISNYKKDGKNDGKNDKFVGLVADSVQMKGINQYII FYKPKPTS FAR
 FRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLP
 GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSRGRFAAKVDFGSKSVDGII
 DSGDGLHMGTKQKFAAIDGNGFKGTWTENGGDVSGKFYGPAGEEVAGKYSYRPTDAEKG
 GFGVFAGKKEQD*

287_2 <SEQ ID 3180>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
 QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNMPQNAADTDSLTPNHTPAS
 NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNQ
 TAGSQNPASSTNPSATNSGGDFGRNTVGNVVIDGPSQNTLTHCKGDS CSGNNFLDEEV
 QLKSEFEKLSADAKISNYKKDGKNDGKNDKFVGLVADSVQMKGINQYII FYKPKPTS FAR
 FRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLP
 GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSRGRFAAKVDFGSKSVDGII
 DSGDGLHMGTKQKFAAIDGNGFKGTWTENGGDVSGKFYGPAGEEVAGKYSYRPTDAEKG
 GFGVFAGKKEQD*

287_21. <SEQ ID 3181>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
 QGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGTDSLTPNHTPDP
 NMLAGNMENQATDAGESSQPANQPDMAAADGMQGGDDPSAGGQAGNTAAQGANQAGNNQ
 AAGSSDPIPASNPAPANGGSNFGRVDLANGVLIDGPSQNTLTHCKGDS CSGNNFLDEEV
 QLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYII FYKPKPTS FARFRRS

ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGSY
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSVDDGIIDSGD
DLHMGTKQKFAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKGFGV
FAGKKEQD*

287_9 <SEQ ID 3182>

MFKRSVIAMACIVALSACGGGGGGSPDVKSADTLSPKPAAPVVTEDVGEEVLPKEKKDEEA
VSGAPQADTQDATAGKGGQDMAAVSAENTGNNGAATTNDPENKDEGPQNDMPQNAADTDS
STPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMAAADGMQGGDPSAGENAGNTADQA
ANQAENNOVGGSQNPASSTNPNATNGGSDFGRIINVANGIKLDSGSENVTLTHCKDKVCDR
DDLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVEKNGTNKYVIIYKDKSAS
SSSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYG
AEKLSGGSYALSQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDFGSKS
VDGIIDSGDDLHMGTKQKFAVIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPT
DAEKGFGVFAGKKEQD*

FA1090 <SEQ ID 3183>

MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPEKKDEEA
AGGAPQADTQDATAGEGSDMAAVSAENTGNNGAATTNDPKNEDAGAQNMPQNAAESAN
QTGNNOQAGSSDSAPASNPAPANGGSDFGRTNVGNSVVIDGPSQNTLTHCKGDSNGDN
LLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVEKNGTNKYIIFYTDKPPTR
SARSRRSLPAEIPVQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGSY
YALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDFGSKSVDDGIIDSG
DDLHMGTKQKFAAIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPTDAEKGFGV
VFAGKKDRD*

Z2491 <SEQ ID 3184>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVSEKETEAKEDAPQAGSQG
QGAPSAQGSQDMAAVSEENTGNNGAVTADNPKNEDEVAQNMPQNAAGTDSSTPNHTPDP
NMLAGNMENQATDAGESSQPANQPDMAAADGMQGGDPSAGGQNAAGNTAAQGANQAGNNQ
AAGSSDPIPASNPAPANGGSNFGRVDLANGVLIDGPSQNTLTHCKGDSGSGNNFLDEEV
QLKSEFEKLSADKISNYKKDGKNDKFVGLVADSVQMGKINQYIIFYKPKPSTSFARFRRS
ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGSY
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSVDDGIIDSGD
DLHMGTKQKFAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKGFGV
FAGKKEQD*

Figure 21 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 287, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 14

Table 5 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 519 among different strains.

Table 5

519 gene variability: List of used *Neisseria* strains

Identification Strains	Source / reference
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number**Group B**

zv01_519	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv02_519	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zv03_519ass	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv04_519	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zv05_519	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zv06_519ass	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zv07_519	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zv11_519	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zv12_519	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zv18_519	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zv19_519	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zv20_519ass	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zv21_519ass	MC58	R. Moxon
zv96_519	2996	Our collection

Group A

zv22_519ass	205900	R. Moxon
z2491_519	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

Others

zv26_519	A22	(group W) R. Moxon / Maiden <i>et al.</i> , 1998
zv27_519	E26	(group X) R. Moxon / Maiden <i>et al.</i> , 1998
zv28_519	860800	(group Y) R. Moxon / Maiden <i>et al.</i> , 1998
zv29_519ass	E32	(group Z) R. Moxon / Maiden <i>et al.</i> , 1998

Gonococcus

zv32_519	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
fa1090_519	FA1090	R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.

Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090_519 <SEQ ID 3185>
 MEFFIILLAAVAVFGFKSFVVIQQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
 KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
 RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE
 KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
 LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
 ISAGMKIIDSSKTAK*

Z2491_519 <SEQ ID 3186>

MEFFIILLAAVVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV01_519 <SEQ ID 3187>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV02_519 <SEQ ID 3188>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV03_519 <SEQ ID 3189>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV04_519 <SEQ ID 3190>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV05_519 <SEQ ID 3191>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV06_519ASS <SEQ ID 3192>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV07_519 <SEQ ID 3193>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV11_519 <SEQ ID 3194>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV12_519 <SEQ ID 3195>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV18_519 <SEQ ID 3196>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV19_519 <SEQ ID 3197>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV20_519ASS <SEQ ID 3198>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSM
ISAGMKIIDSSKTAK*

ZV21_519ASS <SEQ ID 3199>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV22_519ASS <SEQ ID 3200>

MEFFIILLAAVVVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV26_519 <SEQ ID 3201>

MEFFIILLAAVVVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV27_519 <SEQ ID 3202>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV28_519 <SEQ ID 3203>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV29_519ASS <SEQ ID 3204>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREPEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSNKTAK*

ZV32_519 <SEQ ID 3205>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV96_519 <SEQ ID 3206>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

Figure 22 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 519, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 15

Table 6 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 919 among different strains.

Table 6

919 gene variability: List of used *Neisseria* strains

Identification Strains	Source / reference
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number**Gr up B**

zm01	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm02	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zm03	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm04	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zm05	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zm06	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zm07	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zm08n	528	R. Moxon / Seiler <i>et al.</i> , 1996
zm09	NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zm10	BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zm11asbc	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zm12	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zm13	NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zm14	NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zm15	SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zm16	NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zm17	NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zm18	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zm19	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zm20	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zm21	MC58	R. Moxon
zm96	2996	Our collection

Group A

zm22	205900	R. Moxon
zm23asbc	F6124	R. Moxon
z2491	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

Group C

zm24	90/18311	R. Moxon
zm25	93/4286	R. Moxon

Others

zm26	A22	(group W) R. Moxon / Maiden <i>et al.</i> , 1998
zm27bc	E26	(group X) R. Moxon / Maiden <i>et al.</i> , 1998
zm28	860800	(group Y) R. Moxon / Maiden <i>et al.</i> , 1998
zm29asbc	E32	(group Z) R. Moxon / Maiden <i>et al.</i> , 1998
zm31asbc	<i>N. lactamica</i>	R. Moxon

Gonococcus

zm32asbc	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
zm33asbc	Ng SN4	R. Moxon
fa1090	FA1090	R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden et al., Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3207>
 MKKHLRLSALYGIAAAILAACQSRSIQTFFQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
 YTVVPHLSMPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
 YFTPWQVAGNGSLAGTGTGYYEPVLKGDGRTERARFPIYGIPTDDFISVPLPAGLRGGKN
 LVRIQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELASGNEGVPVGALGTPLMGEYAGA
 IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

Z2491 <SEQ ID 3208>
 MKKYLFRALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
 YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
 YFTPWQVAGNGSLAGTGTGYYEPVLKGDRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
 LVRIQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKAYMQNPORLAEVLGQNPSYIFFRELTSNDGVPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM01 <SEQ ID 3209>
 MKKYLFRALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
 YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
 YFTPWQVAGNGSLAGTGTGYYEPVLKGDRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
 LVRIQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELASNDGVPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM02 <SEQ ID 3210>
 MKKYLFRALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
 YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
 YFTPWQVAGNGSLAGTGTGYYEPVLKGDRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
 LVRIQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELASNDGVPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM03 <SEQ ID 3211>
 MKKYLFRALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
 YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
 YFTPWQVAGNGSLAGTGTGYYEPVLKGDRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
 LVRIQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
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ZM04 <SEQ ID 3212>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
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YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
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DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
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VDRHYITLGAPLFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM05 <SEQ ID 3213>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVPVHLSLPHWAAQDFAKSLQSFRLSCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM06 <SEQ ID 3214>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
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DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM07 <SEQ ID 3215>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
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KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM08N <SEQ ID 3216>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
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DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM09 <SEQ ID 3217>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
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YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
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KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM10 <SEQ ID 3218>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
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YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
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KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM11ASBC <SEQ ID 3219>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSQAKQFFER
YFTPWQVAGNAGSLAGTGTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNAGGTHADLSRFPITARTTAIKRFEGRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVVSIGKYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM12 <SEQ ID 3220>

MKKYLFRAALYGI A AAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNAGSLAGTGTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKRFEGRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM13 <SEQ ID 3221>

MKKYLFRAALYGI A AAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNAGSLAGTGTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKRFEGRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM14 <SEQ ID 3222>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
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YFTPWQVAGNAGSLAGTGTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
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DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVVSIGKYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM15 <SEQ ID 3223>

MKKYLFRAALYGI A AAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDLAGTTVGGGGAV
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YFTPWQVAGNAGSLAGTGTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKRFEGRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVVSIGKYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM16 <SEQ ID 3224>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPGRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNAGSLAGTGTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKRFEGRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVVSIGKYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFREL TGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM17 <SEQ ID 3225>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEPEVLKGD RRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFREL TGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPL FVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM18 <SEQ ID 3226>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEPEVLKGD RRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
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DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPL FVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM19 <SEQ ID 3227>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVPVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPEVLKGD RRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPL FVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM20 <SEQ ID 3228>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEPEVLKGD RRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPL FVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM21 <SEQ ID 3229>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEPEVLKGD RRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPL FVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM22 <SEQ ID 3230>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEPEVLKGD RRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMQNPQRLAEVLGQNPSYIFFREL TGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPL FVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM23ASBC <SEQ ID 3231>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEPEVLKGD RRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL

KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGETAGK
MKEPGYVWQLLPNGMKPEYRP*

ZM24 <SEQ ID 3232>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVLEFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGKYMADKGYL
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM25 <SEQ ID 3233>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVLEFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGKYMADKGYL
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM26 <SEQ ID 3234>

MKKYLFRAALYGI AAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVLEFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGTSMQGIKAYMQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM27BC <SEQ ID 3235>

MKKYLFRAALYGI AAILAACQSKSIQTFPQPDTSVINGPDRPAGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVLEFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGETAGK
MKEPGYVWQLLPNGMKPEYRP*

ZM28 <SEQ ID 3236>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVLEFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM29ASBC <SEQ ID 3237>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVLEFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLVATHPITR KALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM31ASBC <SEQ ID 3238>

MKKHLFRAALYGIAAAILAACQSKSIQTFFPQPDTSIIKGPDRPAGIPDPAGTTVGGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
 LVRI RQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYVFFRELAGSGNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM32ASBC <SEQ ID 3239>

MKKHLRSALYGIAAAILAACQSRSIQTFFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRGGKA
 LVRI RQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYI FFRELAGSGGDPVGALGTPLMGGYAGA
 IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM33ASBC <SEQ ID 3240>

MKKHLRSALYGIAAAILAACQSRSIQTFFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
 YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRGGKN
 LVRI RQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYI FFRELAGSGNEGPVGALGTPLMGEYAGA
 IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM96 <SEQ ID 3241>

MKKYLFRAALYGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
 LVRI RQTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYI FFRELAGSSNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

Figure 23 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 919, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 16

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

Table 7: Oligonucleotides used for PCR to amplify complete or partial ORFs

ORF	primer	Sequence	Restriction sites
001	Forward	CGCGGATCCCATATG-TGGATGGTGCTGGTCAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCCGTCTTGTCCAC	XhoI
003	Forward	CGCGGATCCCATATG-GTCGTATTCGTGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAATCATGAACACGCGC	XhoI
005	Forward	CGCGGATCCCATATG-GACAATATTGACATGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATCACATCCGCCCCG	XhoI
006	Forward	CGCGGATCCCATATG-CTGCTGGTGCTGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGTTCCGGCTTTGATGT	XhoI
007	Forward	CGCGGATCCCATATG-GCCGACAACAGCATCAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAGGCGTTCATGATATAAG	XhoI
008	Forward	CGCGGATCCCATATG-AACAACAGACATTTTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCTGTCCGGTAAAAGAC	XhoI
009	Forward	CGCGGATCCCATATG-CCCCGCGCTGCT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGGCTTTTGCCACGTTTT	XhoI
011	Forward	CGCGGATCCCATATG-AAGACACACCGCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCGGTCAGTACGGT	XhoI
012	Forward	CGCGGATCCCATATG-CTCGCCCGTTGCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCGGGGAAGAGGCAC	XhoI
013	Forward	CGCGGATCCCATATG-CCTTTGACCATGCT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGATTCGGCAAAAAAATCT	XhoI
018	Forward	CGCGGATCCCATATG-CAGCAGAGGCAGTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGAGGCGAACGCC	XhoI
019	Forward	AAAGAATTC-CTGCCAGCCGGCAAGACCCCGGC	Eco RI
	Reverse	AAACTGCAG-TCAGCGGGCGGGGACAATGCCCAT	Pst I
023	Forward	AAAGAATTC-AAAGAATATTCGGCATGGCAGGC	Eco RI
	Reverse	AAACTGCAG-TTACCCCCAAATCACTTTAACTGA	Pst I
025	Forward	AAAGAATTC-TGCGCCACCCAACAGCCTGCTCC	Eco RI
	Reverse	AAACTGCAG-TCAGAACGCGATATAGCTGTTCGG	Pst I
031	Forward	CGCGGATCCCATATG-GTCTCCCTTCGCTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATGTAAGACGGGGACAAC	XhoI
032	Forward	CGCGGATCCCATATG-CGGCGAAACGTGC	BamHI-

	Reverse	CCCGCTCGAG-CTGGTTTTTTGATATTTGTG	NdeI
033	Forward	CGCGGATCCCATATG-GCGGCGGCAGACA	XhoI
	Reverse	CCCGCTCGAG-ATTTGCCGCATCCCGAT	BamHI-
034	Forward	CGCGGATCCCATATG-GCCGAAAACAGCTACGG	NdeI
	Reverse	CCCGCTCGAG-TTTGACGATTTGGTTCAATT	XhoI
036	Forward	CGCGGATCCCATATG-CTGAAGCCGTGCG	BamHI-
	Reverse	CCCGCTCGAG-CCGGACTGCGTATCGG	NdeI
038	Forward	CGCGGATCCCATATG-ACCGATTTCGCCA	XhoI
	Reverse	CCCGCTCGAG-TTCTACGCCGTAAGTCC	BamHI-
039	Forward	CGCGGATCCCATATG-CCGTCCGAACCGC	NdeI
	Reverse	CCCGCTCGAG-TAGGATGACGAGGTAGG	XhoI
041	Forward	CGCGGATCCCATATG-TTCGTGCGCGAACCGC	BamHI-
	Reverse	CCCGCTCGAG-GCCCAAAAACCTTTTCAA	NdeI
042	Forward	CGCGGATCCCATATG-ACGATGATTTGCTTGC	XhoI
	Reverse	CCCGCTCGAG-TTTGCAGCCTGCATTTGAC	BamHI-
043	Forward	AAAAAAGGTACC-ATGGTTGTTTCAAATCAAATATC	NdeI
	Reverse	AAACTGCAG-TTATTGCGCTTCACCTTCGCGCGC	XhoI
043a	Forward	AAAAAAGGTACC-GCAAAAGTGCATGGCGGCTTGGACGGTGC	Kpn I
	Reverse	AAAAAACTGCAG-TTAATCCTGCAACACGAATTCGCCCCGTCCG	Pst I
044	Forward	CGCGGATCCCATATG-CCGTCCGACTAGAG	Kpn I
	Reverse	CCCGCTCGAG-ATGCGCTACGGTAGCCA	Pst I
046	Forward	AAAGAATTC-ATGTCGGCAATGCTCCCGACAAG	BamHI-
	Reverse	AAACTGCAG-TCACTCGGCGACCCACACCGTGAA	NdeI
047	Forward	CGCGGATCCCATATG-GTCATCATAACAGGCG	XhoI
	Reverse	CCCGCTCGAG-TCCGAAAAAGCCCATTTTG	Eco RI
048	Forward	AAAGAATTC-ATGCTCAACAAAGGCGAAGAATTGCC	Pst I
	Reverse	AAACTGCAG-TCAAGATTCGACGGGGATGATGCC	Eco RI
049	Forward	AAAGAATTC-ATGCGGGCGCAGGCGTTTGATCAGCC	Pst I
	Reverse	AAACTGCAG-AAGGCGTATCTGAAAAAATGGCAG	BamHI-
050	Forward	CGCGGATCCCATATG-GGCGCGGGCTGG	NdeI
	Reverse	CCCGCTCGAG-AATCGGGCCATCTTCGA	XhoI
052	Forward	AAAAAAGAATTC-ATGGCTTTGGTGCGGAGGAAAC	Eco RI
	Reverse	AAAAAAGTCGAC-TCAGGCGGCGTTTTTCACCTTCCT	Sal I
052a	Forward	AAAAAAGAATTC-GTGGCGGAGGAAACGGAAATATCCGC	Eco RI

	Reverse	AAAAAACTGCAG-TTAGCTGTTTTTGGAAACGCCGTCCAACCC	Pst I
073	Forward	CGCGGATCCCATATG-TGTATGCCATATAAGAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACCGGATTGTCCGAC	XhoI
075	Forward	CGCGGATCCCATATG-CCGTCTTACTTCATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCACCAATGCCGATTATTT	XhoI
077a	Forward	AAAAAAGAATTC-GGCGGCATTTTCATCGACACCTTCCT	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGAACATCTGCACAAACGCAAT	Pst I
080	Forward	AAAGAATTC-GCGTCCGGGCTGGTTTGGTTTACAATTC	Eco RI
	Reverse	AAACTGCAG-CTATTCTTCGGATTCTTTTTCGGG	Pst I
081	Forward	AAAGAATTC-ATGAAACCACTGGACCTAAATTTTCATCTG	Eco RI
	Reverse	AAACTGCAG-TCACTTATCCTCCAATGCCTC	Pst I
082	Forward	AAAGAATTC-ATGTGGTTGTTGAAGTTGCCTGC	Eco RI
	Reverse	AAACTGCAG-TTACGCGGATTTCGGCAGTTGG	Pst I
084	Forward	AAAGAATTC-TATCACCCAGAATATGAATACGGCTACCG	Eco RI
	Reverse	AAACTGCAG-TTATACTTGGGCGCAACATGA	Pst I
085	Forward	CGCGGATCCCATATG-GGTAAAGGGCAGGACT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CAAAGCCTTAAACGCTTCG	XhoI
086	Forward	AAAAAAGGTACC-TATTTGGCATCAAAAGAAGGCGG	Kpn I
	Reverse	AAACTGCAG-TTACTCCACCCGATAACCGCG	Pst I
087	Forward	AAAGAATTC-ATGGGCGGTAAAACCTTTATGC	Eco RI
	Reverse	AAACTGCAG-TTACGCCGCACACGCAATCGC	Pst I
087a	Forward	AAAAAAGAATTC-AAGCTATTAGGCGTGCCGATTGTGATTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCTGCAAGATGCCAGCTTGCC	Pst I
088	Forward	AAAAAAGAATTC-ATGTTTTTATGGCTCGCACATTTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAGCGGATTTTGAGGGTACTCAAACC	Pst I
089	Forward	CGCGGATCCCATATG-CCGCCCAAATCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCGCATACCAAAGCCA	XhoI
090	Forward	CGCGGATCCCATATG-CGCATAGTCGAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAAAACGGCGGTACG	XhoI
091	Forward	AAAGAATTC-ATGGAAATACCCGTACCGCCGAGTCC	Eco RI
	Reverse	AAACTGCAG-TCAGCGCAGGGGGTAGCCCAAGCC	Pst I
092	Forward	AAAGAATTC-ATGTTTTTTTATTTCAATCCG	Eco RI
	Reverse	AAACTGCAG-TCAAATCTGTTTCGACAATGC	Pst I
093	Forward	AAAGAATTC-ATGCAGAATTTTGGCAAAGTGGC	Eco RI
	Reverse	AAACTGCAG-CTATGGCTCGTCATACCGGGC	Pst I
094	Forward	AAAGAATTC-ATGCCGTCACGGAAGCGCATCAACTC	Eco RI
	Reverse	AAACTGCAG-TTATCCCGGCCATACCGCCGAACA	Pst I
095	Forward	AAAGAATTC-ATGTCCTTTTCATTTGAACATGGACGG	Eco RI
	Reverse	AAACTGCAG-TCAACGCCGCAGGCACTAACGCCC	Pst I
096	Forward	AAAGAATTC-ATGGCTCGTCATACCGGGCAGGG	Eco RI

	Reverse	AAACTGCAG-TCAAAGGAAAAGGCCGTCTGAAAAGCG	Pst I
097	Forward	AAAGAATTC-ATGGACACTTCAAAACAAACACTGTTG	Eco RI
	Reverse	AAACTGCAG-TCAGCCCAAATACCAGAATTTTCAG	Pst I
098	Forward	AAAGAATTC-GATGAACGCAGCCCAGCATGGATACG	Eco RI
	Reverse	AAACTGCAG-TTACGACATTCTGATTTGGCA	Pst I
102	Forward	AAAAAAGAATTC-GGCCTGATGATTTTGGAAAGTCAACAC	Eco RI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
105	Forward	CGCGGATCCCATATG-TCCGCAAACGAATACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGTCTGCCAGTTTCAG	XhoI
107	Forward	AAAAAAGAATTC- CTGATGATTTTGGGAAGTCAACACCCATTATCC	Eco RI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
107b	Forward	AAAAAAGAATTC- GATACCCAAGCCCCCGCCGGCACAACACTACTG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGCGTGCCTTTAAAGTATTTGAGCAGGCTGGAGAC	Pst I
108	Forward	AAAGAATTC-ATGTTGCCGGGCTTCAACCG	Eco RI
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Pst I
108a	Forward	AAAAAAGAATTC-GGTAACACATTCGGCAGCTTAGACGGTGG	Eco RI
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Pst I
109	Forward	AAAGAATTC-ATGTATTATCGCCGGGTTATGGG	Eco RI
	Reverse	AAACTGCAG-CTAGCCCAAAGATTTGAAGTGTTT	Pst I
111	Forward	CGCGGATCCCATATG-TGTTCGGAACAAACCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGAGCAGTTTTTCAA	XhoI
114	Forward	CGCGGATCCCATATG-GCTTCCATCACTTCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATCCGCGAAATCGTC	XhoI
117	Forward	AAAAAAGGTACC-ATGGTCGAAGAACTGGAAGTCTG	Kpn I
	Reverse	AAACTGCAG-TTAAAGCCGGGTAACGCTCAATAC	Pst I
118	Forward	AAAGTCGACATGTGTGAGTTCAAGGATATTATAAG	Sal I
	Reverse	AAAGCATGC-CTATTTTTTGTGTGAATAATCAAATC	Sph I
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATAATAATATCCCGCGCCC	XhoI
122	Forward	CGCGGATCCCATATG-GTCATGATTAAAATCCGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AATCTTGGTAGATTGGATTT	XhoI
125	Forward	AAAGAATTC-ATGTCGGGCAATGCCTCCTCTCC	Eco RI
	Reverse	AAACTGCAG-TCACGCCGTTTCAAGACG	Pst I
125a	Forward	AAAAAAGAATTC-ACGGCAGGCAGCACCGCCGCACAGGTTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTATTTTGCCACGTCGGTTTCTCCGGTGAACAACGC	Pst I
126	Forward	CGCGGATCCCATATG-CCGTCTGAAACCC	BamHI-

	Reverse	CCCGCTCGAG-ATATTCCGCCGAATGCC	NdeI
			XhoI
127	Forward	AAAGAATTC-ATGGAAATATGGAATATGTTGGACACTTG	Eco RI
	Reverse	AAACTGCAG-TTAAAGTGTTTCGGAGCCGGC	Pst I
127a	Forward	AAAAAAGAATTC-AAGGAACTGATTATGTGTCTGTCGGG	Eco RI
	Reverse	AAACTGCAG-TTAAAGTGTTTCGGAGCCGGC	Pst I
128	Forward	CGCGGATCCCATATG-ACTGACAACGCACT	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GACCGCGTTGTCGAAA	XhoI
130	Forward	CGCGGATCCCATATG-AAACAACCTCCGCGA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GAATTTTGCACCGGATTG	XhoI
132	Forward	AAAGAATTC-ATGGAACCCTTCAAAACCTTAATTTG	Eco RI
	Reverse	AAAAAACTGCAG-TCACCATGTCTGGCATTGAAAAAC	Pst I
134	Forward	CGCGGATCCCATATG-TCCCAAGAAATCCTC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CAGTTTGACCGAATGTTC	XhoI
135	Forward	CGCGGATCCCATATG-AAATACAAAAGAATCGTATT	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AAATTCGGTCAGAAGCAGG	XhoI
137	Forward	AAAAAAGGTACC-ATGATTACCCATCCCCAATTCGATCC	Kpn I
	Reverse	AAAAAACTGCAG-TCAGTGCTGTTTTTTCATGCCGAA	Pst I
137a	Forward	AAAAAAGAATTC-GGCCGCAAACACGGCATCGGCTTCCT	Eco RI
	Reverse	AAAAAACTGCAG-TTAAGCGGGATGACGCGGCAGCATACC	Pst I
138	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTGGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Xba I
141	Forward	AAAGAATTC-ATGAGCTTCAAAACCGATGCCGAAATCGC	Eco RI
	Reverse	AAACTGCAG-TCAGAACAAGCCGTGAATCACGCC	Pst I
142	Forward	CGCGGATCCCATATG-CGTGCCGATTTCATG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AAACTGCTGCACATGGG	XhoI
143	Forward	AAAAAAGAATTC- ATGCTCAGTTTCGGCTTTCTCGGCGTTCAGAC	Eco RI
	Reverse	AAAAAACTGCAG-TCAAACCCCGCCGTGTGTTTCTTTAAT	Pst I
144	Forward	AAAAAAGAATTC-GGTCTGATCGACGGGCGTGCCGTAAC	Eco RI
	Reverse	AAAAAATCTAGA-TCGGCATCGGCCGGCATATGTCCG	Xba I
146	Forward	AAAAAAGAATTC- CGCCAAGTCGTCATTGACCACGACAAAGTC	Eco RI
	Reverse	AAAAAACTGCAG-TTAGGCATCGGCAAATAGGAAACTGGG	Pst I
147	Forward	AAAAAAGAATTC-ACTGAGCAATCGGTGGATTTGGAAAC	Eco RI
	Reverse	AAAAAATCTAGA-TTAGGTAAAGCTGCGGCCCATTTGCGG	Xba I
148	Forward	AAAAAAGAATTC- ATGGCGTTAAAAACATCAAACCTTGGAACACGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGCCCTTCATACAGCCTTCGTTTTG	Xba I
149	Forward	CGCGGATCCCATATG-CTGCTTGACAACAAAGT	BamHI-

	Reverse	CCCGCTCGAG-AAACTTCACGTTACGCC	NdeI
150	Forward	CGCGGATCCCATATG-CAGAACACAAATCCG	XhoI
			BamHI-
			NdeI
	Reverse	CCCGCTCGAG-ATAAACATCACGCTGATAGC	XhoI
151	Forward	AAAAAAGAATTC- ATGAAACAAATCCGCAACATCGCCATCATCGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAATCCAGCTTTTAAAGTGGCGGCG	Pst I
152	Forward	AAAAAAGAATTC- ATGAAAAACAAAACCAAAGTCTGGGACCTCCC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGGACAGGAGCAGGATGGCGGC	Pst I
153	Forward	AAAAAAGAATTC-ATGGCGTTTGCTTACGGTATGAC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTCATGTTTTTCCGTTTCATT	Pst I
153a	Forward	AAAAAAGAATTC-CGGACTTCGGTATCGGTTCCCCAGCATTG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGCCGACGAAATACTCAGACTTTTCGG	Pst I
154	Forward	CGCGGATCCCATATG-ACTGACAACAGCCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCGGCTTCCTTTTCGGG	XhoI
155	Forward	AAAAAAGAATTC-ATGAAAATCGGTATCCACGCGAGTC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCCTTTCTTAAACATATTTCAGCAT	Pst I
156	Forward	AAAAAAGAATTC-GCACAGCAAAACGGTTTTGAAGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGCAGCCGCGACAAACAGCCC	Pst I
157	Forward	CGCGGATCCCATATG-AGGAACGAGGAAAAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AAAACACAATATCCCCGC	XhoI
158	Forward	AAAAAAGAATTC-GCGGAGCAGTTGGCGATGGCAAATTCTGC	Eco RI
	Reverse	AAAAAATCTAGA-TTATCCACAGAGATTGTTTCCAGTTC	Xba I
160	Forward	CGCGGATCCCATATG-GACATTCTGGACAAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTTTGCCCGCCTTCTTT	XhoI
163	Forward	AAAAAAGGTACC-ACCGTGCCGGATCAGGTGCAGATGTG	Kpn I
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCCACCTGCTCGTG	Xba I
163a	Forward	AAAAAAGAATTC-CGGCTGGTGCAGATAATGAGCCAGAC	Eco RI
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCCACCTGCTCGTG	Xba I
164	Forward	CGCGGATCCCATATG-AACCGGACTTATGCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTGTTTCCGTCAAACCTGC	XhoI
165	Forward	CGCGGATCCGCTAGC-GCTGAAGCGACAGACG	BamHI-
			NheI
	Reverse	CCCGCTCGAG-AATATCCAATACTTTTCGCG	XhoI
206	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTCTGTAAAAAAAGTATGTGC	XhoI
209	Forward	CGCGGATCCCATATG-CTGCGGCATTTAGGA	BamHI-
			NdeI

	Reverse	CCCGCTCGAG-TACCCCTGAAGGCAAC	XhoI
211	Forward	AAAAAAGAATTC-ATGTTGCGGGTTGCTGCTGC	Eco RI
	Reverse	AAAAAACTGCAG-CTATCCTGCGGATTGGCATTGAAA	Pst I
212	Forward	CGCGGATCCCATATG-GACAATCTCGTATGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGGGTTAGATCCTTCC	XhoI
215	Forward	CGCGGATCCCATATG-GCATGGTTGGGTCGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATATCTTTTGTATCATAAATC	XhoI
216	Forward	CGCGGATCCCATATG-GCAATGGCAGAAAACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TACAATCCGTGCCGCC	XhoI
217	Forward	CGCGGATCCCATATG-GCGGATGACGGTGTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACCCCGAATATCGAATCC	XhoI
218	Forward	CGCGGATCCCATATG-GTCGCGGTTCGATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TAACTCATAGAATCCTGC	XhoI
219	Forward	CGCGGATCCGCTAGC-ACGGCAAGGTTAAG	BamHI- NheI
	Reverse	CCCGCTCGAG-TTTAAACCATCTCCTCAAAAC	XhoI
223	Forward	CGCGGATCCCATATG-GAATTCAGGCACCAAGTA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCTTCCCGCGTGTC	XhoI
225	Forward	CGCGGATCCCATATG-GACGAGTTGACCAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTTCAGAAAGCGGGAC	XhoI
226	Forward	AAAGAATTC-CTTGCGATTATCGTGCGCACGCG	Eco RI
	Reverse	AAACTGCAG-TCAAAATCCCAAAACGGGGAT	Pst I
228	Forward	CGCGGATCCCATATG-TCGCAAGAAGCCAAACAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	XhoI
229	Forward	CGCGGATCCCATATG-CAAGAGGTTTTGCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACACAATATAGCGGATGAAC	XhoI
230	Forward	CGCGGATCCCATATG-CATCCGGGTGCCGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAGTTTGGCGGCTTCGG	XhoI
232	Forward	AAAAAAGAATTC-ATGTACGCTAAAAAAGGCGGTTTGGG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGGTTTTTTCCTGATTGCCGCCGC	Pst I
232a	Forward	AAAAAAGAATTC-GCCAAGGCTGCCGATACACAAATTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTAAACATTGTCGTTGCCGCCAGATG	Pst I
233	Forward	CGCGGATCCCATATG-GCGGACAAACCCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGGCATTGAGCAG	XhoI
234	Forward	CGCGGATCCCATATG-GCCGTTTCACTGACCG	BamHI-

	Reverse	GCCCAAGCTT-ACGGTTGGATTGCCATG	NdeI
235	Forward	CGCGGATCCCATATG-GCCTGCCAAGTTCAAA	Hind III
	Reverse	CCCGCTCGAG-TTTGGGCTGCTCTTC	BamHI-
236	Forward	CGCGGATCCCATATG-GCGCGTTTCGCCTT	NdeI
	Reverse	CCCGCTCGAG-ATGGGTCGCGCGCCGT	XhoI
238	Forward	CGCGGATCCGCTAGC-AACGGTTTGGATGCCCCG	BamHI-
	Reverse	CCCGCTCGAG-TTTGTCTAAGTTCCTGATATG	NdeI
239	Forward	CCGGAATTCTACATATG-CTCCACCATAAAGGTATTG	XhoI
	Reverse	CCCGCTCGAG-TGGTGAAGAGCGGTTTAG	EcoRI-
240	Forward	CGCGGATCCCATATG-GACGTTGGACGATTTC	NdeI
	Reverse	CCCGCTCGAG-AAACGCCATTACCCGATG	XhoI
241	Forward	CCGGAATTCTACATATG-CCAACACGTCCAAC	BamHI-
	Reverse	CCCGCTCGAG-GAATGCGCCTGTAATTAATC	NdeI
242	Forward	CGCGGATCCCATATG-ATCGGCAAACCTTGTTG	XhoI
	Reverse	GCCCAAGCTT-ACCGATACGGTCGCAG	BamHI-
243	Forward	CGCGGATCCCATATG-ACGATTTTTTCGATGCTGC	NdeI
	Reverse	CCCGCTCGAG-CGACTTGGTACCGCG	HindIII
244	Forward	CGCGGATCCCATATG-CCGTCTGAAGCCC	BamHI-
	Reverse	CCCGCTCGAG-TTTTTTCGGTAGGGGATTT	NdeI
246	Forward	CGCGGATCCCATATG-GACATCGGCAGTGC	XhoI
	Reverse	CCCGCTCGAG-CCCGCGCTGCTGGAG	BamHI-
247	Forward	CGCGGATCCCATATG-GTCGGATCGAGTTAC	NdeI
	Reverse	CCCGCTCGAG-AAGTGTTCTGTTTGCGCA	XhoI
248	Forward	CGCGGATCCCATATG-CGCAAACAGAACACT	BamHI-
	Reverse	CCCGCTCGAG-CTCATCATTATTGCTAACA	NdeI
249	Forward	CGCGGATCCCATATG-AAGAATAATGATTGCTTC	XhoI
	Reverse	CCCGCTCGAG-TTCCCGACCTCCGAC	BamHI-
251	Forward	CGCGGATCCCATATG-CGTGCTGCGGTAGT	NdeI
	Reverse	CCCGCTCGAG-TACGAAAGCCGGTCGTG	XhoI
253	Forward	AAAAAAGAATTC-ATGATTGACAGGAACCGTATGCTGCG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Pst I

253a	Forward	<u>AAAAAAGAATTC</u> -AAAATCCTTTTGAAAACAAGCGAAAACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Pst I
254	Forward	<u>AAAAAAGAATTC</u> -ATGTATACAGGCGAACGCTTCAATAC	Eco RI
	Reverse	AAAAAAATCTAGA-TCAGATTACGTAACCGTACACGCTGAC	Xba I
255	Forward	CGCGGATCCCATATG-GCCGCGTTGCGTTAC	BamHI-
	Reverse	CCCGCTCGAG-ATCCGCAATACCGACCAG	NdeI
			XhoI
256	Forward	CGCGGATCCGCTAGC-TTTTAACACCGCCGGAC	BamHI-
	Reverse	CCCGCTCGAG-ACGCCTGTTTGTGCGG	NheI
			XhoI
257	Forward	CGCGGATCCCATATG-GCGGTTTCTTTCTCCTG	BamHI-
	Reverse	CCCGCTCGAG-GCGCGTGAATATCGCG	NdeI
			XhoI
258	Forward	<u>AAAAAAGAATTC</u> -GATTATTTCTGGTGGATTGTTGCGTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
258a	Forward	<u>AAAAAAGAATTC</u> -GCGAAGGCGGTGGCGCAAGGCGA	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
259	Forward	CGCGGATCCCATATG-GAAGAGCTGCCTCCG	BamHI-
	Reverse	CCCGCTCGAG-GGCTTTTCCGGCGTTT	NdeI
			XhoI
260	Forward	CGCGGATCCCATATG-GGTGCGGGTATGGT	BamHI-
	Reverse	CCCGCTCGAG-AACAGGGCGACACCCT	NdeI
			XhoI
261	Forward	<u>AAAAAAGAATTC</u> -CAAGATACAGCTCGGGCATTTCG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAACCAACAAGCCTTGGTCACT	Pst I
263	Forward	CGCGGATCCCATATG-GCACGTTTAACCGTA	BamHI-
	Reverse	CCCGCTCGAG-GGCGTAAGCCTGCAATT	NdeI
			XhoI
264	Forward	<u>AAAAAAGGTACC</u> -GCCGACGCAGTGGTCAAGGCAGAA	Kpn I
	Reverse	AAACTGCAG-TCAGCCGGCGGTCAATACCGCCCG	Pst I
265	Forward	<u>AAAAAAGAATTC</u> -GCGGAGGTCAAGAGAAGGTGTTTG	Eco RI
	Reverse	AAAAAACTGCAG-TTACGAATACGTCGTCAAAATGGG	Pst I
266	Forward	<u>AAAGAATTC</u> -CTCATCTTTGCCAACGCCCCCTTC	Eco RI
	Reverse	AAACTGCAG-CTATTCCCTGTTGCGCGTGTGCCA	Pst I
267	Forward	<u>AAAGAATTC</u> -TTCTTCCGATTTCGATGTTAATCG	Eco RI
	Reverse	AAACTGCAG-TTAGTAAAAACCTTTCTGCTTGGC	Pst I
269	Forward	<u>AAAGAATTC</u> -TGCAAACCTTGCGCCACGTGCCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
269a	Forward	<u>AAAAAAGAATTC</u> -GACTTTATCCAAAACACGGCTTCGCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
270	Forward	<u>AAAGAATTC</u> -GCCGTCAAGCTCGTTTTGTGCAATG	Eco RI
	Reverse	AAACTGCAG-TTATTCGGCGGTAAATGCCGTCTG	Pst I
271	Forward	CGCGGATCCCATATG-CCTGTGTGCAGCTCGAC	BamHI-
	Reverse	CCCGCTCGAG-TCCCAGCCCCGTGGAG	NdeI
			XhoI

272	Forward	AAAGAATTC-ATGACCGCAAAGGAAGAACTGTTTCGC	Eco RI
	Reverse	AAACTGCAG-TCAGAGCAGTTCCAAATCGGGGCT	Pst I
273	Forward	AAAGAATTC-ATGAGTCTTCAGGCGGTATTTATATACCC	Eco RI
	Reverse	AAACTGCAG-TTACGCGTAAGAAAAAACTGC	Pst I
274	Forward	CGCGGATCCCATATG-ACAGATTTGGTTACGGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGCTTTCAGTATTATTGAA	XhoI
276	Forward	AAAAAAGAATTC- ATGATTTTGCCGTCGTCATCACGATGATGCG	Eco RI
	Reverse	AAAAAACTGCAG-CTACACCACCATCGGCGAATTTATGGC	Pst I
277	Forward	AAAAAAGAATTC-ATGCCCCGCTTTGAGGACAAGCTCGTAGG	Eco RI
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Pst I
277a	Forward	AAAAAAGAATTC-GGGGCGGCGGCTGGGTTGGACGTAGG	Eco RI
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Pst I
278	Forward	AAAAAAGGTACC-GTCAAAGTTGTATTAATCGGGCCTTTGCC	Kpn I
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Pst I
278a	Forward	AAAAAAGAATTC-AAAACTCTCCTAATTCGTCATAGTCG	Eco RI
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Pst I
279	Forward	CGCGGATCCCATATG-TTGCCTGCAATCACGATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTAGAAGCGGGCGGCAA	XhoI
280	Forward	AAAAAAGGTACC-GCCCCCTGCCGTTGTAACCAG	Kpn I
	Reverse	AAAAAACTGCAG-TTATTGCTTCATCGCGTTGGTCAAGGC	Pst I
281	Forward	AAAAAAGAATTC-GCACCCGTCGGCGTATTCCTCGTCATGCG	Eco RI
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Xba I
281a	Forward	AAAAAAGAATTC-TCCTACCACATCGAAATTCCTTCCGG	Eco RI
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Xba I
282	Forward	AAAAAAGAATTC-CTTTACCTTGACCTGACCAACGGGCACAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAACCTGCCAGTTGCGGGAATATCGT	Pst I
283	Forward	CGCGGATCCCATATG-GCCGTCTTTACTTGGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGGCAGTATTTGTTTACG	XhoI
284	Forward	CGCGGATCCCATATG-TTGCCTGCAAAAGAATCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCGACTTTGCAAAAAGT	XhoI
286	Forward	CGCGGATCCCATATG-GCCGACCTTCCGAAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAAGCGCGTTCCCAAG	XhoI
287	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG	EcoRI- NheI
	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTTGCC	XhoI
288	Forward	CGCGGATCCCATATG-CACACCGGACAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGTATCAAAGACTTGCGT	XhoI
290	Forward	CGCGGATCCCATATG-GCGGTTTGGGGCGGA	BamHI-

	Reverse	CCCGCTCGAG-TCGGCGCGGCGGGC	NdeI
292	Forward	CGCGGATCCCATATG-TGCGGGCAAACGCCC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTGATTTTTGCGGATGATTT	NdeI
294	Forward	AAAAAAGAATTC-GTCTGGTCGATTCGGGTTGTCAGAAC	XhoI
	Reverse	AAAAAACTGCAG-TTACCAGCTGATATAAAACATCGCTTT	Eco RI
295	Forward	CGCGGATCCCATATG-AACCGGCCGGCCTCC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CGATATTTGATTCCGTTGC	NdeI
297	Forward	AAAAAAGAATTC-GCATAATTGCTTCGACAGAGAG	XhoI
	Reverse	AAAAAACTGCAG-TCAATCCGATTGCGACACGGT	Eco RI
298	Forward	AAAAAAGAATTC-CTGATTGCCGTGTGGTTCAGCCAAAACCC	Pst I
	Reverse	AAAAAACTGCAG-TCATGGCTGTGTACTTGATGGTTGCGT	Eco RI
299	Forward	CGCGGATCCGCTAGC-CTACCTGTCGCCTCCG	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-TTGCCTGATTGCAGCGG	NheI
302	Forward	AAAAAAGAATTC-ATGAGTCAAACCGATACGCAACG	XhoI
	Reverse	AAAAAACTGCAG-TTAAGGTGCGGGATAGAATGTGGGCGC	Eco RI
305	Forward	AAAAAAGGTACC-GAATTTTTACCGATTTCAGCACCGGA	Pst I
	Reverse	AAAAAACTGCAG-TCATTCCCAACTTATCCAGCCTGACAG	Kpn I
305a	Forward	AAAAAAGGTACC-TCCCGTTCGGGCAGTACGATTATGGG	Pst I
	Reverse	AAAAAACTGCAG-TTACAAACCGACATCATGCAGGGTGAA	Kpn I
306	Forward	CGCGGATCCCATATG-TTTATGAACAAATTTTCCC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CCGCATCGGCAGAC	NdeI
308	Forward	CGCGGATCCCATATG-TTAAATCGGGTATTTTATC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-ATCCGCCATTCCCTGC	NdeI
311	Forward	AAAAAAGGTACC-ATGTTCAAGTTTTGGCTGGGTGTTT	XhoI
	Reverse	AAACTGCAG-ATGTTTCATATTCCTTCGCTTCGGC	Kpn I
312	Forward	AAAAAAGGTACC-ATGAGTATCCCATCCGGCGAAATT	Pst I
	Reverse	AAACTGCAG-TCAGTTTTTCATCGATTGAACCGG	Kpn I
313	Forward	AAAAAAGAATTC-ATGGACGACCCGCGCACCTACGGATC	Pst I
	Reverse	AAAAAACTGCAG-TCAGCGGCTGCCGCCGATTTTGCT	Eco RI
401	Forward	CGCGGATCCCATATG-AAGGCGGCAACACAGC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CCTTACGTTTTTCAAAGCC	NdeI
402	Forward	AAAAAAGAATTC-GTGCCTCAGGCATTTTCATTTACCCTTGC	XhoI
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	Eco RI
402a	Forward	AAAAAAGAATTC-AGGCTGATTGAAAACAAACACGG	Xba I
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	Eco RI
406	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG	Xba I
			BamHI-
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG	NdeI
			XhoI

501	Forward	CGCGGATCCCATATG-GCAGGCGGAGATGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGTGTGATGTTCACCC	XhoI
502	Forward	CGCGGATCCCATATG-GTAGACGCGCTTAAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCTGCATGGCGGCG	XhoI
503	Forward	CGCGGATCCCATATG-TGTTCTGGGGAAAGGCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCGCGCATTCCTCGCA	XhoI
504	Forward	CGCGGATCCCATATG-AGCGATATTGAAGTGACG	BamHI- NdeI
	Reverse	GCCCAAGCTT-TGATTCAAGTCCTTGCCG	HindIII
505	Forward	CGCGGATCCCATATG-TTTCGTTTACAATTCAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGTTTTATAGCGG	XhoI
510	Forward	CGCGGATCCCATATG-CCTTCGCGGACAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCACTGGCAGCG	XhoI
512	Forward	CGCGGATCCCATATG-GGACATGAAGTAACGGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGAATAGCCTTTGACG	XhoI
515	Forward	CGCGGATCCCATATG-GAGGAAATAGCCTTCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAATGCCGCAAAGCATC	XhoI
516	Forward	CGCGGATCCCATATG-TGTACGTTGATGTTGTGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGCGGGCGGCATC	XhoI
517	Forward	CGCGGATCCCATATG-GGTAAAGGTGTGGAAATA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGCGCCCAGCCGT	XhoI
518	Forward	AAAGAATTC-GCTTTTTTACTGCTCCGACCGGAAGG	Eco RI
	Reverse	AAACTGCAG-TCAAATTTCACTCTGCCAC	Pst I
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC	XhoI
520	Forward	CGCGGATCCCATATG-CCTGCGCTTCTTTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATATTTACATTTCACTCGGC	XhoI
521	Forward	CGCGGATCCCATATG-GCCAAAATCTATACCTGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATACGCCCCAGTTCC	XhoI
522	Forward	CGCGGATCCCATATG-ACTGAGCCGAAACAC	BamHI- NdeI
	Reverse	GCCCAAGCTT-TTCTGATTTCAAATCGGCA	HindIII
523	Forward	CGCGGATCCCATATG-GCTCTGCTTTCCGCG	BamHI- NdeI

	Reverse	CCCGCTCGAG-AGGGTGTGTGATAATAAGAAG	XhoI
525	Forward	CGCGGATCCCATATG-GCCGAAATGGTTCAAATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCCGTGCATATCATAAA	XhoI
527	Forward	AAAGAATTC-TTCCCTCAATGTTGCCGTTTTTCG	Eco RI
	Reverse	AAACTGCAG-TTATGCTAAACTCGAAACAAATTC	Pst I
529	Forward	CGCGGATCCGCTAGC-TGCTCCGGCAGCAAAAC	BamHI- NheI
	Reverse	GCCCAAGCTT-ACGCAGTTCGGAATGGAG	HindIII
530	Forward	CGCGGATCCCATATG-AGTGCGAGCGCGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGACCGACTGATTCCG	XhoI
531	Forward	AAAAAAGAATTC-TATGCCGCCGCCTACCAAATCTACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAAACACAGCGCCGTGCCGACGACAAG	Pst I
532	Forward	AAAAAAGAATTC-ATGAGCGGTCAGTTGGGCAAAGGTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTGTTCCAAGTGGTCGGTATCAAA	Pst I
532a	Forward	AAAAAAGAATTC-TTGGGTGTCGCGTTTGAGCCGGAAGT	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTGTTCCAAGTGGTCGGTATCAAA	Pst I
535	Forward	AAAGAATTC-ATGCCCTTTCCCGTTTTTCAGAC	Eco RI
	Reverse	AAACTGCAG-TCAGACGACCCCGCCTTCCCC	Pst I
537	Forward	CGCGGATCCCATATG-CATACCCAAAACCAATCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCCTGCAAATAAAGGGTT	XhoI
538	Forward	CGCGGATCCCATATG-GTCGAGCTGGTCAAAGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGGCATTTCGGTTTCGTC	XhoI
539	Forward	CGCGGATCCGCTAGC-GAGGATTTGCAGGAAA	BamHI- NheI
	Reverse	CCCGCTCGAG-TACCAATGTCGGCAAATC	XhoI
542	Forward	AAAGAATTC-ATGCCGTCTGAAACCGTGTC	Eco RI
	Reverse	AAACTGCAG-TTACCGCGAACCGGTCAGGAT	Pst I
543	Forward	AAAAAAGAATTC-GCCTTCGATGGCGACGTTGTAGGTAC	Eco RI
	Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
543a	Forward	AAAAAAGAATTC-GGCAAAACTCGTCATGAATTTGC	Eco RI
	Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
544	Forward	AAAGAATTC-GCGCCCGCCTTCTCCCTGCCCGACCTGCACGG	Eco RI
	Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
544a	Forward	AAAAAAGAATTC- GCAAATGACTATAAAAAACAAAAACTTCCAAGTACTTGC	Eco RI
	Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
547	Forward	AAAGAATTC-ATGTTCTGTAGATAACGGATTTAATAAAAC	Eco RI
	Reverse	AAACTGCAG-TTAACAACAAAAACAAACCGCTT	Pst I
548	Forward	AAAGAATTC-GCCTGCAACCTCAAGACAACAGTGCGGC	Eco RI

	Reverse	AAACTGCAG-TCAGAGCAGGGTCCTTACATCGGC	Pst I
550	Forward	AAAAAAGTCGAC- ATGATAACGGACAGGTTTCATCTCTTTTCATTTTCC	Sal I
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAAATCCCC	Pst I
550a	Forward	AAAAAAGAATTC-GTAAATCACGCCTTTGGAGTCGCAAACGG	Eco RI
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAAATCCCC	Pst I
552	Forward	AAAAAAGAATTC-TTGGCGCGTTGGCTGGATAC	Eco RI
	Reverse	AAACTGCAG-TTATTTCTGATGCCTTTTCCCAAC	Pst I
554	Forward	CGCGGATCCCATATG-TCGCCCCGCGCCCAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCCCTGTCAGACAC	XhoI
556	Forward	AAAGAATTC-GCGGGCGGTTTTGTTTGGACATCCCG	Eco RI
	Reverse	AAACTGCAG-TTAACGGTGCGGACGTTTCTGACC	Pst I
557	Forward	CGCGGATCCCATATG-TGCGGTTTCCACCTGAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCCGCCTTCAGAAAGG	XhoI
558	Forward	AAAGAATTC-GAGCTTTATATGTTTCAACAGGGGACGGC	Eco RI
	Reverse	AAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
558a	Forward	AAAAAAGAATTC-ATTAGATTCTATCGCCATAAACAGACGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
560	Forward	AAAAAAGAATTC- TCGCCTTTCCGGGACGGGGCGCACAAGATGGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATGCGGTTTCAGACGGCATTTTGGC	Pst I
561	Forward	CCGGAATTCTACATATG-ATACTGCCAGCCCGT	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCAAGCTTTCTTCAGATG	XhoI
562	Forward	CGCGGATCCCATATG-GCAAGCCCGTCGAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGACCAACTCCAACCTCGT	XhoI
565	Forward	CGCGGATCCCATATG-AAGTCGAGCGCGAAATAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCATTGATCGGCGGC	XhoI
566	Forward	CGCGGATCCCATATG-GTCGGTGGCGAAGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCATGGGCGAAGTCA	XhoI
567	Forward	CCGGAATTCTACATATG-AGTGCGAACATCCTTG	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCCCCGACACCCTCG	XhoI
568	Forward	CGCGGATCCCATATG-CTCAGGGTCAGACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGCGGCGTTTCAG	XhoI
569	Forward	AAAAAAGAATTC-CTGATTGCCTTGTGGGAATATGCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TTATGCATAGACGCTGATAACGGCAAT	Pst I
570	Forward	CGCGGATCCCATATG-GACACCTTCCAAAAAATCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGGCGTTTCATTTCTTT	XhoI

571	Forward	AAAAAAGAATTC- ATGGGTATTGCCGGCGCCGTAAATGTTTTGAACCC	Eco RI
	Reverse	AAAAAACTGCAG-TTATGGCCGACGCGCGGCTACCTGACG	Pst I
572	Forward	CGCGGATCCCATATG-GCGCAAAAAGGCAAAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCAGTGTGCCGATA	XhoI
573	Forward	CGCGGATCCCATATG-CCCTGTTTGTGCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGGTGTTCATTTCCGCC	XhoI
574	Forward	CGCGGATCCCATATG-TGGTTTGCCGCCCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACTTCGATTTTATTCGGG	XhoI
575	Forward	CGCGGATCCCATATG-GTTTCGGGCGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGAATCTGAACAG	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATTTACTTTTTTGATGTCGAC	XhoI
577	Forward	CGCGGATCCCATATG-GAAAGGAACGGTGTATTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGCTGTTTGGTAGATTCCG	XhoI
578	Forward	CGCGGATCCCATATG-AGAAGGTTCGTACAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCAACGCCTCCACG	XhoI
579	Forward	CGCGGATCCCATATG-AGATTGGGCGTTTCCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGAATTGATGATGTGTATGT	XhoI
580	Forward	CGCGGATCCCATATG-AGGCAGACTTCGCCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACTTCCCCCGAAGTG	XhoI
581	Forward	CGCGGATCCCATATG-CACTTCGCCCAGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCCGTTTGGCTTTGG	XhoI
582	Forward	AAAAAAGAATTC-TTTGGAGAGACCGCGCTGCAATGCGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATGCCGTCCAGTCGTTGAA	Xba I
583	Forward	AAAAAAGAATTC-ACTGCCGGCAATCGACTGCATAATCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGGAGGTCAATATGATGAAATTG	Pst I
584	Forward	AAAAAAGAATTC- GCGGCTGAAGCATTGAATTACAATATTGTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGAACTGAACCGTCCCATTGACGCT	Pst I
585	Forward	AAAAAAGGTACC-TCTTTCTGGCTGGTGCAGAACACCCTTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTTCGCACTTTTTTCTGTTTGGGA	Pst I
586	Forward	CGCGGATCCCATATG-GCAGCCCATCTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTCAGCGAATCAAGTTTC	XhoI
587	Forward	CGCGGATCCCATATG-GACCTGCCCTTGACGA	BamHI-

	Reverse	CCCGCTCGAG-AAATGTATGCTGTACGCC	NdeI
			XhoI
588	Forward	AAAAAAGAATTC-GCCGTCCTGACTTCCTATCAAGAACCAGG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTGTTTTTGGGCAGTTTCACTTC	Pst I
589	Forward	AAAAAAGAATTC- ATGCAACAAAAAATCCGTTTCCAAATCGAAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAATCGATTTTTACCCGTTTCAGGCG	Pst I
590	Forward	AAAAAAGAATTC-ATGAAAAAACCTTTGATTTCAAGTTGCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTGCTGCGGCTCTGAAACCAT	Pst I
591	Forward	AAAAAAGAATTC-CACTACATCGTTGCCAGATTGTGCGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAACCGAGCAGCCGGGTAACGTCGTT	Pst I
592a	Forward	AAAAAAGAATTC-CGCGATTACACCGCCAAGCTGAAAATGGG	Eco RI
	Reverse	AAAAAACTGCAG-TTACCAAACGTCGGATTGATACG	Pst I
593	Forward	CGCGGATCCGCTAGC-CTTGAACCTGAACGGACTC	BamHI- NheI
	Reverse	CCCGCTCGAG-GCGGAAGCGGACGATT	XhoI
594a	Forward	AAAAAAGAATTC-GGTAAGTTCGCCGTTTCAGGCCTTTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCGCCGTTTCTGACACTCGCG	Pst I
595	Forward	AAAAAAGAATTC-TGCCAGCCGCCGGAGGCGGAGAAAGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCAAGCCGAGTATGCCGCG	Pst I
596	Forward	CGCGGATCCCATATG-TCCCAACAATACGTC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCGTTACCGGTTTGT	XhoI
597	Forward	CGCGGATCCCATATG-CTGCTTCATGTCAGC	BamHI- NdeI
	Reverse	GCCCAAGCTT-ACGTATCCAGCTCGAAG	HindIII
601	Forward	CGCGGATCCCATATG-ATATGTTCCCAACCGGCAAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAACAATCCTCAGGCAC	XhoI
602	Forward	CGCGGATCCGCTAGC-TTGCTCCATCAATGC	BamHI- NheI
	Reverse	CCCGCTCGAG-ATGCAGCTGCTAAAAGCG	XhoI
603	Forward	AAAAAAGAATTC-CTGTCTCGCGTAGGCGGGGACGGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAGATGCCGGCAAGTTCGGC	Pst I
604	Forward	CGCGGATCCGCTAGC-CCCGAAGCGCACTT	BamHI- NheI
	Reverse	CCCGCTCGAG-GACGGCATCTGCACGG	XhoI
606a	Forward	AAAAAAGAATTC-CGCGAATACCGCGCCGATGCGGGCGC	Eco RI
	Reverse	AAAAAACTGCAG-TTAAAGCGATTTGAGGCGGGCGATACG	Pst I
607	Forward	AAAAAAGAATTC-ATGCTGCTCGACCTCAACCGCTTTTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGGCCTTATGCGATCTGAC	Pst I
608	Forward	AAAAAAGAATTC-ATGTCCGCCCTCCTCCCCATCATCAACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGTCTATCCAAATGTCGCGTTC	Pst I
609	Forward	CGCGGATCCCATATG-GTTGTGGATAGACTCG	BamHI- NdeI

	Reverse	CCCGCTCGAG-CTGGATTATGATGTCTGTC	XhoI
610	Forward	CGCGGATCCCATATG-ATTGGAGGGCTTATGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCTTCAACATCTTTGCC	XhoI
611	Forward	CGCGGATCCCATATG-CCGTCTCAAACGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACGACTTTGAACGCGCAA	XhoI
613	Forward	CGCGGATCCCATATG-TCGCGTTCGAGCCG3	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCCTGTAAAATAAGCGGC	XhoI
614	Forward	CGCGGATCCCATATG-TCCGTCTGTGAGCGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCATACTGCGGCGTTC	XhoI
616	Forward	AAAAAAGAATTC-ATGTCAAACACAATCAAATGGTTGTCGG	Eco RI
	Reverse	AAAAAATCTAGA-TTAGTCCGGGCGGCAGGCAGCTCG	Xba I
619a	Forward	AAAAAAGAATTC-GGGCTTCTCGCCGCCTCGCTTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATTTTTTGTGTTTTAAACGAGATA	Pst I
622	Forward	CGCGGATCCCATATG-GCCGCCCTGCCTAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGTCCAAATGATAAATCTG	XhoI
624	Forward	CGCGGATCCCATATG-TCCCCGCGCTTTTACCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGATTCGGGCCTGCGC	XhoI
625	Forward	CGCGGATCCCATATG-TTTGCAACCAGGAAAATG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCAAATACCGCCTT	XhoI
627a	Forward	AAAAAAGAATTC-AAAGCAGGCGAGGCAGGCGCGCTGGG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGAATGAAACAGGGTACCCGTCATCAAGGC	Pst I
628	Forward	AAAAAAGGTACC-GCCTTACAAACATGGATTTTGCGTTC	Kpn I
	Reverse	AAAAAACTGCAG-CTACGCACCTGAAGCGCTGGCAA	Pst I
629a	Forward	AAAAAAGAATTC-GCCACCTTTATCGCGTATGAAAACGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACAACACCGCCGTCCGGTTCAAACC	Pst I
630a	Forward	AAAAAAGAATTC-GCGGCTTTGGGTATTTCTTTTCGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGGAGACTTCGCCAATGGAGCCGGG	Pst I
635	Forward	AAAAAAGAATTC- ATGACCCAGCGACGGGTCTGGCAAGCAAAACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAATCCACTATAATCCTGTTGCT	Pst I
638	Forward	AAAAAAGAATTC-ATGATTGGCGAAAAGTTTATCGTAGTTGG	Eco RI
	Reverse	AAAAAACTGCAG-TCACGAACCGATTATGCTGATCGG	Pst I
639	Forward	CGCGGATCCCATATG-ATGCTTTATTTTGTTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCGCGGCTGCCGAC	XhoI
642	Forward	CGCGGATCCCATATG-CGGTATCCGCCGCAAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGATTGCGGGGCATTA	XhoI

643	Forward	CGCGGATCCCATATG-GCTTCGCCGTCGGCAG	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-AACCGAAAAACAGACCGC	
644	Forward	AAAAAAGAATTC- ATGCCGTCTGAAAGGTCGGCGGATTGTTGCCC	Eco RI
	Reverse	AAAAAATCTAGA-CTACCCGCAATATCGGCAGTCCAATAT	Pst I
645	Forward	AAAAAAGAATTC-GTGGAACAGAGCAACACGTAAATCG	Eco RI
	Reverse	AAAAAACTGCAG-CTACGAGGAAACCGAAGACCAGGCCGC	Pst I
647	Forward	AAAAAAGAATTC-ATGCAAAGGCTCGCCGCAGACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGATTATCAGGGATATCCGGTAGAA	Pst I
648	Forward	AAAAAAGAATTC- ATGAACAGGCGCGACGCGCGGATCGAACG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGCTGTGTGCTGATTGAATGCGAC	Pst I
649	Forward	AAAAAAGAATTC-GGTACGTCAGAACCCGCCACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGGCGGAAACTGCCGCCGTC	Pst I
650	Forward	AAAAAAGAATTC-ATGTCCAACTCAAACCATCGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGGCATGGCGGTCTGTTTT	Pst I
652	Forward	AAAAAAGGTACC- GCTGCCGAAGACTCAGGCCTGCCGCTTTACCG	Kpn I
	Reverse	AAAAAACTGCAG-TTATTTGCCCAGTTGGTAGAATGCGGC	Pst I
653	Forward	AAAAAAGAATTC-GCGGCTTTGCCGTAATTTTCATCGG	Eco RI
	Reverse	AAAAAACTGCAG-CTATGCCGGTCTGGTTGCCGGCGGCGA	Pst I
656a	Forward	AAAAAAGAATTC-CGGCCGACGTCGTTGCGTCCTAAGTC	Eco RI
	Reverse	AAAAAACTGCAG-CTACGATTTCGGCGATTTCACATCGT	Pst I
657	Forward	AAAAAAGAATTC-GCAGAATTTGCCGACCGCCATTTGTGCGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATAGGGACTGATGCAGTTTTTTTGC	Pst I
658	Forward	CGCGGATCCCATATG-GTGTCCGGAATTGTG	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-GGCAGAATGTTTACCGTT	
661	Forward	AAAAAAGAATTC- ATGCACATCGGCGGCTATTTTATCGACAACCC	Eco RI
	Reverse	AAAAAACTGCAG-TCACGACGTGTCTGTTTCGCCGTCGGGC	Pst I
663	Forward	CGCGGATCCCATATG-TGTATCGAGATGAAATT	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-GTAAAAATCGGGGCTGC	
664	Forward	CGCGGATCCCATATG-GCGGCTGGCGCGGT	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-AAATCGAGTTTTACACCAC	
665	Forward	AAAAAAGAATTC-ATGAAATGGGACGAAACGCGCTTCGG	Eco RI
	Reverse	AAAAAACTGCAG-TCAATCCAAAATTTTGCCGACGATTTC	Pst I
666	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTGGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Xba I
667	Forward	AAAAAAGAATTC- CCGCATCCGTTTGATTTCATTTCGTATTCGTCCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAATGACACAATAGGCGCAAGTC	Pst I

669	Forward	AAAAAAGAATTC-ATGCGCCGCATCATTAAAAAACACCAGCC	Eco RI
	Reverse	AAAAAACTGCAG-TTACAGTATCCGTTTGATGTCGGC	Pst I
670a	Forward	AAAAAAGAATTC-AAAAACGCTTCGGGCGTTTCGTCTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTAGGAGCTTTTGGAACGCGTCGGACTGGC	Pst I
671	Forward	CGCGGATCCCATATG-ACCAGCAGGGTAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAACTATAAAAAACGCAAG	XhoI
672	Forward	CGCGGATCCCATATG-AGGAAAATCCGCACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGGGATAGGCGGTTG	XhoI
673	Forward	AAAAAAGAATTC-ATGGATATTGAAACCTTCCTTGCAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAACCCAGCTCGCGCAGGAA	Pst I
674	Forward	AAAAAAGAATTC-ATGAAAACAGCCCGCCGCGTTCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TCAACGGCGTTTGGGCTCGTCGGG	Pst I
675	Forward	CGCGGATCCCATATG-AACACCATCGCCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCTTCGTCTTCAAACCTGT	XhoI
677a	Forward	AAAAAAGAATTC-AGACGGCATTCCCGATCAGTCGATTTTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGTATGCGCGAAATCGACCGCCGC	Pst I
680	Forward	CGCGGATCCGCTAGC-ACGAAGGGCAGTTCGG	BamHI- NheI
	Reverse	CCCGCTCGAG-CATCAAAAACCTGCCGC	XhoI
681	Forward	AAAAAAGAATTC-ATGACGACGCCGATGGCAATCAGTGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCGTCTTCCGCAAAAAACAGC	Pst I
683	Forward	CGCGGATCCCATATG-TGCAGCACACCGGACAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAGTTTTTTTCCGCATACG	XhoI
684	Forward	CGCGGATCCCATATG-TGCGGTACTGTGCAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTCGACCATCTGTTGCG	XhoI
685	Forward	CGCGGATCCCATATG-TGTTTGCTTAATAATAAACATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTTTTTCCCCGCCGCA	XhoI
686	Forward	CGCGGATCCCATATG-TGCGGCGGTTTCGGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGATTCTGATGAAG	XhoI
687	Forward	CGCGGATCCCATATG-TGCGACAGCAAAGTCCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCGCGGCTTTTTGTT	XhoI
690	Forward	CGCGGATCCCATATG-TGTTCTCCGAGCAAAGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TATTCGCCCCGTGTTTGG	XhoI
691	Forward	CGCGGATCCCATATG-GCCACGGCTTATATCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAGGCAGGAAGAAAG	XhoI

694	Forward	CGCGGATCCCATATG-TTGGTTTCCGCATCCGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCTGCGTCGGTGCGGT	XhoI
695	Forward	CGCGGATCCCATATG-TTGCCTCAAACCTCGTCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGTTTGCGCACGGCT	XhoI
696	Forward	CGCGGATCCCATATG-TTGGGTTGCCGGCAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGATTGCCGCAATGATG	XhoI
700a	Forward	AAAAAAGAATTC-GCATCGACAGACGGTGTGTCGTGGAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCTACCGGCACGACTTCCAAACC	Pst I
701	Forward	CGCGGATCCCATATG-AAGACTTGTTTGGATACTTC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCCGACAACAGCCTC	XhoI
702	Forward	AAAAAAGAATTC-ATGCCGTGTTCCAAAGCCAGTTGGATTTC	Eco RI
	Reverse	AAAAAACTGCAG-TTAACCCCATTCACCCGGAGAACCGA	Pst I
703	Forward	CGCGGATCCGCTAGC-CAAACGCTGGCAACCG	BamHI- NheI
	Reverse	CCCGCTCGAG-TTTTGCAGGTTTGATGTTTG	XhoI
704a	Forward	AAAAAAGAATTC-GCTTCTACCGGTACGCTGGCGCG	Eco RI
	Reverse	AAAAAACTGCAG- TTAGTTTTGCCGGATAATATGGCGGGTGCG	Pst I
707	Forward	CGCGGATCCGCTAGC-GAAATTATTAACGATGCAGA	BamHI- NheI
	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGA	XhoI
708	Forward	CGCGGATCCGCTAGC-CCTTTTAAGCCATCCAAAA	BamHI- NheI
	Reverse	CCCGCTCGAG-TTGACCGGTGAGGACG	XhoI
710	Forward	CGCGGATCCCATATG-GAAACCCACGAAAAAATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACGGTTTTCGGTCAG	XhoI
714	Forward	CGCGGATCCCATATG-AGCTATCAAGACATCTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGTAGGTAAATCGGAT	XhoI
716	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTAGAACCGCATTTGCC	XhoI
718	Forward	CGCGGATCCCATATG-GAGCCGATAATGGCAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCGCGGGCATGGTCTTGTC	XhoI
720	Forward	CGCGGATCCCATATG-AGCGGATGGCATAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTTGCATAGCTGTTGACCA	XhoI
723	Forward	CGCGGATCCCATATG-CGACCCAAGCCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AATGCGAATCCGCCGCC	XhoI

725	Forward	CGCGGATCCCATATG-GTGCGCACGGTTAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGCTTATCCTTAAGGGTTA	XhoI
726	Forward	CGCGGATCCCATATG-ACCATCTATTTCAAAAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCGATGTTTAGCGTCC	XhoI
728	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	XhoI
729	Forward	CGCGGATCCCATATG-TGCACCATGATTCCCCA	BamHI- NdeI
	Reverse	GCCCAAGCTT-TTGTCGGTTTGGGTATC	HindIII
731	Forward	CGCGGATCCGCTAGC-GCCGTGCCGGAGG	BamHI- NheI
	Reverse	CCCGCTCGAG-ACGGGCGCGGCAG	XhoI
732	Forward	CCGGAATTCTACATATG-TCGAAACCTGTTTTTAAGAA	EcoRI- NdeI
	Reverse	CCCGCTCGAG-CTTCTTATCTTTTTTATCTTTC	XhoI
733	Forward	CGCGGATCCCATATG-GCCTGCGGCGGCAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGCTTGCCCTCCTTTAC	XhoI
734	Forward	CGCGGATCCCATATG-GCCGATACTTACGGCTAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAGATTTTGAATCAAAGAG	XhoI
735	Forward	CGCGGATCCCATATG-AAGCAGCAGGCGGTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATTTCCGTAGCCGAGGG	XhoI
737	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTCGTCGCGGCGGGA	XhoI
739	Forward	CGCGGATCCCATATG-GCAAAAAAACCGAACA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAAGAGTTTGTGCGAGAATT	XhoI
740	Forward	CGCGGATCCCATATG-GCCAATCCGCCCGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAACGCGCCAAAATAGTG	XhoI
741	Forward	CGCGGATCCCATATG-TGCAGCAGCGGAGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGCTTGCGGCAAGGC	XhoI
743	Forward	CGCGGATCCCATATG-GACGGTGTGTGCCTGTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTTACGGATCAAATTGACG	XhoI
745	Forward	CGCGGATCCCATATG-TTTTGGCAACTGACCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CAAATCAGATGCCTTTAGG	XhoI
746	Forward	CGCGGATCCCATATG-TCCGAAAACAAACAAAAC	BamHI-

	Reverse	CCCGCTCGAG-TTCATTCGTTACCTGACC	NdeI
			XhoI
747	Forward	CCGGAATTCTAGCTAGC-CTGACCCCTTGGG	EcoRI-
			NheI
	Reverse	GCCCAAGCTT-TTTTGATTTTAATTGACTATAGAAC	HindIII
749	Forward	CGCGGATCCCATATG-TGCCAGCCGCCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTCAAGCCGAGTATGC	XhoI
750	Forward	CGCGGATCCCATATG-TGTCGCCCCGAACCTG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CTTTTCCCCGCCGCAA	XhoI
758	Forward	CGCGGATCCCATATG-AACAATCTGACCGTGTT	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TGGCTCAATCCTTTCTGC	XhoI
759	Forward	CGCGGATCCGCTAGC-CGCTTCACACACACCAC	BamHI-
			NheI
	Reverse	CCCGCTCGAG-CCAGTTGTAGCCTATTTTG	XhoI
763	Forward	CGCGGATCCCATATG-CTGCCTGAAGCATGGCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTCCGCAAATACCGTTTCC	XhoI
764	Forward	CGCGGATCCCATATG-TTTTCTCCGCCCTGA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCGCTCCCTAAAGCTTTC	XhoI
765	Forward	CGCGGATCCCATATG-TTAAGATGCCGTCCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-ACGCCGACGTTTTTTATTAA	XhoI
767	Forward	CGCGGATCCCATATG-CTGACGGAAGGGGAAG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTCTGTACAGCAGGGG	XhoI
768	Forward	CGCGGATCCCATATG-GCCCCGAAAAACCCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTCATCCCTTTTTTGAGC	XhoI
770	Forward	CGCGGATCCCATATG-TGCGGCAGCGGCGAA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GCGTTTGTGAGATTTTC	XhoI
771	Forward	CGCGGATCCCATATG-TCCGTATATCGCACCTTC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CGGTTCTTTAGGTTTGAG	XhoI
772	Forward	CGCGGATCCCATATG-TTGCGGCGTTGGTGG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CAATGCCGACATCAAACG	XhoI
774	Forward	CGCGGATCCCATATG-TCCGTTTCACCCGTTCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCGTTTGCGCACGGCT	XhoI
790	Forward	CGCGGATCCCATATG-GCAAGAAGGTCAAAAAC	BamHI-
			NdeI

	Reverse	CCCGCTCGAG-GGCGTTGTTCGGATTTCG	XhoI
900	Forward	CGCGGATCCCATATG-CCGTCTGAAATGCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATATGGAAAAGTCTGTTGTC	XhoI
901	Forward	CGCGGATCCCATATG-CCCGATTTTTCGATG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAATGGAACAATACCAGG	XhoI
902	Forward	CCGGAATTCTACATATG-TTGCACCTTCAAAGGATAATC	EcoRI- NdeI
	Reverse	CCCGCTCGAG-AAAAATGTACAATGGCGTAC	XhoI
903	Forward	CCGGAATTCTAGCTAGC-CAGCGTCAGCAGCACAT	EcoRI- NheI
	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGAA	XhoI
904	Forward	AAAAAAGGTACC-ATGATGCAGCACAAATCGTTTC	Kpn I
	Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
904a	Forward	AAAAAAGAATTC-CGGCTCGGCATTGTGCAGATGTTGCA	Eco RI
	Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
905	Forward	CGCGGATCCCATATG-AACAAAATATACCGCATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCACTGATAACCGACAGAT	XhoI
907	Forward	CGCGGATCCCATATG-GGCGCGCAACGTGAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCCACTGCCAGCG	XhoI
908	Forward	AAAGAATTC-GCAGAGTTAGTAGGCGTTAATAAAAATAC	Eco RI
	Reverse	AAACTGCAG-TTAATATGGTTTTGTCTGTTTCG	Pst I
909	Forward	CGCGGATCCCATATG-TGCGCGTGGGAAACTTAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGGTTTTGAAACTTTGGTTTT	XhoI
910	Forward	AAAGAATTC-GCATTGCGGCGACTCTGCCGAGCG	Eco RI
	Reverse	AAACTGCAG-TCAGCGATCGAGCTGCTCTTT	Pst I
911	Forward	AAAGAATTC-GCTTTCGCGTGGCCGGCGGTGC	Eco RI
	Reverse	AAAAAACTGCAG-GTCGACTTATTCGGCGGCTTTTCCGC	Pst I
912	Forward	AAAAAAGAATTC- CAAATCCGTCAAACGCCACTCAAGTATTGAG	Eco RI
	Reverse	AAAAAACTGCAG-TTACAGTCCGTCCACGCCTTTCGC	Pst I
913	Forward	CGCGGATCCCATATG-GAAACCCGCCCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGTTGTGTTCCAGGTTG	XhoI
915	Forward	CGCGGATCCCATATG-TGCCGGCAGGCGGAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAAAATATAGGTATCAGG	XhoI
914	Forward	AAAGAATTC-GACAGAATCGGCGATTGGAAGCACG	Eco RI
	Reverse	AAACTGCAG-CTATATGCGCGGCAGGACGCTCAACGG	Pst I
916	Forward	CGCGGATCCCATATG-GCAATGATGGCGGCTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	XhoI

917	Forward	AAAAAAGAATTC-CCTGCCGAAAAACCGGCACCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCCCCGCCTTCACATCCTG	Pst I
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC	BamHI-
	Reverse	CCCGCTCGAG-CGGGCGGTATTCGGG	NdeI
920	Forward	CGCGGATCCCATATG-CACCGCGTCTGGGTC	XhoI
	Reverse	CCCGCTCGAG-ATGGTGCGAATGACCGA	BamHI-
921	Forward	AAAAAAGAATTC-TTGACGGAAATCCCCGTGAATCC	NdeI
	Reverse	AAAAAACTGCAG-TCATTTCAAGGGCTGCATCTTCAT	XhoI
922	Forward.	CGCGGATCCGCTAGC-TGTACGGCGATGGAGGC	Eco RI
2	Reverse	CCCGCTCGAG-CAATCCCGGGCCGCC	Pst I
923	Forward	CGCGGATCCCATATG-TGTTACGCAATATTGTCCC	BamHI-
	Reverse	CCCGCTCGAG-GGACAAGGCGACGAAG	NheI
925	Forward	CGCGGATCCCATATG-AAACAAATGCTTTTAGCCG	XhoI
	Reverse	CCCGCTCGAG-GCCGTTGCATTTGATTTC	BamHI-
926	Forward	CGCGGATCCCATATG-TGCGCGCAATTACCTC	NdeI
	Reverse	CCCGCTCGAG-TCTCGTGCGCGCCG	XhoI
927	Forward	CGCGGATCCCATATG-TGCAGCCCCGCAGC	BamHI-
	Reverse	CCCGCTCGAG-GTTTTTTGCTGACGTAGT	NdeI
929a	Forward	AAAAAAGAATTC-CGCGGTTTGCTCAAAACAGGGCTGGG	XhoI
	Reverse	AAAAAATCTAGA-TTAAGAAAGACGGAACTACTGCC	Eco RI
931	Forward	AAAAAAGAATTC-GCAACCCATGTTTTGATGGAAAC	Xba I
	Reverse	AAAAAACTGCAG-TTACTGCCCCGACAACAACGCGACG	Eco RI
935	Forward	AAAAAAGAATTC-GCGGATGCGCCCGCGATTTTGGATGACAAGGC	Pst I
	Reverse	AAAAAACTGCAG-TCAAACCGCCAATCCGCCGACAC	Eco RI
936	Forward	CGCGGATCCCATATG-GCCGCCGTCGGCGC	Pst I
	Reverse	CCCGCTCGAG-GCGTTGGACGTAGTTTTG	BamHI-
937	Forward	AAAAAAGAATTC-CCGTTTACATTCAAACCGGCGCAAC	NdeI
	Reverse	AAAAAACTGCAG-TTAAAATGTATGCTGTACGCCAAA	XhoI
939a	Forward	AAAAAAGAATTC-GGTTCGGCAGCTGTGATGAAACC	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGCAAACCTTGGATAAAGTTGGC	Pst I
950	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	BamHI-
	Reverse	CCCGCTCGAG-TTTagAACCGCATTTGCC	NdeI
953	Forward	CGCGGATCCCATATG-GCCACCTACAAAGTGGAC	XhoI
	Reverse	CCCGCTCGAG-TTGTTTGGCTGCCTCGAT	BamHI-
957	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	NdeI
			XhoI
			BamHI-

	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	NdeI
958	Forward	CGCGGATCCCATATG-GCCGATGCCGTTGCG	XhoI
			BamHI-
			NdeI
	Reverse	GCCCAAGCTT-GGGTCGTTTGTTCGTC	HindIII
959	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GTCGTCGCGGCGGGA	XhoI
961	Forward	CGCGGATCCCATATG-GCCACAAGCGACGACG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CCACTCGTAATTGACGC	XhoI
972	Forward	AAAAAAGAATTC- TTGACTAACAGGGGGGGGAGCGAAATTAAAAAC	Eco RI
	Reverse	AAAAAATCTAGA-TTAAAAATAATCATAATCTACATTTTG	Xba I
973	Forward	AAAAAAGAATTC-ATGGACGGCGCACAAACGAAAAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTTCACGCGGGTCGCCATCAGCGT	Pst I
982	Forward	CGCGGATCCCATATG-GCAGCAAAAGACGTAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CATCATGCCGCCCATCC	XhoI
983	Forward	CGCGGATCCCATATG-TTAGCTGTTGCAACAACAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GAACCGGTAGCCTACG	XhoI
987	Forward	CGCGGATCCCATATG-CCCCACTGGAAGAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TAATAAACCTTCTATGGGC	XhoI
988	Forward	CGCGGATCCCATATG-TCTTTAAATTTACGGGAAAAAG	BamHI-
			NdeI
	Reverse	GCCCAAGCTT-TGATTTGCCTTTCCGTTTT	HindIII
989	Forward	CCGGAATTCTACATATG-GTCCACGCATCCGGCTA	EcoRI-
			NdeI
	Reverse	CCCGCTCGAG-TTTGAATTTGTAGGTGTATTGC	XhoI
990	Forward	CGCGGATCCGCTAGC-TTCAGAGCTCAGCTT	BamHI-
	2		NheI
	Reverse	CCCGCTCGAG-AAACAGCCATTTGAGCGA	XhoI
992	Forward	CGCGGATCCCATATG-GACGCGCCCGCCCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CCAAATGCCCAACCATTC	XhoI
993	Forward	CGCGGATCCCATATG-GCAATGCTGATTGAAATCA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GAACACATCGCGCCCG	XhoI
996	Forward	CGCGGATCCCATATG-TGCGGCAGAAAATCCGC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCTAAACCCCTGTTTTCTC	XhoI
997	Forward	CCGGAATTCTAGCTAGC-CGGCACGCCGACGTT	EcoRI-
			NheI
	Reverse	CCCGCTCGAG-GACGGCATCGCTCAGG	XhoI

Underlined sequences indicate restriction recognition sites.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1>:

```
g001.seq
  1  ATGCTGCCGC AGGGGAAGGC GCGCGGAGG GTGTCGGCGA ACGAGGTGTC
 51  CGGCAGGGCT TCGCGCCGGA TGGTGCTGGT CATCTGCCAG ACGCTGCCGA
101  AACGCGATAC TTTAAACGGC TCGGGTACGC ATACTTTACC GGTTTGGGCG
151  ATTTTGCCGA GGTCTGTGCG CAGCAAATCG ACAATCATCA CGTTTTCGGC
201  GCGGTTTTTC GGGTCGGTTT GTAACTCGGC GCGCGGCGT TCGTCTTGTC
251  CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTCCGT GCTGATGGTG
301  CCGTCTGAAG CGATGTTGAG GAAGAGTTCG GCGGAGAAAC ACAGCGTCCA
351  CGCGGATTGC CCGGCTTCAT CGGGCAGGTG GGACAATACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 2; ORF 001.ng>:

```
g001.pep
  1  MLPOGKAARR VSANEVSGRA CARMVLVICQ TLPKRDTLNG SGHTLTPVWA
 51  ILPRSLRSKS TIITFSARFF GSVCNSAARR SSCPSPKIGA VPFIGSVLMV
101  PSEAMLRKSS GEKHSVHAD C PASSGRWDNT A*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3>:

```
m001.seq
  1  ATGCTGCCGC AGGGGAAGGC GCGCGGAGG ATGTCGGCGA ACGAGGTGTC
 51  CGGcAssCTT ss.GCTTGGA yGGTGCTGGT CATCTGCCAA ACGCTGCCGA
101  AACGCGATAC TTTAAACGGT TCGGGTACGC ATACTGTGCC GGTTTGGGCG
151  ATTTTGCCGA GATCGTTACG CAGCAAATCG ACAATCATCA CGTTTTCGGC
201  GCGGTTTTTC GGGTCTGCTT GCAACTCGGC GCGCGGCGT TCGTCTTGTC
251  CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTCCGT GCTGATGGTG
301  CCGTCCGAAC CGATTTTGAG GAAGAGTTCG GCGGAGAAAC ACAGCGTCCA
351  CGCGGATTGC CCCTCCGCAT CGGGCAGGTG GGACAAGACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 4; ORF 001>:

```
m001.pep
  1  MLPOGKAARR MSANEVCGXL XAWXVLVICQ TLPKRDTLNG SGHTVVPVWA
 51  ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101  PSEPILRKSS GEKHSVHAD C PSASGRWDKT A*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 5>:

```
a001.seq
  1  ATGCTGCCGC AGGGGAAGGC GCGCGGAGG ATGTCGGCGA ACGAGGTGTC
 51  CGGCAAGGCT TGGGCTTGGA TGGTGCTGGT CATCTGCCAA ACGCTGCCGA
101  AACGCGATAC TTTAAACGGT TCGGGTACGC ATACTGTGCC GGTTTGGGCG
151  ATTTTGCCGA GGTCTGTACG CAGCAAATCG ACAATCATCA CGTTTTCGGC
201  GCGGTTTTTC GGGTCTGCTT GCAACTCGGC GCGCGGCGT TCGTCTTGTC
251  CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTCCGT GCTGATGGTG
301  CCGTCCGAAC CGATTTTGAG GAAGAGTTCG GCGGAGAAAC ACAGCGTCCA
351  CGCGGATTGC CCTTGTGCAT CGGGCAGGTG GGACAAAACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 6; ORF 001.a>:

```
a001.pep
  1  MLPOGKAARR MSANEVCGKA WAWMVLVICQ TLPKRDTLNG SGHTVVPVWA
 51  ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101  PSEPILRKSS GEKHSVHAD C PASGRWDKT A*
```

m001/a001 96.2% identity over a 131 aa overlap

```

              10          20          30          40          50          60
m001.pep  MLPOGKAARRMSANEVCGXLXAWXVLVICQTLPKRDTLNGSGHTVVPVWAILPRSLRSKS
            |||||
a001.pep  MLPOGKAARRMSANEVCGKAWAWMVLVICQTLPKRDTLNGSGHTVVPVWAILPRSLRSKS
```

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	10	20	30	40	50	60
m001.pep	70	80	90	100	110	120
	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
a001.pep	70	80	90	100	110	120
	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
m001.pep	130					
	PSASGRWDKTAX					
a001.pep	130					
	PCASGRWDKTAX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 001 shows 89.3% identity over a 131 aa overlap with a predicted ORF (ORF 001.ng) from *N. gonorrhoeae*:

m001/g001

	10	20	30	40	50	60
m001.pep	70	80	90	100	110	120
	MLPQGKAARRMSANEVCGXLXAWXVLVICQTLPKRDTLNGSGHTVPVWAILPRSLRSKS					
g001	70	80	90	100	110	120
	MLPQGKAARRVSANEVSGRACARMVLVICQTLPKRDTLNGSGHTLPVWAILPRSLRSKS					
m001.pep	130					
	PSASGRWDKTAX					
	: :					
g001	130					
	PASSGRWDNTAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 7>:

g003.seq

```

1  ATGGTCGTAT TCGTGGCTGA AGGCGTATTC GGTCCGCTG TTTTGGGTCA
51  CTTGGTATTG CTCTTCGGTC AGGGTGC GTT TGAGTTCGGC GTCACTCGGT
101 TTTTATACG TTGCCGCGTC GAAGCCTTTG CCTTGCGGTG CGGCTTTGGT
151 TTTGCCCGGC AGCGGTTTCG CCGCTTTGCG GATGTCGATG TGGCAGTAGC
201 CGTTGGGGTT TTTAATCAGG TAGTCCTGAT GGTATTCCTC GGCGTCGTAG
251 AAGTTTTTCA GCGGTTTCGT TTCAACAACG AGGGGCAGTT GGTATTTTTG
301 CTGCTCGCGT TTGAGGGCGG CGGCGATGAC GGCTTTTTTC GCGGGGTCGG
351 TGTA GTACAC GCCGCTGCGG TATTGCGTGC CGGTGTCTGT ACCCTGTTTG
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAA TAATATTGCA GGATGTCGTC
451 CAGgCTGagt TTGTCGGCAT CGTaggtcac tTTGACGGTC TCGGCATGAC
501 CCGTATGGCG GTaggacact tctTCgtanc TcGGGtTTTC CGTgttGCCG
551 TTGGCgttac cGGATACCGC gtcaACCACG CCGTcgatgc gttggaAATa
601 ggCTTCCAAg ccccaaaaagc agccgccggc gaagtaaagt gtgcccgtgt
651 tcatgattGC TGA

```

This corresponds to the amino acid sequence <SEQ ID 8; ORF 003.ng>:

g003.pep

```

1  MVVFVAEGVF GRAVLGHLVL LFGQGA FEFG VTRFFIRCRV EAFALRCGFG
51  FARQRFVGFA DVDVAVAVGV FNOQVLMVFL GVVEVFQRFV FNNEGQLVFL
101 LLAFEGGGDD GFFGGVGVVH AA AVL RAGVV TLFVEAGRIN DAEIILQDVV

```

151 QAEFVGIVGH FDGLGMTRMA VGHFFVRVFR VAVGVTGYRV NHAVDAL EIG
201 FQAPKAAAGE VNGARVHDC

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 9>:

```
m003.seq
1   ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTGCGCTG TTTTGGGTAA
51  CTTGstATTG CTCTTCGGTC AGGGTGCGTT TGAGTTCGGC GTCAC TCGGT
101 TTTTATACG TTGCCGCGTC GAAGCCTTTG CCTGCGGGG CGGTCTTGGT
151 TTTGCCCGGC AGCGGTTCTG CAGCkTTGCG GATGTCGATG TGGCAGTAGC
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG
251 AAGTTTTtCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTTG
301 CTGCTCGCGT TTGAGGCGCk CGGCGATGAC GGCTTTTTTCG kCGGGGTCGG
351 TG TAGTACAC GCCGCTGCGG TATTGCGTAC CGGTGTCGTT GCCCTGTTTG
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC
451 TAGGCTGAGT TTGTCGGCAT CGTAGGTCAC TTTGACGGTT TCGGCGTGGC
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTTT CGTGTGCGCG
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGGAAATA
601 GGCTTCCAAG CCCAGAAGC AGCg.CCGGC GAGGTAAATG GTGCGCGTGT
651 TCATGATTTT TGA
```

This corresponds to the amino acid sequence <SEQ ID 10; ORF 003>:

```
m003.pep Length: 221
1   MVVFVAEGIF GRAVLGNLXL LFGQGAFFEG VTRFFIRCRV EAFALRGGLG
51  FARQRFVSXA DVDVAVAVGV FNQVLMVFL GIVEVFQRLV FNNEGQLVFL
101 LLAFEGXGDD GFFXGVGVVH AA AVLRTGVV ALFVEAGRIN DAEEILQDVV
151 *AEFVGIVGH FDGFGVARMA VGHVFIARIF RVAVGVAGYR VNHAVDAL E I
201 GFQAPEAAXG EVNGARVHDF *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 11>:

```
a003.seq
1   ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTGCGCTG TTTTGGGTAA
51  CTTGGTATTG CTCTTCGGTC AGGGTGCGTT TGAGTTCGGC GTCAC TCGGT
101 TTTTATACG TTGCCGCGTC GAAGCCTTTG CCTGCGGTG CGGTCTTGGT
151 TTTGCCCGGC AGCGGTTCTG CGGCTTTGCG GATATCGATG TGGCAGTAGC
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG
251 AAGTTTTtCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTTG
301 CTGCTCGCGT TTGAGGCGCG CGGCGATGAC GGCTTTTTTCG GCGGGGTCGG
351 TG TAGTACAC GCCGCTGCGG TATTGCGTAC CGGTGTCGTT GCCCTGTTTG
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC
451 TAGGCTGAGT TTGTCGGCAT CGTAGGTCAC TTTGACGGTT TCGGCGTGGC
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTTT CGTGTGCGCG
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGGAAATA
601 GGCTTCCAAG CCCAGAAGC AGCCGCCGGC GAGGTAGATG GTGCGCGTGT
651 TCATGATTTT TGA
```

This corresponds to the amino acid sequence <SEQ ID 12; ORF 003.a>:

```
a003.pep
1   MVVFVAEGIF GRAVLGNLVL LFGQGAFFEG VTRFFIRCRV EAFALRCGLG
51  FARQRFVGFA DIDVAVAVGV FNQVLMVFL GIVEVFQRLV FNNEGQLVFL
101 LLAFEGGGDD GFFGGGVGVH AA AVLRTGVV ALFVEAGRIN DAEEILQDVV
151 *AEFVGIVGH FDGFGVARMA VGHVFIARIF RVAVGVAGYR VNHAVDAL E I
201 GFQAPEAAAAG EVDGARVHDF *
```

m003/a003 95.9% identity over a 220 aa overlap

```

              10      20      30      40      50      60
m003.pep  MVVFVAEGIFGRAVLGNLXL LFGQGAFFEGVTRFFIRCRVEAFALRGGLGFARQRFVSXA
            | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a003      MVVFVAEGIFGRAVLGNLVL LFGQGAFFEGVTRFFIRCRVEAFALRCGLGFARQRFVGFA
              10      20      30      40      50      60
```

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	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNQQLVFLLLAFEGXGDDGFFXGVGVVH					
a003	DIDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNQQLVFLLLAFEGGGDDGFFGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGRINDAEEILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
a003	AAAVLRTGVVALFVEAGRINDAEEILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVIDALEIGFQAPEAAXGEVNGARVHDFX					
a003	RVAVGVAGYRVNHAVIDALEIGFQAPEAAXGEVDGARVHDFX					
	190	200	210	220		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 003 shows 88.6% identity over a 219 aa overlap with a predicted ORF (ORF 003.ng) from *N. gonorrhoeae*:

m003/g003

	10	20	30	40	50	60
m003.pep	MVVFVAEGIFGRAVLGNLXLLFGQGAFFGVTRFFIRCRVEAFALRGGLGFARQRFVXSXA					
g003	MVVFVAEGVFGRAVLGHLVLLFGQGAFFGVTRFFIRCRVEAFALRCGFGFARQRFVGFFA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNQQLVFLLLAFEGXGDDGFFXGVGVVH					
g003	DVDVAVAVGVFNQVVLVFLGVVEVFQRFVFNQQLVFLLLAFEGGGDDGFFGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGRINDAEEILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
g003	AAAVLRAGVVTLFVEAGRINDAEEILQDVVQAEFVGIVGHFDGLGMTRMAVGHFFV-RVF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVIDALEIGFQAPEAAXGEVNGARVHDFX					
g003	RVAVGVAGYRVNHAVIDALEIGFQAPKAAAGEVNGARVHDC					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 13>:

g004.seq

```

1  ATGgtagAAC  GGCATATCCA  GCATTTCGGG  AACGGTCATC  TTCATTTGAT
51  GCGCCCATGC  CAACAagtgA  gccAAAtgtT  CGCGCGCAGG  GCCTacgatT
101 TCCGCGCCGA  TAAagcggcc  gGTGgctTTT  tcgGCataca  ggcgcaTatg
151 gCCTTTGTTT  ACCAgcatca  cgcggtgctg  accttgaTTT  TTGAACGATA
201 CTTTCGCCgAT  GACAAATTCCG  TCGGCTTGGT  ATTGCGCGGC  AACCTGCGCG
251 TATTTCAAAC  CGACAAAGCC  GATTTCGcga  ctggttaaACA  CCACGCCAAT
301 GGTgctgcgg  cGCAAACCGC  TGCCGATAt  cgGgtagcgg  ccccgctta
351 ttgcccggca  atcttacctt  ggtcggcggc  ttcATGCAGC  AGGGGcagtt
401 ggttggacgc  gtcgcccgcA  ataAAGATAT  GCGGAATgct  ggtCTGCATg
451 gtCAGCGGAT  CGGCAACGGG  tacgccgcgc  gcgtctttgT  CGATATTGAT
501 GTTTTCCAAA  CCGATATtgT  CAACGTTCCG  ACGGCgACCT  ACGGCTGCCA

```

```

551 ACATATATTC GGCAACAAAT ACGCCTTTTT CGCCATCCTG CTCCCAATGG
601 ACTtctACAT TGCCGTCTGC GTCGAGTTTG ACCTCGGTTT TAGCATCCAG
651 ATGCAGTTTC AATtctTCTC CGAACACGGC TTTCGCCTCG TCTGAAACAA
701 CGGGGTCGGA AATGCCGCCG ATGATTCCGC CCAAACCGAA AATTTCAACT
751 TTCACACCCA AACGGTGCAA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 14; ORF 004.ng>:

g004.pep

```

1 MVERHIQHLR NGHLLHMRPC QQVSQMFGR AYDFRADKAA GGFFGIQAHM
51 AFVYQHHAHA TLIFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGKHHAN
101 GAAAQTAADI RVAAPRYCPA ILPWSAASCS RGSWLDASPA IKICGMLVCM
151 VSGSATGTPR ASLSILMFSK PILSTFGRRP TAANIYSATN TPFSPSCSQW
201 TSTLPSASSL TSVLASRCSF NSSPNTAFAS SETTGSEMP MIPPKPKIST
251 FPKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 15>:

m004.seq

```

1 ATGGTAGAAC GGCATATCCA GCATTTGCGG AACGGTCATC TTCATTTGAT
51 GTGCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCAGG GCCTACGATT
101 TCCGCGCCGA TAAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTC ACCAGCATCA CGCGGCTGCG GCCTTGTTT TTGAACGATA
201 CTTCGCCGAT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TAGTTTCAGAC CGACAAAGCC GATTTGCGGA CTGGTAAACA CCACGCCGAT
301 GGTGCTGCGC CGCAAACCGC CGCCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGCAATC TTGCCTTGGT CGGCAGCTTC ATGCAGCAGA GGCAGTTGGT
401 TGGACGCATC GCCTGCGATG AAGATATGCG GAATACTGGT CTGCATGGTC
451 AGCGGTCGG CAACAGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATATT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCCACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCATC GAGTTTGACC TCGGTTTTAG CATCCAGATG
651 CAGTTTCAAT TCTTCGCCGA ACACGGCGTT CGCCTCGTCT GAAACGACGG
701 GGTGCGAAAT GCCGCCGATG ATTCGCCCCA AACCGAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 16; ORF 004>:

m004.pep

```

1 MVERHIQHLR NGHLLMCPS QQVRQMFGR AYDFRADKAA GGFFGIQAHM
51 AFVHQHHAHA ALVFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGKHHAD
101 GAAPQTAADI RVAAALSPAI LPWSAASCSR GSWLDASPA KICGILVCMV
151 SGSATGTPRA SFSILIFSKP ILSTFGRRPT AASIYSATNT PFSFSCSQWT
201 STLPSASSLT SVLASRCSFN SSPNTAFASS ETTGSEMP MIPPKPKISTF
251 TPKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 17>:

a004.seq

```

1 ATGGTAGAAC GGCATATCCA GCATTTGCGG AACGGTCATC TTCATTTGAT
51 GTGCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCCGG ACCTACGATT
101 TCTGCGCCGA TGAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTC ACCAGCATCA CGCGGCTGCG GCCTTGTTT TTGAACGATA
201 CTTCGCCGAT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTCAAAC CGACAAAGCC GATTTGCGGA CTGGTGAACA CTACGCCGAT
301 GGTGCTGCGG CGCAAACCGC CGCCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGCAATC TTGCCTTGGT CGGCGGCTTC ATGCAGCAGG GGCAGTTGGT
401 TGGACGCGTC GCGGCAATA AAGATATGCG GAATACTGGT CTGCATAGTC
451 AGCGGATCGG CAACGGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATGTT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCCTACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCGTC GAGTTTGGCC TCGGTTTTAG CATCCAAATG
651 CAGTTTCAAT TCTTACCGA ACACGGCTTT CGCCTCGTCT GAAACGACGG
701 GGTGCGAAAT GCCGCCGATG ATGCCACCCA AACCGAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 18; ORF 004.a>:

```

a004 . pep
  1  MVERHIQHLR  NGLHLMCP  SQQVRQMF  GGR  TYDFCADE  AAGFFGIQ  AHMAFV  HQHHAAA
 51  AFVYQHAAA  ALVFER  YFAD  DKFVGL  VLRG  NLRVFQ  TDKA  DLRTGE  HYAD
101  GAAQTAADI  RVAAAL  SPAI  LPWSAAS  CSR  GSWLDAS  PAI  KICGIL  VCIV
151  SGSATGT  PRA  SFSILM  FSKP  ILSTFG  RRP  AASIYS  ATNT  PFSPSC  SQWT
201  STLPSASS  LA  SVLASK  CSFN  SSPNTA  FASS  ETTGSE  MP  MPPKPK  ISTF
251  TPKRCNA*

```

m004/a004 94.9% identity over a 257 aa overlap

```

              10      20      30      40      50      60
m004 . pep    MVERHIQHLRNGHLHLMCP  SQQVRQMF  GGRAYDFRADKAAGFFGIQAHMAFVHQHHAAA
              |||||
a004          MVERHIQHLRNGHLHLMCP  SQQVRQMF  GGRTYDFCADEAAGFFGIQAHMAFVYQHAAA
              10      20      30      40      50      60

              70      80      90      100     110     120
m004 . pep    ALVFER  YFADDKFVGLVLRGNLRVFQTDKADLRTGKHHADGAAPQTAADIRVAAALSPAI
              |||||
a004          ALVFER  YFADDKFVGLVLRGNLRVFQTDKADLRTGEHYADGAAQTAADIRVAAALSPAI
              70      80      90      100     110     120

              130     140     150     160     170     180
m004 . pep    LPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGT  PRASF  SILIFSKPILSTFGRRP
              |||||
a004          LPWSAASCSRGSWLDASPAIKICGILVCIVSGSATGT  PRASF  SILMFSKPILSTFGRRP
              130     140     150     160     170     180

              190     200     210     220     230     240
m004 . pep    AASIYSATNTPFSPSCSQWTSTLPSASSLT  SVLASRCSFNSSPNTAFASSETTGSEMP  PM
              |||||
a004          AASIYSATNTPFSPSCSQWTSTLPSASSL  ASVLASKCSFNSSPNTAFASSETTGSEMP  PM
              190     200     210     220     230     240

              250
m004 . pep    IPPKPKISTFTPKRCNAX
              :
a004          MPPKPKISTFTPKRCNAX
              250

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 004 shows 93.4% identity over a 258 aa overlap with a predicted ORF (ORF 004.ng) from *N. gonorrhoeae*:

m004/g004

```

              10      20      30      40      50      60
m004 . pep    MVERHIQHLRNGHLHLMCP  SQQVRQMF  GGRAYDFRADKAAGFFGIQAHMAFVHQHHAAA
              |||||
g004          MVERHIQHLRNGHLHLMR  PCQQV  SQMF  GGRAYDFRADKAAGFFGIQAHMAFVYQHAAA
              10      20      30      40      50      60

              70      80      90      100     110     119
m004 . pep    ALVFER  YFADDKFVGLVLRGNLRVFQTDKADLRTGKHHADGAAPQTAADIRVAAA-LSPA
              :
g004          TLIFERYFADDKFVGLVLRGNLRVFQTDKADLRTGKHHANGAAAQTAADIRVAAPRYCPA
              70      80      90      100     110     120

              120     130     140     150     160     170     179
m004 . pep    ILPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGT  PRASF  SILIFSKPILSTFGRRP

```

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```

|||||
g004      ILPWSAASCSRGSWLDASPAIKICGMLVCMVSGSATGTPRASLSILMFSKPILSTFGRRP
              130      140      150      160      170      180

180      190      200      210      220      230      239
m004.pep  TAASIYSATNTPFSPSCSQWTSTLPSASSLTSVLASRCSFNSSPNTAFASSETTGSEMP
|||||
g004      TAANIYSATNTPFSPSCSQWTSTLPSASSLTSVLASRCSFNSSPNTAFASSETTGSEMP
              190      200      210      220      230      240

240      250
m004.pep  MIPPKPKISTFTPKRCNAX
|||||
g004      MIPPKPKISTFTPKRCNA
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 19>:

```

g005.seq
1  ATGGGGATGG ACAATATTGA TATGTTTCATG CCTGAACAAG AGGAAATCCA
51  ATCAATGTGG AAAGAAATTT TACTGAATTA CGGTATTTTC CTGCTCGAAC
101 TGCTTACCGT GTTCGGCGCA ATTGCGCTGA TTGTGTTGGC TATCGTACAG
151 AGTAAGAAAC AGTCGGAAG CGGCAGTGTC GTACTGACAG ATTTTTCGGA
201 AAATTATAAA AAACAGCGGC AATCGTTTGA AACATTCTTT TTAAGCGAGG
251 AAGAGACAAA ACATCAGGAA AAAAAAGAAA AGAAAAAGGA AAAGCGGAA
301 GCCAAAGCAG AGAAAAAGCG TTTGAAGGAG GCGGGGAGA AATCTGCCGA
351 AACGCAAAAA TCCCGCCTTT TTGTGTTGGA TTTTGACGGC GATTGTATG
401 CACACGCCGT AGAATCCTTG CGTCATGAGA TTACGCGCGT GCTTTTGATT
451 GCCAAGCCTG AAGATGAGGT TCTGCTCAGA TTGGAAAGTC CGGGCGCGCT
501 GGTTACCGGT TACGGTTTGG CGGCTTCGCA GCTTAGGCGT TTGCGCGAAC
551 GCAATATTCC GCTGAccgtc gccgTCGATA AGGTCGCGGC AAGCGgccgc
601 tatatgatgg cgtgtgtgGC GGATAAAATT GTTTCGCTc cgtttgccgt
651 catcggttcg gtgggtgtgg tgGcggaagt gcCGAATATC CaccGctGT
701 TGAAAAACA TGATATTGAT GTGGATGTA TGACGCGCGG CGAATTTAAG
751 CGCACGGTTA CTTTATTGGG TGAAATACG GAAAAGGGCA AACAGAAATT
801 CCGGCAGGAA CTGGAGGAAA CGCATCAGTT GTTCAAGCAG TTTGTCAGTG
851 AAAACCGCCC CGGGTTGGAT ATTGAAAAA TAGCGACGGG CGAGCATTGG
901 TTCGGCCGGC AGGCGTTGGC GTTGAAGTT ATTGACGAGA TTTCGACCAG
951 TGATGATTG TTGTTGAAAG CGTTTGAAA CAAACAGGtt aTCGAAGTGA
1001 AATATCAGGA GAAGCGAAGC CTGATCCAGC GCATTGGTTT GCAGGCGGAA
1051 GCTTCCGTTG AAAAGTTGTT TGCCAAACTT GTCAACCGGC GAGCGGATGT
1101 GATGTAG

```

This corresponds to the amino acid sequence <SEQ ID 20; ORF 005.ng>:

```

g005.pep
1  MGMNDNIDMF PEQEIIQSMW KEILLNYGIF LLELLTVFGA IALIVLAIQV
51  SKKQSESGSV VLTDFSENYK KQRQSFETFF LSEETHKHQE KKEKKKEKAE
101 AKAEKKRLKE GGEKSAETQK SRLFVLDFDG DLYAHAVESL RHEITAVLLI
151 AKPEDEVLLR LESPGGVVHG YGLAASQLRR LRERNIPLTV AVDKVAASGG
201 YMMACVADKI VSAPFAVIGS VGVVAEVPNI HRLKKHDID VDVMTAGEFK
251 RTVTFMGENT EKGKQKFRQE LEETHQLFKQ FVSENRPGLD IEKIATGEHW
301 FGRQALALNL IDEISTSDDL LLKAFENKQV IEVKYQEKRS LIQRIGLQAE
351 ASVEKLFACL VNRRADVM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 21>:

```

m005.seq
1  ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51  GTGGAAAGAA ATTTTACTGA ATTACGGTAT TTTCTGCTC GAACTGCTTA
101 CCGTGTTCCG CGCAATTGCG CTGATTGTGT TGGCTATCGT ACAGAGTAAG
151 AAACAGTCGG AwAGCGGCAG TGTCGTACTG ACGGATTTT CGGAAATTA
201 TAAAAACAG CGGCAATCGT TTGAAGCATT CTTTTTAAGC GGGGAAGAGG
251 CACAACATCA GGAAAAAGAG GAAAAGAAAA AGGAAAAGGC GGAAGCCAAA

```

```

301 GCAGAGAAAA A.CGTTTGAA GGAGGGTGGG GAGAAATCTG CCGAAACGCA
351 nAAATCACGC CTTTTGTGT TGGANNNNNN NNNNNNNNNN NNNNNNNNNN
401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNGCGAGCGG CGGTTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGCTTCC GCTCCGTTTG CGATTGTCTG
651 TTCGGTGGGT GTGGTGGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGGCGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGGAAGAG GGCAAACAGA AATTCCGACA
801 GGAACGTGGG GAAACGCATC AGTTGTTCAA GCAGTTTGTC AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGGCGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCGA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTTG AAAACAAACA GGTATCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTGCAGGC GGAAGCTTCT
1051 GTTGAAAAGT TGTTTGCCAA ACTTGTC AAC CGGCGGGCGG ATGTGATGT A
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 22; ORF 005>:

m005.pep

```

1 MDNIDMFPE QEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 QQSXSGSVVL TDFSENYKKQ RQSFEAFFLS GEEAQHQEKE EKKKEKAEAK
101 AEKXRLKEGG EKSAETXKSR LFVLXXXXXX XXXXXXXXXX XXXXXXXXXX
151 XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXASGGYM
201 MACVADKIAS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG
301 RQALALNLID EISTDDLLL KAFENKQVIE VKYQEKQSLI QRIQLQAEAS
351 VEKLFKLVN RRADVM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 23>:

a005.seq

```

1 ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51 GTGGAAAGAA ATTTTACTGA ATTACGGTAT TTTCTGCTC GAACTGCTTA
101 CCGTGTTCGG CGCAATTGCG CTGATTGTGT TGGCTATCGT ACAGAGTAAG
151 AAACAGTCGG AAAGCGGCAG TGTCGTA CTG ACGGATTTT CGGAAATAATTA
201 TAAAAACAG CGGCAATCGT TTGAAGCATT CTTTTTAAGC GGGGAAGAGG
251 CAAAACATCA GGAAAAAGAG GAAAAGAAA AGGAAAAGGC GGAAGCCAAA
301 GCAGAGAAAA AGCGTTTGAA GGAGGGTGGG GAGAAATCTT CCGAAACGCA
351 AAAATCCCGC CTTTTGTGT TGGATTTTGA CGGCGATTG TATGCACACG
401 CCGTAGAATC CTTGCGTCAT GAGATTACGG CGGTGCTTTT GATTGCCAAG
451 CCTGAAGATG AGGTTCTGCT TAGATTGGAA AGTCCGGGCG GCGTGTTTCA
501 CGGTTACGGT TTGGCGGCTT CGCAGCTTAG GCGTTGCGC GAACGCAATA
551 TTCCGCTGAC CGTCGCCGTC GATAAGGTGG CGGCGAGCGG TGTTTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGTTTCC GCTCCGTTTG CGATTGTCTG
651 TTCGGTGGGT GTTGTAGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGGCGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGGAAGAG GGCAAACAGA AATTCGACA
801 GGAACGTGGG GAAACGCATC AGTTGTTCAA GCAGTTTGTC AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGGCGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCGA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTTG AAAACAAACA GGTATCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTGCAGGC GGAAGCTTCT
1051 GTTGAAAAGT TGTTTGCCAA ACTTGTC AAC CGGCGGGCGG ATGTGATGTA
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 24; ORF 005.a>:

a005.pep

```

1 MDNIDMFPE QEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 QQSESGSVVL TDFSENYKKQ RQSFEAFFLS GEEAKHQEKE EKKKEKAEAK
101 AEKKRLKEGG EKSETQKSR LFVLDFDGD L YAHAVESLRH EITAVLLIAK
151 PEDEVLLRLE SPGGVVHGYG LAASQLRRLR ERNIPLTVAV DKVAASGGYM
201 MACVADKIVS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG

```


301 RQALALNLID EISTSDDLK KAFENKQVIE VKYQEKQSLI QRIGLQAEAS
 351 VEKLFKLVN RRADM*

m005/a005 79.2% identity over a 366 aa overlap

	10	20	30	40	50	60
m005.pep	MDNIDMFMPQE	EIQSMWKEILL	NYGIFLLELL	TVFGAIALIV	LAIVQSKQ	SXSGSVVL
a005	MDNIDMFMPQE	EIQSMWKEILL	NYGIFLLELL	TVFGAIALIV	LAIVQSKQ	SESGSVVL
	10	20	30	40	50	60
	70	80	90	100	110	120
m005.pep	TDFSENYKKQR	QSFEAFFLSG	EAAHQHKEE	KKKEKAEAK	AEKXRLKEG	GEKSAETXKSR
a005	TDFSENYKKQR	QSFEAFFLSG	EAAHQHKEE	KKKEKAEAK	AEKXRLKEG	GEKSSSETQKSR
	70	80	90	100	110	120
	130	140	150	160	170	180
m005.pep	LFVLXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX	XXXXXXXXXXXX
		:				
a005	LFVLDFDGDLY	AHAVESLRHEI	TAVLLIAKPE	DEVLLRLESP	GGVVHGYGLA	ASQLRRLR
	130	140	150	160	170	180
	190	200	210	220	230	240
m005.pep	XXXXXXXXXXXX	ASGGYMMACV	ADKIASAPFA	IVGSGVVAE	VPNIHRLKK	HDIDVD
	:					
a005	ERNIPLTVAV	DKVAASGGY	MMACVADKIV	SAPFAIVGS	GVVAEVPNI	HRLKKHDIDVD
	190	200	210	220	230	240
	250	260	270	280	290	300
m005.pep	VMTAGEFKRTV	TFMGENTEK	GKQKFRQEL	EETHQLFKQ	FVSENRPQ	LDIEEVATGEHWFG
a005	VMTAGEFKRTV	TFMGENTEK	GKQKFRQEL	EETHQLFKQ	FVSENRPQ	LDIEEVATGEHWFG
	250	260	270	280	290	300
	310	320	330	340	350	360
m005.pep	RQALALNLID	EISTSDDLK	KAFENKQVIE	VKYQEKQSLI	QRIGLQAEAS	VEKLFKLVN
a005	RQALALNLID	EISTSDDLK	KAFENKQVIE	VKYQEKQSLI	QRIGLQAEAS	VEKLFKLVN
	310	320	330	340	350	360
m005.pep	RRADMVX					
a005	RRADMVX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 005 shows 77.0% identity over a 366 aa overlap with a predicted ORF (ORF 005.ng) from *N. gonorrhoeae*:

m005/g005

	10	20	30	40	50
m005.pep	MDNIDMFMPQE	EIQSMWKEILL	NYGIFLLELL	TVFGAIALIV	LAIVQSKQ
g005	MGMDNIDMFMP	QEIQSMWKEILL	NYGIFLLELL	TVFGAIALIV	LAIVQSKQ
	10	20	30	40	50
	60	70	80	90	100
m005.pep	VLTDSENYKKQ	RQSFEAFFLS	GEEAQQHKEE	KKKEKAEAK	AEKXRLKEG
g005	VLTDSENYKKQ	RSFETFFLSE	EETKHQEKKE	KKKEKAEAK	AEKXRLKEG
	70	80	90	100	110
	120				

	120	130	140	150	160	170
m005.pep	SRLFVLXX					
			:			
g005	SRLFVLDFDGDLYAHAVESLRHEITAVLLIAKPEDEVLLRLESPPGGVVHGYGLAASQLRR					
		130	140	150	160	170
						180
m005.pep	180	190	200	210	220	230
	XXXXXXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSVGVVAEVPNIHRLKKHDID					
	:					
g005	LRERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAVIGSVGVVAEVPNIHRLKKHDID					
		190	200	210	220	230
						240
m005.pep	240	250	260	270	280	290
	VDVMTAGEFKRTVTFMGENTEKKGKQKFRQELEETHQLFKQFVSENRPQLDIEEVATGEHW					
g005	VDVMTAGEFKRTVTFMGENTEKKGKQKFRQELEETHQLFKQFVSENRPGLDIEKIATGEHW					
		250	260	270	280	290
						300
m005.pep	300	310	320	330	340	350
	FGRQALALNLIDEISTSDDLKAFENKQVIEVKYQEKQSLIQRIGLQAEASVEKLFACL					
g005	FGRQALALNLIDEISTSDDLKAFENKQVIEVKYQEKRSLIQRIQLQAEASVEKLFACL					
		310	320	330	340	350
						360
m005.pep	360	VNRRADVMX				
g005	VNRRADVMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 25>:

g006.seq

```

1  ATGCTGCTGG TGCTggaatt ttggttCGGc gtGtCGGCGG TGGGCatact
51  tgCGTTGTTT TTATGGCttt TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTCCG CCTGAACAAC AGCTTGAAC gcgACAACCA CTTTATCCGA
151 AAAGGCGACG AGCGGCAGCT GTACCGCCAT TACGGACTGG TTTCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TGCGTCGGCG
251 CGGCGATGGG TATTTTGTTT GGCTTTGCTT TTGTGATGAT GACGCTCAA
301 GGCTACGGCA GCGCGGGGCA TATTTATTCG GTCGGCACTT ATCTGTGGAT
351 GTTTGCCATG AGTTTGACG ATGTGCCGCG ATTGGTCGAA CAATATTCCA
401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTGGAACG GAACATCAA
451 GCCGGAACCTT GA

```

This corresponds to the amino acid sequence <SEQ ID 26; ORF 006.ng>:

g006.pep

```

1  MLLVLEFWFG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR
51  KGDERQLYRH YGLVSRLRVL ISNREAFGYL CVGAAMGILF GFAFVMTLK
101 GYGSAGHIYS VGTYLWMFAM SLDDVPRIVE QYSNLKDIGO RIEWSERNIK
151 AGT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 27>:

m006.seq

```

1  ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT
51  TGCGTTGTTT TTATGGCTTT TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTCCG CCTGAACAAC AGCTTGAAC GCGACAACCA CTTTATCCGA
151 AAAGGCGACC GCGCGGAGCT GTACCGCCAT TACGGACTGC TTGCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TGCGTCGGCA
251 CGGCGATGGG TATTTTGTTT GGCTTTGCTT TTGTGATGAT GACGCTCAA
301 GGCTACAGCA GCGCGGGGCA TGCTTATTCG GTCGGCACTT ATCTGTGGAT

```

```

351  GTTTGCCATG AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA
401  ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTCCGAACG GAACATCAAA
451  GCCGGAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 28; ORF 006>:

```

m006.pep
  1  MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR
51  KGDRRQLYRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMMTLK
101 GYSSAGHVYS VGTYLWMFAM SLDDVPRLVE QYSLNKDIGQ RIEWSERNIK
151 AGT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 29>:

```

a006.seq
  1  ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT
51  TGC GTTGT TTATGGCTTT TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTCCG CCTGAAGAAC AGCTTGGAAC GCGACAACCA CTTTATCCGA
151 AAAGGCGACG AGCGGCAGCT GGACCGCCAT TACGGACTGC TTGCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TGCGTCGGCA
251 CCGCGATGGG TATTTTGCTT GGCTTTGCTT TTGTGATGAT GACGCTCAAA
301 GGCTACAGCA GCGCGGGGCA TGTCTATTCG GTCGGCACTT ATCTGTGGAT
351 GTTTGCCATA AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA
401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTCCGAACG GAACATCAAA
451 GCCGGAACTT GA

```

This corresponds to the amino acid sequence <SEQ ID 30; ORF 006.a>:

```

a006.pep
  1  MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLKN SLERDNHFIR
51  KGDERQLDRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMMTLK
101 GYSSAGHVYS VGTYLWMFAI SLDDVPRLVE QYSLNKDIGQ RIEWSKRNIK
151 AGT*

```

m006/a006 96.7% identity over a 153 aa overlap

m006.pep	10	20	30	40	50	60
	MLLVLEFWVGVS					
a006	10	20	30	40	50	60
	MLLVLEFWVGVS					
m006.pep	70	80	90	100	110	120
	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYS					
a006	70	80	90	100	110	120
	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYS					
m006.pep	130	140	150			
	SLDDVPRLVEQYSLNKDIGQRIEWSERNIKAGTX					
a006	130	140	150			
	SLDDVPRLVEQYSLNKDIGQRIEWSKRNIKAGTX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 006 shows 95.4% identity over a 153 aa overlap with a predicted ORF (ORF 006.ng) from *N. gonorrhoeae*:

m006/g006

```

m006.pep
  1  MLLVLEFWVGVS
```

g006-1.seq

1	ATGTGGA AAA	TGTTGAAACA	CATAGCCAAA	ACCCACCGCA	AGCGATTGAT
51	TGGCACATTT	TCCCCGGTGC	GACTGGAAAA	CCTTTTGATG	CTGGGGTATC
101	CGGTGTTTGG	CGGTGTTGGC	ATTAATGCCG	TGATTGCGGG	GAGGGTGTGG
151	CAGGCGTTGC	TGTACGCTTT	GGTTGTATTT	TTGATGTGGC	TGGTCGGTGC
201	GGCACGGCGG	ATTGCCGATA	CGCGCACGTT	TACGCGGATT	TATACCGAAA
251	TCGCCGTGCC	GGTTGTGTTG	GAACAACGGC	AGCGGCAAGT	CCCGCATTCA
301	GCGGTAAC TG	CACGGGTTGC	CCTGTGCGCT	GAATTTGTCA	GCTTTTTTGA
351	AGAACACCTG	CCGATGTCCG	CGACATCCGT	CGTATCCATA	TTCGGCGCGT
401	GCATCATGCT	GCTGGTGCCT	GAATTTTGGG	TCGGCGGTGC	GCGGGTGGGC
451	ATACTTGCGT	TGTTTTTATG	GCTTTTGCCA	CGTTTTGCCG	CCATCAGCGA
501	AAACCTGTAT	TTCCGCCTGA	ACAACAGCTT	GGAACGCGAC	AACCACCTTA
551	TCCGAAAAGC	CGACGAGCGG	CAGCTGTACC	GCCATTACGG	ACTGGTTTCG
601	CGCCTGCGTG	TGCTGATTTT	C AACCGGAA	GCCTTCGGGT	ATCTCTGCGT
651	CGGCGCGGCG	ATGGGTATTT	TGTTCCGGCT	TGCTTTTGTG	ATGATGACGC
701	TCAAAGGCTA	CGGCAGCGCG	GGGCATATTT	ATTCCGGTCG	CACTTATCTG
751	TGGATGTTTT	CCATGAGTTT	GGACGATGTG	CCGCGATTGG	TCGAACAATA
801	TTCCAATTTT	AAAGACATCG	GACAACGGAT	AGAGTGGTCG	GAACGGAACA
851	TCAAAGCCGG	AACTTGA			

g006-1.pep

1	MWKMLKHIAK	THRKRLLIGTF	SPVGLENLLM	LGYPVFGGWA	INAVIAGRNV
51	<u>QALLYALVVF</u>	<u>LMWLVGAAARR</u>	IADTRTFTRI	YTEIAVPVVL	EQRQRQVPHS
101	AVTARVALSR	EFVSFFEEHL	PIAATSVVSI	<u>FGACIMLLVL</u>	EFWVGVSavg
151	<u>ILALFLWLLP</u>	RFAAISENLY	FRLNLSLERD	NHFIRKGDER	QLYRHYGLVS
201	RLRLVISNR	AFGYLCVGAA	MGILFGFAFV	MMTLKGYGSA	GHIYSVGTYL
251	WMFAMSLDDV	PRLVEQYSNL	KDIGORIEWS	ERNIKAGT*	

m006-1.seq

1	ATGTGGA AAA	TGTTGAAACA	CATAGCCCAA	ACCCACC GCA	AGCGATTGAT
51	TGGCACATTT	TCCCTGGTGC	ATCATGGA AAA	CCTTTTGATG	CTGGGTGATC
101	CGGTGTTTGG	CGGCCGGGCG	ATCAATGCCG	TGATTGCGGG	GGAGGTGTGG
151	CAGGCGTTGC	TGTACGCTTT	GGTTGTGCTT	TTGATGTGCG	TGGTCGGTGC
201	GGTGCGGCGG	ATTGCCGATA	CGCGCACGTT	TACGCGGATT	TATACCGAAA
251	TCGCCGTGCC	GGTCGTGTTG	GAACAGCGGC	AGCGACAAGT	CCCGCATTCG
301	GCGGTAAC TG	CGCGGGTTGC	CCTGTCGCGT	GAGTTTGTC A	GCTTTTTTGA
351	AGAACAC T G	CCGATTG CCG	CGACATCGGT	CGATCCGATA	TTCCGGCGCT
401	GCATCATGCT	GCTGGTGCTG	GAATTTTGGG	TCGGCGTGTC	GGCGGTGGGC
451	ATACTTGCGT	TGTTTTTATG	GCTTTTGCCA	CGTTTTGCGG	CCATCAGCGA
501	AAACCTGTAT	TTCCCGCTGA	ACAACAGTAT	GGAACCGCAG	AACCACTTTA
551	TCGGA AAAAG	CGACCGGCGG	CAGCTGTACC	GCCATTACGG	ACTGCTTGGC
601	CGCTGCGTGC	TGCTGATTT C	CAACCGCGAA	GCCTTCGGCT	ATCTCTGCGC

```

651 CGGCACGGCG ATGGGTATTT TGTTCCGGCTT TGCTTTTGTG ATGATGACGC
701 TCAAAGGCTA CAGCAGCGCG GGGCATGTCT ATTCGGTCGG CACTTATCTG
751 TGGATGTTTG CCATGAGTTT GGACGACGTG CCGCGATTGG TCGAACAATA
801 TTCCAATTTG AAAGACATCG GACAACGGAT AGAGTGGTCG GAACGGAACA
851 TCAAAGCCGG AACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 34; ORF 006-1>:

```

m006-1.pep
  1 MWKMLKHIAQ THRKRLIGTF SLVGLENLLM LVYPVFGGRA INAVIAGEVW
  51 QALLYALVVL LMWLVGAVRR IADTRTFTRI YTEIAVPVVL EQRQRQVPHS
 101 AVTARVALSR EFVSFFEEHL PIAATSVVSI FGACIMLLVL EFWVGVSavg
 151 ILALFLWLLP RFAAISENLY FRLNNSLERD NHFIRKGD RR QLYRHYGLLA
 201 RLRVLISNRE AFGYLCVGTA MGILFGFAFV MMTLKGYSSA GHVYSVGTYL
 251 WMFAMSLDDV PRLVEQYSNL KDIGQRIEWS ERNIKAGT*

```

m006-1/g006-1 95.5% identity in 288 aa overlap

m006-1.pep	10	20	30	40	50	60
	MWKMLKHIAQTHRKRLIGTFSLVGLENLLMLVYPVFGGRAINAVIAGEVWQALLYALVVL					
g006-1	10	20	30	40	50	60
	MWKMLKHIAKTHRKRLIGTFSPVGLENLLMLGYPVFGGWAINAVIAGRNVQALLYALVVF					
m006-1.pep	70	80	90	100	110	120
	LMWLVGAVRRIADTRTFTRIYTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL					
g006-1	70	80	90	100	110	120
	LMWLVGAARRIADTRTFTRIYTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL					
m006-1.pep	130	140	150	160	170	180
	PIAATSVVSIFGACIMLLVLEFWVGVSavgILALFLWLLPRFAAISENLYFRLNNSLERD					
g006-1	130	140	150	160	170	180
	PIAATSVVSIFGACIMLLVLEFWVGVSavgILALFLWLLPRFAAISENLYFRLNNSLERD					
m006-1.pep	190	200	210	220	230	240
	NHFIRKGD RR QLYRHYGLLARLRVLISNREAFGYLCVGTA MGILFGFAFV MMTLKGYSSA					
g006-1	190	200	210	220	230	240
	NHFIRKGD RR QLYRHYGLVSR LRVLISNREAFGYLCVGAAMGILFGFAFV MMTLKGYGSA					
m006-1.pep	250	260	270	280	289	
	GHVYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					
g006-1	250	260	270	280		
	GHIYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 35>:

```

a006-1.seq (partial)
  1 ..AGCCAAAACC ACCGCAAGCG ATTGATTGGC ACATTTTTTC TGGTCGGACT
  51 GGAAAACCTT TTGATGCTGG TGTATCCGGT GTTTGGCGGC TGGGCGATTA
 101 ATGCCGTGAT TGCGGGGCG GCGTGCGAGG CGTTGCTGTA CGCTTTGGTT
 151 GTGCTTTTGA TGTGGCTGGT CCGTGCGGCG CGGCGGATTG CCGATACGCG
 201 CACGTTTACG CGGATTATA CCGAAATCGC CGTGCCGGTT GTGTTGGAAC
 251 AGCGGCAGCG GCAAGTCCCG CATTGCGCGG TAACTGCGCG GGTGCCCCTG
 301 TCGCGTGAGT TTGTCAGCTT TTTTGAAGAA CACCTGCCGA TTGCCGCGAC
 351 ATCCGTCGTA TCCATATTCG GCGCGTGCAT CATGCTGCTG GTGCTGGAAT
 401 TTTGGGTCGG CGTGTGCGCG GTGGGCATAC TTGCGTTGTT TTTATGGCTT
 451 TTGCCACGTT TTGCCGCCAT CAGCGAAAAC CTGTATTTCG GCCTGAAGAA
 501 CAGCTTGGA ACGGACAACC ACTTTATCCG AAAAGGCGAC GAGCGGCAGC
 551 TGGACCGCCA TTACGGACTG CTTGCGCGCC TCGGTGTGCT GATTTCCAAC
 601 CGCGAAGCCT TCGGCTATCT CTGCGTCGGC ACGGCGATGG GTATTTTGTT
 651 CGGCTTTGCT TTTGTGATGA TGACGCTCAA AGGCTACAGC AGCGCGGGGC

```

701 ATGTCTATTC GGTCGGCACT TATCTGTGGA TGTTTGCCAT AAGTTTGGAC
 751 GACGTGCCGC GATTGGTCGA ACAATATTCC AATTGAAAG ACATCGGACA
 801 ACGGATAGAG TGGTCGAAAC GGAACATCAA AGCCGGAAC TGA

This corresponds to the amino acid sequence <SEQ ID 36; ORF 006-1.a>:

a006-1.pep (partial)

1 ..SQNHRKRLIG TFFLVGLENL LMLVYPVFGG WAINAVIAGQ AWQALLYALV
 51 VLLMWLVGAA RRIADTRTFT RIYTEIAVPV VLEQRQRQVP HSAVTARVAL
 101 SREFVSFFEE HLPAAATSVV SIFGACIMLL VLEFWVGUSA VGILALFLWL
 151 LPRFAAISEN LYFRLKNSLE RDNHFIRKGD ERQLDRHYGL LARLRVLISN
 201 REAFGYLCVG TAMGILFGFA FVMMLTKGYS SAGHVYSVGT YLWMFAISLD
 251 DVPRLVEQYS NLKDIGQRIE WSKRNIKAGT *

a006-1/m006-1 95.7% identity in 280 aa overlap

	10	20	30	40	50
a006-1.pep	SQNHRKRLIGTFFLVGLENLLMLVYPVFGGWAINAVIAGQAWQALLYALVVL				
m006-1	MWKMLKHIAQTHRKRLIGTFFSLVGLNLLMLVYPVFGGRAINAVIAGEVWQALLYALVVL				
	10	20	30	40	50
	60	70	80	90	100
a006-1.pep	LMWLVGAAARRIADTRTFTRIYTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL				
m006-1	LMWLVGAVRRIADTRTFTRIYTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL				
	70	80	90	100	110
	120	130	140	150	160
a006-1.pep	PIAATSVVSIFGACIMLLVLEFWVGSAVGILALFLWLLPRFAAISENLYFRLKNSLERD				
m006-1	PIAATSVVSIFGACIMLLVLEFWVGSAVGILALFLWLLPRFAAISENLYFRLNNSLERD				
	130	140	150	160	170
	180	190	200	210	220
a006-1.pep	NHFIRKGDERRQLDRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMLTKGYSSA				
m006-1	NHFIRKGDERRQLDRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMLTKGYSSA				
	190	200	210	220	230
	240	250	260	270	280
a006-1.pep	GHVYSVGTYLWMFAISLDDVPRLVEQYSNLKDIGQRIEWSKRNIKAGTX				
m006-1	GHVYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX				
	250	260	270	280	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 37>:

g007.seq

1 atgaACACAA CCCGACTGCC GACCGCCTTC ATCTTGTGCT GCCTCTGcgC
 51 CGCcGCTTCT GCCGccgaca acAGCatcat gaCaAAAGGG CAAAAAGTGT
 101 ACGAATCcAa ctGCATCGCC TGCCACGGCA AGAAAGGGGA AGGGCGCGGC
 151 ACTGCGtTTC CTccgctTTT CCggtcgGac tgtattatga acaAACCGCa
 201 cgTCctgctg cacagcatgg tcaaaggcAt cgacgggaca ttaaagtgg
 251 agcggcaaaa cctacgacgg atttatgCcc gcaaccgcca tcagcgATGC
 301 GGACATTGCC GCCGTCGCCA CTTATATCAT GAACGCCTTT GA

This corresponds to the amino acid sequence <SEQ ID 38; ORF 007.ng>:

g007.pep

1 MNTTRLPTAF ILCLCAAAS AADNSIMTKG QKVYESNCIA CHGKKGEGRG
 51 TAFPPLFRSD CIMNKPHVLL HSMVKGIDGT FKVERQNLRR IYARNRHQRC
 101 GHCRRRHLYH ERL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 39>:

This corresponds to the amino acid sequence <SEQ ID 40; ORF 007>:

m007.pgp

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 41>:

a007.seq

This corresponds to the amino acid sequence <SEQ ID 42; ORF 007.a>:

a007.pgp

m007/a007 97.3% identity over a 113 aa overlap

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 007 shows 86.7% identity over a 113 aa overlap with a predicted ORF (ORF 007.ng) from *N. gonorrhoeae*:

m007/g007

```

      10      20      30      40      50      60
m007.pep  MNTRLPTALVLGCFCAAASAADNSIMTKGQKVYESNCVACHGKKGEGRGTMFPPLYRSD
          |||||::||:|||||||||||||||::|||:|||||
g007       MNTRLPTAFILCCLCAAASAADNSIMTKGQKVYESNCIACHGKKGEGRGTAFPPFLFRSD
          10      20      30      40      50      60

      70      80      90     100     110
m007.pep  FIMKKPQVLLHSMVKGINGTIKVXRQNLQRIHARNRHQRCGHCRRRHLYHERLX
          ||::||:|||||||:|||||:|||||:|||||

```

g007 CIMNKPHVLLHSMVKGIDGTFKVERQNLRRYARNRHQRCGHCRRRHLYHERL
 70 80 90 100 110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 43>:

g007-1.seq (partial)

```

1  ATGAACACAA CCCGACTGCC GACCGCCTTC ATCTTGTGCT GCCTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCATCGCC TGCCACGGCA AGAAAGGGGA AGGCGCGGCG
151 ACTGCGTTTC CTCCGCTTTT CCGGTCGGAC TATATTATGA ACAAACCGCA
201 CGTCCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCC CAACCGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAAACA GGCAAAAGGC AAAAAAAC.
```

This corresponds to the amino acid sequence <SEQ ID 44; ORF 007-1.ng>:

g007-1.pep (partial)

```

1  MNTTRLPTAF ILCCLCAAAS AADNSIMTKG QKVYESNCIA CHGKKGEGRG
51  TAFPPLFRSD YIMNKPHVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKG KKN...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 45>:

m007-1.seq

```

1  ATGAACACAA CCCGACTGCC GACCGCCCTC GTCTTGGGCT GCTTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAAACGCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCC CAACCGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAAACA GGCAAAAGC AAAAAAACT
401 AA
```

This corresponds to the amino acid sequence <SEQ ID 46; ORF 007-1>

m007-1.pep

```

1  MNTTRLPTAL VLGCFCAAAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51  TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKS KKN*
```

m007-1 / g007-1 91.7% identity in 133 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTTRLPTALVLGCFCAAAS	AADNSIMTKGQKVYESNCVACHGKKGEGRG	TMFPPLYRSD			
g007-1	MNTTRLPTAFILCCLCAAAS	AADNSIMTKGQKVYESNCIACHGKKGEGRG	TAFPPLFRSD			
	10	20	30	40	50	60
	70	80	90	100	110	120
m007-1.pep	FIMKKPQVLLHSMVKGINGTIKVNGKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV					
g007-1	YIMNKPHVLLHSMVKGINGTIKVNGKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV					
	70	80	90	100	110	120
	130					
m007-1.pep	TEKDVQAKSKKNX					
g007-1	TEKDVQAKGKKN					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 47>:

a007-1.seq (partial)

```

1  ATGAACACAA CCCGACTGCC GACCGCCCTC GTCTTGGGCT GCCTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
```



```

151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACC GCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CCACTGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAAAACA GGCAAAAAAC AAAAAA..

```

This corresponds to the amino acid sequence <SEQ ID 48; ORF 007-1.a>:

a007-1.pep (partial)

```

1 MNTTRLPTAL VLGCLCAAAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKN KK..

```

m007-1/a007-1 98.5% identity in 132 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTTRLPTALVLGCFCAAAS	AADNSIMTKGQKVYESNCVACHGKKGEGRG	TMFPPLYRSD			
a007-1	MNTTRLPTALVLGCLCAAAS	AADNSIMTKGQKVYESNCVACHGKKGEGRG	TMFPPLYRSD			
	10	20	30	40	50	60
	70	80	90	100	110	120
m007-1.pep	FIMKKPQVLLHSMVKGINGT	IKVNGKTYNGFMPATAISDADIAAVATYIM	NAFDNGGGSV			
a007-1	FIMKKPQVLLHSMVKGINGT	IKVNGKTYNGFMPATAISDADIAAVATYIM	NAFDNGGGSV			
	70	80	90	100	110	120
	130					
m007-1.pep	TEKDVQAKSKKNX					
a007-1	TEKDVQAKNKK					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 49>:

g008.seq

```

1 ATGAACAACA GACATTTTGC CGTCAtcgCC TTGGGCAGCA ACCTTGACAA
51 CCCGCACAA CAAATacgcg gcgcattaga cgcgctctcg tcccatcctg
101 acatccggct tgaaCagggt tcctcactgt aTatgaccgc acctgtcggt
151 tacgAcaaTC agcccgATTT CATCaatgcc gTCTgcaccg TTTCCACCAC
201 CtTGGACGGC ATTGcccTGC TTGCCgaACT CAAccgTATC GAAGCCGATT
251 TCGGACGCGA aCGCAGTTTC CGCAATGCAC CGCGCACATT GGATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACCCCGGCC TTACCCTGCC
351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATACGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTTTG GGAAAATACG GAAAGGTTGT CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGACA GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 50; ORF 008.ng>:

g008.pep

```

1 MNNRHFVIA LGSNLDNPAQ QIRGALDALS SHPDIRLEQV SSLYMTAPVG
51 YDNQPDFINA VCTVSTLDG IALLAELNRI EADFRERSF RNAPRTLDLD
101 IIDFDGISSD DPRLTLEHPR AHERSFVIRP LAEILPDFIL GKYGKVVLS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 51>:

m008.seq

```

1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
51 CCCTGCTCAA CAGGTACGCG CCGCATTGGA CACGCTGTCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATTT TGTCATGCC GTCTGCACCG TTCCACCAC
201 TCTGGACGGC ATTGCCyTGC TTGCCGAAC CAACCGTATC GAGGCTGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GkATTTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACACsCGAC TcACctTGCC

```

```

351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATCCGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTGTTTTA GGAAACACG GAAAGGTGC CGAATTGTCA
451 AAACGGyTGG GCAATCAAGG TATCCGTCTT TTACCGGACA GGTAAAT

```

This corresponds to the amino acid sequence <SEQ ID 52; ORF 008>:

```

m008.pep
  1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
 51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFGRETSF RNAPRTLXLD
101 IIDFDGISSD DTRLTLPHPR AHERSFVIRP LAEILPDFVL GKHGKVAELS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis*<SEQ ID 53>:

```

a008.seq
  1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
 51 CCCTGCCCAA CAGGTACGCG CCGCATTGGA CACGCTGTCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATTG CGTCAATGCC GTCTGCACCG TTTCCACCAC
201 CTTGGACGGC ATTGCCCTGC TTGCCGAAT CAACCGTATC GAAGCCGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GGATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACCCCGGAC TCACCTGCC
351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATAACGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTTTG GGAAACACG GAAAGGTGC CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGATA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 54; ORF 008.a>:

```

a008.pep
  1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
 51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFGRETSF RNAPRTLXLD
101 IIDFDGISSD DTRLTLPHPR AHERSFVIRP LAEILPDFIL GKHGKVAELS
151 KRLGNQGIRL LPDK*

```

m008/a008 97.6% identity over a 164 aa overlap

	10	20	30	40	50	60
m008.pep	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYNQPDFVNA					
a008	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYNQPDFVNA					
	10	20	30	40	50	60
m008.pep	VCTVSTTLDGIALLAELNRIEADFGRETSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
a008	VCTVSTTLDGIALLAELNRIEADFGRETSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
	70	80	90	100	110	120
m008.pep	VCTVSTTLDGIALLAELNRIEADFGRETSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
a008	VCTVSTTLDGIALLAELNRIEADFGRETSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
	70	80	90	100	110	120
m008.pep	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
a008	AHERSFVIRPLAEILPDFILGKHGKVAELSKRLGNQGIRLLPDKX					
	130	140	150	160		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 008 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF008.ng) from *N. gonorrhoeae*:

m008/g008

	10	20	30	40	50	60
m008.pep	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYNQPDFVNA					
g008	MNNRHFAVIALGSNLDNPAQQIRGALDALSSHPDIRLEQVSSLYMTAPVGYNQPDFINA					

183

	10	20	30	40	50	60
	70	80	90	100	110	120
m008.pep	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
g008	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDPRLTLPHPR					
	70	80	90	100	110	120
	130	140	150	160		
m008.pep	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
	: : :					
g008	AHERSFVIRPLAEILPDFILGKYGKVVELSKRLGNQGIRLLPDRX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 55>:

g009.seq

```

1  ATGCCCCGCG CTGCCGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51 CGAACAAAAT ACCCATCGCC GCGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGGAAA TCAGCACACG CAGGCGCGAA ACCAGTCCGT AATGGCGGTA
151 CAGCTGCCGC TCGTCGCCTT TTCGGATAAA GTGGTTGTcg cGTTCCAAGC
201 TGTGTTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AaaaGCCATA A

```

This corresponds to the amino acid sequence <SEQ ID 56; ORF 009.ng>:

g009.pep

```

1  MPRAAFAFER HHHKSKEQN THRRADAEIA EGFAVGNQHT QARNQSVMAV
51 QLPLVAFSDK VVVAFAQVVQ AEIQVFADGG KTWQKP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 57>:

m009.seq

```

1  ATGCCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51 CGAACAAAAT ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGGAAA TCAGCACACG CAGGCGCGCA AGCAGTCCGT AATGGCGGTA
151 CAGCTGCCGC CGGTGCGCCTT TTCGGATAAA GTGGTTGTCTG CGTTCGAAGC
201 TGTGTTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AAAAGCCATA A

```

This corresponds to the amino acid sequence <SEQ ID 58; ORF 009>:

m009.pep

```

1  MPRAAFAFER HHHKSKEQN THRRADAEIA EGFAVGNQHT QARKQSVMAV
51 QLPPVAFSDK VVVAFAQVVQ AEIQVFADGG KTWQKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 009 shows 97.7% identity over a 86 aa overlap with a predicted ORF (ORF 009.ng) from *N. gonorrhoeae*:

m009/g009

	10	20	30	40	50	60
m009.pep	MPRAAFAFERHHHKSKEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK					
	:					
g009	MPRAAFAFERHHHKSKEQNTHRRADAEIAEGFAVGNQHTQARNQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
	70	80				
m009.pep	VVVAFAQVVQAEIQVFADGGKTWQKPX					
g009	VVVAFAQVVQAEIQVFADGGKTWQKPX					
	70	80				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 59>:

```
a009.seq
  1 ATGCCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
 51 CGAACAAAAT ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGGAAA TCAGCACACG CAGGCGCGCA AGCAGTCCGT AATGGCGGTC
151 CAGCTGCCGC TCGTCGCCTT TTCGGATAAA GTGGTTGTCG CGTTCCAAGC
201 TGTTCCTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AAAAGCCATA A
```

This corresponds to the amino acid sequence <SEQ ID 60; ORF 009.a>:

```
a009.pep
  1 MPRAAFAFER HHHKSKAEQN THRRADAEIA EGFVGNQHT QARKQSVMAV
 51 QLPLVAFSDK VVVAFAQVLQ AEIQVFADGG KTWQKP*
```

m009/a009 97.7% identity over a 86 aa overlap

	10	20	30	40	50	60
m009.pep	MPRAAFAFERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK					
a009	MPRAAFAFERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
	70	80				
m009.pep	VVVAFAQVQAEIQVFADGGKTWQKPX					
a009	VVVAFAQVLQAEIQVFADGGKTWQKPX					
	70	80				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 61>:

```
g010.seq
  1 ATGGGTTTTTC CTGTTTCGCAA GTTTGATGCC GTGATTGTCG GCGGTGGCGG
 51 TGCAGGTTTA CGTGCAGCCC TCCAATTATC CAAATCCGGT TTGAATTGTG
101 CCGTTTTTGT CTAAGTGTTT CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GGCAGTATTT CCGCCTCTCT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGCTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGTCGC GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGCGTTGAA AGCGGCAAAA TTTATCAGCG
351 TCCTTTTCGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG GCGGCGGTCT TATTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACCGGT GACGGTTTGG GCATTGCGC CCGTGCGGGC ATTCGGTTGG
701 AAGATATGGA ATTCTGGCAA TTCCACCGA CCGGCGTGGC GGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GGCGGTATTC TGTGAacgc
801 cgacggcgaa cgcTTTATGG AAcgctatgc GCcgACCGta aAagaCTTGG
851 CTTCTCGCga cgtGGTTTTCA CgcgcGatgG CGatggaAat ctatgaaggt
901 cgcggtctgTG GtaaAAAcAa agaCCacgtC TTACTGAAAA TCGACcAtAt
951 cggtGCAGAA AAAATTATGG AAAAAGTACC GGGCATCCGC GAGATTCCA
1001 TTCagtttgc cGGTATCGAT CCGATTAAAG ACCCGATTcc ggttgTGCCG
1051 ACTACCCACT ATATGATGGG CGGCATTcgc aCCAATTATC ACGGTGAAGT
1101 TGTTGTTCCG CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTCCGTAC ACGGTGCGAA CCGTTTGGGT
1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga
```

This corresponds to the amino acid sequence <SEQ ID 62; ORF 010.ng>:

g010.pep

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDWHMY DTVKGSDDLWLG DQDAIEFMCR AAPEAVIELE
101 HMGMFPDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNVRRANTQF FVEWTAQDLI RDENGDDVGV TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RGCCKNKDHFV LLKIDHIGAE KIMEKLPKIR EISIQFAGID PIKDPPIVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 63>:

m010.seq (PARTIAL)

```

1  ..nTCCAATTAT CCAAATCCGG TCTGAATTGT GCCGTTTGT CTAAAGTGT
51  CCCGACCCGT TCGCATACCG TAGCGGCGCA GGGCGGTATT TCCGCCTCTn
101 TGGGTAATGT GCAGGAAGAC CGTTGGGACT GGCACATGTA CGATACCGTG
151 AAAGGTTCCG ACTGTTGGG CGACCAAGAT GCGATTGAGT TTATGTGCCG
201 CGCCGCGCCT GAAGCCGTAA TTGAGTTGGA ACACATGGGT ATGCCTTTTG
251 ACCGTGTGGA AAGCGGTAAA ATTTATCAGC GTCCTTTCGG CGGCCATACT
301 GCCGAACACG GTAAACGCGC GGTAGAACGC GyCTGTGCGG TTGCCGACCG
351 TACAGGTCAT GCGATGCTGC ATACTTTGTA CCAACAAAAC GTCCGTGCCA
401 ATACGCAATT CTTTGTGGAA TGGACGGCAC AAGATTTGAT TCGTGATGAA
451 AACGGCGATG TCGTCGGCGT AACCGCCATG GAAATGGAAA CCGGCGAaT
501 TTATATTTTC CACGCTAAAG CTGTGATGTT TGCTACCGGC GCGGCGGTC
551 GTATTTATGC GTCTTCTACC AATGCCTATA TGAATACCGG CGATGGTTTG
601 GGTATTTGTG CGCGTGCAGG TATCCCGTTG GAAGACATGG AATTCTGGCA
651 ATTCCAGCCG ACCGGCGTGG CGGGTGCGGG CGTGTGATT ACCGAA...

```

This corresponds to the amino acid sequence <SEQ ID 64; ORF 010>:

m010.pep (PARTIAL)

```

1  ..XQLSKSGLNC AVLSKVFPTR SHTVAAQGGI SASXGNVQED RWDWHMYDTV
51  KGSDWLGDQD AIEFMCRAAP EAVIELEHMG MPFDRVESGK IYQRPFGGHT
101 AEHGKRAVER XCAVADRTGH AMLHTLYQQN VRANTQFFVE WTAQDLIRDE
151 NGDVVGVTAM EMETGEVYIF HAKAVMFATG GGGRIYASST NAYMNTGDGL
201 GICARAGIPL EDMFQWQFQP TGVAGAGVLI TE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 65>:

a010.seq

```

1  ATGGGCTTTC CTGTTCCGAA GTTTGATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTC CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GGCGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACCGG
401 CCTGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCCG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCGA CCGGCGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGCGT ACGGCGCGAG GCGGTATTC TGTTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCA CGTTGTTC CCGCGATGG CGATGGAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTAAGTAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTACC GGGCATCCGC GAGATTTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CGGTATTCG ACCAAGTACC ATGGCGAAGT
1101 TGTGTTTCTT CAAGGCGACG AATACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CGGCGAGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACGAACTCCC TGCTGGACTT AGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAACCT TTGCCTGCTA

```

```

1301 ATGCCGGCGA ACTGACCCGC CAACGTATCG AGCGTTTGGG CAATCAAAC
1351 GATGGTGAAA ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GGCGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TGCGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATCA GATGCCAATA CCTTGTCCTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 66; ORF 010.a>:

```

a010.pep
  1  MGFPVRKFDA VIVGGGGAGL RAXLQLSKSG LNCVLSKVF PTRSHTVAAQ
 51  GGISASLGNV QEDRWDWHMY DTVKGS DWLG DQDAIEFMCR AAPEAVIELE
101  HMGMPFDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151  QQNV RANTQF FVEWTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201  ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251  VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301  RGCGKNKDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPIPVVP
351  TTHYMMGGIP TNYHGEVVVP QGDEYEVVPK GLYAAGECAC ASVHGANRLG
401  TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT
451  DGENVDALRR ELQRSVQLHA GVFR TDEILS KGVREVMATA ERVKRTEIKD
501  KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERDDE
551  NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKRVY*

```

m010/a010 98.7% identity over a 231 aa overlap

```

                                10      20      30
m010.pep                      XQLSKSGLNCAVLSKVF PTRSHTVAAQGGISASXGNV
                                |||
a010      MGFPVRKFDAVIVGGGGAGLRAXLQLSKSGLNCAVLSKVF PTRSHTVAAQGGISASLGNV
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m010.pep      QEDRWDWHMYDTVKGSDWLG DQDAIEFMCR AAPEAVIELEHMGMPFDRVESGKIYQRPFG
                                |||
a010      QEDRWDWHMYDTVKGSDWLG DQDAIEFMCR AAPEAVIELEHMGMPFDRVESGKIYQRPFG
                                70      80      90      100     110     120

                                100     110     120     130     140     150
m010.pep      GHTAEHGKRAVERXCAVADRTGHAMLHTLYQQNV RANTQFFVEWTAQDLIRDENG DVVG V
                                |||
a010      GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNV RANTQFFVEWTAQDLIRDENG DVVG V
                                130     140     150     160     170     180

                                160     170     180     190     200     210
m010.pep      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
                                |||
a010      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
                                190     200     210     220     230     240

                                220     230
m010.pep      FQPTGVAGAGVLITE
                                |: |||
a010      FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG
                                250     260     270     280     290     300

```

Computer analysis of this amino acid sequence gave the following results:

m010.pap/q010.pap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 67>:

g010-1.seq..

1	ATGGGTTTTTC	CTGTTTCGCAA	GTTTGATGCC	GTGATTGTCTG	GCGGTGGCGG
51	TGCAGGTTTTA	CGTGCAGCCC	TCCAATTATC	CAAATCCGGT	TTGAATTGTG
101	CCGTTTTTGTC	CAAAGTGTCTC	CCGACCCCGT	CGCATACCGT	AGCGGCGCAG
151	GGCGGTATTT	TCCCGCTCTCT	GGGTAATGTG	CAGGAGGACC	GTTGGGACTG
201	GCACATGTAC	GATACCGTGA	AAGGTTCCGA	TCTGGCTGGGC	GACCAAGATG
251	CGATTGAGTT	TATGTGTCGC	GCTGCGCCTG	AAGCGGTGAT	TGAGTTGGAA
301	CACATGGGTA	TGCCTTTTTGA	CCGCGTTGAA	AGCGGCAAAA	TTTATCAGCG
351	TCCTTTCCGC	GGACATACTG	CCGAACATGG	TAAACGTGCG	GTAGAACGTG
401	CATGTGCGGT	TGCCGACCGT	ACCGGTCATG	CGATGTTGCA	TACTTTGTAC
451	CAACAAAACG	TCCGTGCCAA	TACACAATTC	TTTGTGGAAT	GGACGGCGCA
501	AGATTTGATT	CGTGATGAAA	ACGGCGATGT	CGTCGGCGTA	ACCGCCATGG
551	AAATCGGAAAC	GGGCGCAAGTT	TATATTTTCC	ACGCCAAGGC	CGTGATGTTT
601	GCTACCGGTG	GCGGCGGTGCG	TATTTATGCT	TCTTCTACCA	ATGCTTATAT
651	GAATACCGGT	GACGGTTTTGG	GCATTTGCGC	CCGTGCGGGC	ATTCGGTTGG
701	AAGATATGGA	ATTCTGGCAA	TTCCACCCGA	CCGGCGTGGC	GGGTGCGGGC
751	GTGTTGATTA	CCGAAGGCGT	ACGCGGCGAG	GGCGGTATTC	TGTTGAACGC
801	CGACGGCGGAA	CGCTTTATGG	AACGCTATGC	GCCGACCGTA	AAAGACTTGG
851	CTTCTCGCGA	CGTGTTTTCA	CGCGCATATG	CGATGGAAT	CTATGAAGGT
901	CGCGGCTGTG	GTAAAAACAA	AGACACCGTC	TTACTGAAAA	TCGACCATAT
951	CGGTGCAGAA	AAAATTATGG	AAAAACTGCC	GGGCATCCGC	GAGATTTCCA
1001	TTCAAGTTTGC	CGGTATCGAT	CCGATTAAAG	ACCCGATTCC	GGTTGTGCCG
1051	ACTACCCACT	ATATGATGGG	CGGCATTCCG	ACCAATTATC	ACGGTGAAGT
1101	TGTTGTTCCG	CAAGGCGACG	AGTACGAAAT	ACCTGTAAAC	GGCTGTGATG
1151	CCGCAGGTGA	GTGCGCCTGT	GCTTCCGTAC	ACGGTGCGAA	CCGTTTTGGG

1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga

This corresponds to the amino acid sequence <SEQ ID 68; ORF 010-1.ng>:

g010-1.pep

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKV F PTRSHTVAAQ
51  GGISASLGNV QEDRWDWHMY DTVKGS DWLG DQDAIEFMCR AAPEAVIELE
101 HMGMPPFDRVE SGKIYQRPFG GHAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNV RANTQF FVEWTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RCGGKNKDHV LLKIDHIGAE KIMEKLP GIR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEV PVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*

```

g010-1 / P10444

sp|P10444|DHSA_ECOLI SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT
 gnl|PID|d1015210 (D90711) Succinate dehydrogenase, flavoprotein [Escherichia coli] gi|1786942
 (AE000175) succinate dehydrogenase flavoprotein subunit [Escherichia coli] Length = 588
 Score = 1073 (495.6 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169
 Identities = 191/303 (63%), Positives = 238/303 (78%)

```

Query: 1 MGFPVRKFDAVIVXXXXXXXXXXXXXSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV 60
      M PVR+FDAV++ S+SG CA+LSKVFPTRSHTV+AQGGI+ +LGN
Sbjct: 1 MKLPVREFDAVVIGAGGAGMRAALQISQSQTCALLSKVFPTRSHTVSAQGGITVALGNT 60

Query: 61 QEDRWDWHMYDTVKGSDWLG DQDAIEFMCR AAPEAVIELEHMGMPFDRVESGKIYQRPFG 120
      ED W+WHMYDTVKGSD++GDQDAIE+MC+ PEA++ELEHMG+PF R++ G+IYQRPFG
Sbjct: 61 HEDNWEWHMYDTVKGSDYIGDQDAIEYMCKTGPEAILELEHMG L PFSRLDDGRIYQRPFG 120

Query: 121 GHAEHGKRAVERACAVADRTGHAMLHTLYQQNV RANTQFFVEWTAQDLIRDENG DVVG V 180
      G + G R A ADRTGHA+LHTLYQQN++ +T F EW A DL++++G VVG
Sbjct: 121 GQSKNFGGEQAARTAAADRTGHALLHTLYQQNLKNHTTIFSEWYALDLVKNQDGA VVGC 180

Query: 181 TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ 240
      TA+ +ETGEV F A+A + ATGG GRIY S+TNA++NTGDG+G+ RAG+P++DME WQ
Sbjct: 181 TALCIETGEVVYFKARATVLTGGAGRIYQSTTNAHINTGDGVGM AIRAGVPVQDMEMWQ 240

Query: 241 FHPTGVAGAGVVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG 300
      FHPTG+AGAGVL+TEG RGE GG LLN GERFMERYAP KDLA RDVV+R++ +EI EG
Sbjct: 241 FHPTGIAGAGVVLVTEGCRGEGGYLLNKHGERFMERYAPNAKDLAGR DVVARSIMIEIREG 300

Query: 301 RGC 303
      RGC
Sbjct: 301 RGC 303

```

Score = 249 (115.0 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169
 Identities = 53/102 (51%), Positives = 62/102 (60%)

```

Query: 309 HVLLKIDHIGAEKIMEKLP GIREISIQFAGXXXXXXXXXXXXTTHYMMGGIPTNYHGEVV 368
      H LK+DH+G E + +LPGI E+S FA T HYMMGGIPT G+ +
Sbjct: 310 HAKLKL D HLGKEVLESRLPGILELSRTFAHVD PVKEPIPV IPTCHYMMGGIPTKV T GQAL 369

Query: 369 VPQGDEYEV PVKGLYAAGECACASVHGANRLGTNSLLDLVVF 410
      +V V GL+A GE AC SVHGANRLG NSLLDLVVF
Sbjct: 370 TVNEKGEDVVVPGLFAVGEIACSVHGANRLGGNSLLDLVVF 411

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 69>:

m010-1.seq..

```

1  ATGGGTTTTC CTGTCGCAA GTTTGATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCAGCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GGCGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCGGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC

```



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451 CAACAAAACG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGTCT TATTTATGCG TCTTCTACCA ATGCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGCGGCGAG GGCGGTATTC TGTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTAAGTAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTGGC GGGCATCCGC GAGATTTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CGGCATTCCG ACCAATTACC ACGCGAAGT
1101 TGTCGTCCG CAAGGTGAAG ATTACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CGGCAGGTGA GTGCGCTTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACCAACTCCC TGTGGACTT GGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAAACCT TTGCCTGCTA
1301 ATGCAGGTGA GTGACCCGCG CAACGTATCG AGCGTTTGGG CAACCAAACC
1351 GATGGTGAAA ACGTTGATGC ATTGCGTCCG GAAGTGAAC GCTCTGTACA
1401 ACTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTGGG AATTGGATAA
1551 CCTGATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TGCGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATATCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGATGA

```

This corresponds to the amino acid sequence <SEQ ID 70; ORF 010-1>:

m010-1.pep..

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCAVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDWHMY DTVKGS DWLG DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNV RANTQF FVEWTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPT V KDLASRDVVS RAMAMEIYEG
301 RGCGKNKDHV LLKIDHIGAE KIMEKLP GIR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEV VVP QGEDYEVPVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVQLHA GVFTDEILS KGVREVMAlA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERDDE
551 NWMKHTLYHS DINTLSYKPV HTKPLSVEYI KPAKRVY*

```

m010-1 / g010-1 99.5% identity in 410 aa overlap

	10	20	30	40	50	60
m010-1.pep	MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCAVLSKVF PTRSHTVAAQGGISASLGNV					
g010-1	MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCAVLSKVF PTRSHTVAAQGGISASLGNV					
	10	20	30	40	50	60
m010-1.pep	QEDRWDWHMYDTVKGS DWLG DQDAIEFMCR AAPEAVIELEHMGMPFDRVESGKIYQRPFG					
g010-1	QEDRWDWHMYDTVKGS DWLG DQDAIEFMCR AAPEAVIELEHMGMPFDRVESGKIYQRPFG					
	70	80	90	100	110	120
m010-1.pep	GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNV RANTQF FVEWTAQDLIRDENG DVVG V					
g010-1	GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNV RANTQF FVEWTAQDLIRDENG DVVG V					
	130	140	150	160	170	180
m010-1.pep	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTG DGLGICARAGIPLEDMEFWQ					
g010-1	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTG DGLGICARAGIPLEDMEFWQ					
	190	200	210	220	230	240
m010-1.pep	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTG DGLGICARAGIPLEDMEFWQ					
g010-1	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTG DGLGICARAGIPLEDMEFWQ					

190

	190	200	210	220	230	240
m010-1.pep	250	260	270	280	290	300
	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG					
g010-1	250	260	270	280	290	300
	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG					
m010-1.pep	310	320	330	340	350	360
	RGCCKNKHVLLKIDHIGA EKIMEKLP GIREISIQFAGIDPIKDFIPVVP TTHYMMGGIP					
g010-1	310	320	330	340	350	360
	RGCCKNKHVLLKIDHIGA EKIMEKLP GIREISIQFAGIDPIKDFIPVVP TTHYMMGGIP					
m010-1.pep	370	380	390	400	410	420
	TNYHGEVVVPQGEDYEVPV KGLYAAGECACASV HGANRLGTNSLLDLV VF GKAA GDSMIK					
g010-1	370	380	390	400	410	
	TNYHGEVVVPQGEDYEVPV KGLYAAGECACASV HGANRLGTNSLLDLV VFRPTPRX					
m010-1.pep	430	440	450	460	470	480
	FIKEQSDWKPLPANAGELTRQRIERLDNQTDGENVDALRRELQRSVQLHAGVFRTDEILS					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 71>:

a010-1.seq..

```

1  ATGGGCTTTC CTGTTTCGCAA GTTTGATGCC GTGATTGTCTG GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTGTTC TAAAGTGTTC CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GCGCGTATTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCCG TATTTATGCG TCTTCTACCA ATGCCATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGCGCT ACGGCGCGAG GCGGATATTC TGTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTACTGAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTACC GGGCATCCGC GAGATTTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CCGTATTCCG ACCAAGTACC ATGGCGAAGT
1101 TGTGTTTCC CTCAAGCGACG AATACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CGGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACGAACTCCC TGCTGGACTT AGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAAACCT TTGCCTGCTA
1301 ATGCCGGCGA ACTGACCCGC CAACGTATCG AGCGTTTGGA CAATCAAAGT
1351 GATGGTGAAA ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TGCGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCG GATGCCAATA CTTGCTCCTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 72; ORF 010-1.a>:

a010-1.pep..

```

1  MGFPVRKFDA VIVGGGGAGL RAXLQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDDHMY DTVKGSDDLW DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIIYQRPFG GHAEHGKRA VERACAVADR TGHAMLHTLY

```

151 QQNV RANTQF FVEWTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RGCGKNKDHV LLKIDHIGAE KIMEKLP GIR EISIQFAGID PIKDPVPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEV PVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWK P LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVQLHA GVFR TDEILS KGVREVM AIA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERDDE
551 NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKRVY*

m010-1 / a010-1 99.3% identity in 587 aa overlap

	10	20	30	40	50	60
a010-1.pep	MGFPVRKFD	AVIVGGGGAGL	RAXLQLSKSGLN	CAVLSKVFP	TRSHTVAAQGGIS	ASLSGNV
a010-1	MGFPVRKFD	AVIVGGGGAGL	RAALQLSKSGLN	CAVLSKVFP	TRSHTVAAQGGIS	ASLSGNV
	10	20	30	40	50	60
a010-1.pep	70	80	90	100	110	120
a010-1.pep	QEDRWDWHMY	DTVKGSDWLG	QDQDAIEFMCRAA	PEAVIELEHM	GMPFDRVESG	KIYQRPFG
m010-1	QEDRWDWHMY	DTVKGSDWLG	QDQDAIEFMCRAA	PEAVIELEHM	GMPFDRVESG	KIYQRPFG
	70	80	90	100	110	120
a010-1.pep	130	140	150	160	170	180
a010-1.pep	GHTAEHGKRA	VERACAVADRT	GHAMLHTLYQ	QNV RANTQFF	V E W T A Q D L I	R D E N G D V V G V
m010-1	GHTAEHGKRA	VERACAVADRT	GHAMLHTLYQ	QNV RANTQFF	V E W T A Q D L I	R D E N G D V V G V
	130	140	150	160	170	180
a010-1.pep	190	200	210	220	230	240
a010-1.pep	TAMEMETGEV	YIFHAKAVMF	FATGGGGRIY	ASSTNAYMNT	GDGLGICARAG	I P L E D M E F W Q
m010-1	TAMEMETGEV	YIFHAKAVMF	FATGGGGRIY	ASSTNAYMNT	GDGLGICARAG	I P L E D M E F W Q
	190	200	210	220	230	240
a010-1.pep	250	260	270	280	290	300
a010-1.pep	FHPTGVAGAG	V L I T E G V R G E	G G I L L N A D G E	R F M E R Y A P T V	K D L A S R D V V S	R A M A M E I Y E G
m010-1	FHPTGVAGAG	V L I T E G V R G E	G G I L L N A D G E	R F M E R Y A P T V	K D L A S R D V V S	R A M A M E I Y E G
	250	260	270	280	290	300
a010-1.pep	310	320	330	340	350	360
a010-1.pep	RGCGKNKDHV	L L K I D H I G A E	K I M E K L P G I R	E I S I Q F A G I D	P I K D P I P V V P	T T H Y M M G G I P
m010-1	RGCGKNKDHV	L L K I D H I G A E	K I M E K L P G I R	E I S I Q F A G I D	P I K D P I P V V P	T T H Y M M G G I P
	310	320	330	340	350	360
a010-1.pep	370	380	390	400	410	420
a010-1.pep	TNYHGEVVVP	Q G D E Y E V P V K	G L Y A A G E C A C	A S V H G A N R L G	T N S L L D L V V F	G K A A G D S M I K
m010-1	TNYHGEVVVP	Q G D E Y E V P V K	G L Y A A G E C A C	A S V H G A N R L G	T N S L L D L V V F	G K A A G D S M I K
	370	380	390	400	410	420
a010-1.pep	430	440	450	460	470	480
a010-1.pep	FIKEQSDWK	P L P A N A G E L T R	Q R I E R L D N Q T	D G E N V D A L R R	E L Q R S V Q L H A	G V F R T D E I L S
m010-1	FIKEQSDWK	P L P A N A G E L T R	Q R I E R L D N Q T	D G E N V D A L R R	E L Q R S V Q L H A	G V F R T D E I L S
	430	440	450	460	470	480
a010-1.pep	490	500	510	520	530	540
a010-1.pep	KGVREVM A I A E R V K R T E I	K D K S K V W N T A R I E	A L E L D N L I E V A K A T L V S A E	A R K E S R G A H A		
m010-1	KGVREVM A I A E R V K R T E I	K D K S K V W N T A R I E	A L E L D N L I E V A K A T L V S A E	A R K E S R G A H A		
	490	500	510	520	530	540
a010-1.pep	550	560	570	580		
a010-1.pep	SDDHPERDDE	N W M K H T L Y H S D A N T L S Y K P V H T K P L S V E Y I K P A K R V Y X				

m010-1 SDDHPPERDDENWMKHTLYHSDINTLSYKPVHTKPLSVEYIKPAKRVYX
550 560 570 580

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 73>:

g011.seq
1 ATGAAGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTTG CTTTTCAGAC
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA
101 GCCTGAAAAC CCGCCTTACC GAAGATATGA AAACCGCGAT GCGCGCCAAA
151 GATCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAATGCCG CCGTCAAACA
201 GTTTGAAGTA GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA
251 TCCTGACCAA AATGGTCAAA CAGCGCAAAG ACGGCGCGAA AATCTACACT
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGACGT
351 GCTGCACCGC TACCTGCCGC AAATGCTCTC CGCCGGCGAA ATCCGCACCG
401 CCGTCGAAGC AGCCGTTGCC GAAACCGGCG CGGCAGGTAT GCGGGATATG
451 GGCAAAGTGA TGGTCGTATT GAAAACccGC CTCGCCGGCA AAGccgATAT
501 GGGCGAAGTC AACAAAATCT TGAAAAccGt aCTGACCGCC tga

This corresponds to the amino acid sequence <SEQ ID 74; ORF 011.ng>:

g011.pep
1 MKTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKTRLT EDMKTAMRAK
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDGAKIYT
101 EAGRQDLADK ENAEIDVLHR YLPQMLSAGE IRTAVEAAVA ETGAAGMADM
151 GKVMVVLKTR LAGKADMGEV NKILKTVLTA *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 75>:

m011.seq (partial)
1 ATGAGGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTTG CTTTTCAGAC
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA
101 GCCTGAAAAT CCGCCTTACC GAAGACATGA AAACCGCGAT GCGCGCCAAA
151 GACCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAACGCCG CCGTCAAACA
201 GTTTGAAGTG GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA
251 TCCTGACCAA AATGGTCAAA CAGCGAAAAG ACAGCGCGAA AATCTACACT
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGAGGT
351 ACTGCACCGC TACCTTCCCC AAATGCTTTC CGCCGGCGAA ATCCGTACCG
401 AGGTCGAAGC TGCCGTTGCC GAAACCGGCG CGGCAGGTAT GCGGGATATG
451 GGTAAAGTCA TGGGGCTGCT GAAAACCCGC CTCGCAGGTA AAGCCGA...

This corresponds to the amino acid sequence <SEQ ID 76; ORF 011>:

m011.pep (partial)
1 MRTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKIRLT EDMKTAMRAK
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDSAKIYT
101 EAGRQDLADK ENAEIEVLHR YLPQMLSAGE IRTEVEAAVA ETGAAGMADM
151 GKVMGLLKTR LAGKA.....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 011 shows 95.8% identity over a 165 aa overlap with a predicted ORF (ORF 011.ng) from *N. gonorrhoeae*:

m011/g011

	10	20	30	40	50	60
m011.pep	MRTHRKTCSAVCF	AFQTASKPAVSIR	HPSE	DIMSLKIRLT	EDMKTAMRAK	DQVSLGTIRL
g011	MKTHRKTCSAVCF	AFQTASKPAVSIR	HPSE	DIMSLKTRLT	EDMKTAMRAK	DQVSLGTIRL
	10	20	30	40	50	60
	70	80	90	100	110	120
m011.pep	INAAVKQFEV	DERTEADDAK	ITAILTKMVK	QRKDSAKIY	TEAGRQDLADK	ENAEIEVLHR
g011	INAAVKQFEV	DERTEADDAK	ITAILTKMVK	QRKDGAKIY	TEAGRQDLADK	ENAEIDVLHR

193

	70	80	90	100	110	120
	130	140	150	160		
m011.pep	YLPQMLSAGEIRTEVEAAVAETGAAGMADMGKVMGLLKTRLAGKA					
	:					
g011	YLPQMLSAGEIRTAVEAAVAETGAAGMADMGKVMVVLKTRLAGKADMGEVNKILKTVLTA					
	130	140	150	160	170	180
g011	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 77>:

g012.seq

```

1   ATGCTCGCCC GTCGCTATTT TTTCAATATC CAACCCGGGG CGGTTTTTCAC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGCCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTGCGCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACa
201 gGcggTGGAT ATTCGgcact tccgCcacca caccaccga accgatgacc
251 gcaaacggaG CGGAACAAT TTTATCCGCC acacacgcca tcatatagcc
301 gCCGCTTGCC GCGACCTTAT CGAcggcgac ggTCAGCGGA ATATTGCGTT
351 CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT GAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATTT TTGCGTTTCG
551 GCAGATTTCT CCCC GCCCTC CTTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CTTTTTTTTC CTGATGTTT GTCTCTTCTC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 78; ORF 012.ng>:

g012.pep

```

1   MLARRYFFNI QPGAVFTDKL LEQLMRFLQF LPEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRHFRHHTHR TDDRKRSGNN FIRHTRHHIA
101 AACRDLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS EQNLIFRLGN
151 QKHRRLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRFLPAL LQTLFLCFGF
201 RLFLFLFFFF LMFCLFLA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 79>:

m012.seq

```

1   ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTGCGCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GGCGGTGGAT ATTCGGTACT TCCGCCACCA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAGCAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 GCCGCTCGCn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
351 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
401 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
451 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
501 nnnnnnnnnn nnnnnnnnnn AACACAAAAA GGCGTGATTT nTGC GTTTCG
551 GCAGATTTCT CCCCACCCCTC CTTCAAACGT TTTTCcTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTGT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 80; ORF 012>:

m012.pep

```

1   MLARCHFLNI QLR AVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRYFRHHTHR TDNRKRSGSN FIRHTRHHIT
101 AARXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
151 XXXXXXXXXXX XXXXXXXXXXX XXXQHKKA*F XRFGRFLPTL LQTFFLCFGF
201 RLFLFLFLFF LMLCLFPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 81>:

```
a012.seq
1   ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GGCGGTGGAT ATTCCGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGGCGAC GGTGAGCGGA ATATTGCGTT
351 CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCCTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATTT TTGCGTTTCG
551 GAAGATTCTC CCCCACCCTC CTTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTTT GCCTCTTCCC
651 CGCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 82; ORF 012.a>:

```
a012.pep
1   MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRYFRYNTHR TDNRKRSGNN FIRHTRHHIT
101 TARRHLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS KQNLIFRLGN
151 QKHRRLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRFLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFCLFPA*
```

m012/a012 64.2% identity over a 218 aa overlap

	10	20	30	40	50	60
m012.pep	MLARCHFLNIQLRAVLADKLLLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
a012	MLARCHFLNIQLRAVLADKLLLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m012.pep	NIMFFQQAVIDIRYFRHHTHRTDNRKRSGSNFIRHTRHHITAAARXXXXXXXXXXXXXXXXXXXX					
a012	NIMFFQQAVIDIRYFRYNTHRTDNRKRSGNNFIRHTRHHITTARRHLIDGDGQRNIAFAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m012.pep	XXXQHKKAXF					
a012	PKLRSRQTVTVNHAARTFQSKQNLIFRLGNQKHRRLMTQGFYGVCIQIAVKIQHKKAGF					
	130	140	150	160	170	180
	190	200	210	219		
m012.pep	XRFGRLPTLLQTFFLCFGRFLFLFLFLFFLMCLFPAX					
a012	LRFGRFLPTLLQTLFLCFGRFLFLFLFLFFLMFCLFPAX					
	190	200	210			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 012 shows 58.7% identity over a 218 aa overlap with a predicted ORF (ORF 012.ng) from *N. gonorrhoeae*:

m012/g012

	10	20	30	40	50	60
m012.pep	MLARCHFLNIQLRAVLADKLLLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
g012	MLARRYFFNIQPGAVFTDKLLEQLMRFLQFLPEFLFALFRIFTHKSNRALKFARRHHIHI					

195

	10	20	30	40	50	60
m012.pep	70	80	90	100	110	120
	NIMFFQQAVDIRYFRHHHTRTDNRKSGSNFIRHTRHHITAARXXXXXXXXXXXXXXXXXXXXX					
	: : : : : :					
g012	70	80	90	100	110	120
	NIMFFQQAVDIRHFRHHHTRTDDRKRSGNNFIRHTRHHIAAACRDLIDGDGQRNIAFAQT					
	130	140	150	160	170	180
m012.pep	XXQHKKAXF					
	:	:	:	:	:	
g012	130	140	150	160	170	180
	PKLRSRQTVTVNHAARTFQSEQNLI FRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					
	190	200	210	219		
m012.pep	XRFGRFLPTLLQTFFLCFGRFLFLFLFLFLMLCLFPAX					
	: : : : :					
g012	190	200	210			
	LRFGRLPALQLTFLCFGRFLFLFLFLFLMFLCLFLAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 83>:

m012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGTTTCTCGC
51  TGACAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CTTTTCCTGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGCGTGGAT ATTCGGTACT TCCGCCACCA CACCCACCGA ACCGACAATC
251 GCAAACGAG CGGAAGCAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 GCCGCTCGCC GCCACCTTAT CGACGGCGAC GGTCAGCGGA ATATTGCGTT
351 CGCGCAAACG CyTAAGCTGC GAAGCCGCCA AACCCTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT GAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GCGGGGATTT TTGCGTTTCG
551 GCAGATTTCT CCCCACCTTC CTTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 84; ORF 012-1>:

m012-1.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRHHHTR TDNRKSGSN FIRHTRHHIT
101 AARRHLIDGD GQRNIAFAQT XKLSRQTVT VNHAARTFQS EQNLIFRLGN
151 QKHRRNLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFLFLFA*

```

m012-1/g012 91.7% identity in 218 aa overlap

	10	20	30	40	50	60
m012-1.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	: : : : :					
g012	10	20	30	40	50	60
	MLARRYFFNIQPGAVFTDKLLEQLMRFLQFLPEFLFALFRIFTHKSNRALKFARRHHIHI					
	70	80	90	100	110	120
m012-1.pep	NIMFFQQAVDIRYFRHHHTRTDNRKSGSNFIRHTRHHITAARRHLIDGDGQRNIAFAQT					
	: : : : :					
g012	70	80	90	100	110	120
	NIMFFQQAVDIRHFRHHHTRTDDRKRSGNNFIRHTRHHIAAACRDLIDGDGQRNIAFAQT					
	130	140	150	160	170	180
m012-1.pep	XKLSRQTVTVNHAARTFQSEQNLI FRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					
	: : : : :					
g012	PKLRSRQTVTVNHAARTFQSEQNLI FRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					

196

	130	140	150	160	170	180
	190	200	210	219		
m012-1.pep	LRFG	RFLP	TLQL	FLCF	GRFL	FLFLFLFLMFCLFPAX
g012	LRFG	RFLP	ALLQ	TLFL	CFGR	FLFLFLFLFLMFCLFLAX
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 85>:

a012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTTCACCA
201 GCGCGTGGAT ATTCGGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGGCGAC GGTCAGCGGA ATATTGCGTT
351 CGCGCAAACG CTTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGCCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATT TCGCGTTTCG
551 GAAGATTCTC CCCACCCCTC CTTCAAACGC TTTTCTCTCT CTTTGCGTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTC CTGATGTTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 86; ORF 012-1.a>:

a012-1.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRYNTHR TDNRKRSGNN FIRHTRHHIT
101 TARRHLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS KQNLIFRLGN
151 QKHRRLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRLPTL LQTLFLCFGP
201 RLFLFLFLFF LMFCFLFPA*

```

a012-1/m012-1 97.2% identity in 218 aa overlap

	10	20	30	40	50	60
a012-1.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
m012-1	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
a012-1.pep	NIMFFQQAVDIRYFRYNTHRTDNRKRSGNNFIRHTRHHITTARRHLIDGDGQRNIAFAQT					
m012-1	NIMFFQQAVDIRYFRHHTHRTDNRKRSGSNFIRHTRHHITAARRHLIDGDGQRNIAFAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a012-1.pep	PKLRSRQTVT VNHAARTFQSKQNLIFRLGNQKHRRLMTQGFGYGVCIQIAVKIQHKKAGF					
m012-1	XKLRSRQTVT VNHAARTFQSEQNLIFRLGNQKHRRLMTQGFGYGVCIQIAVKIQHKKAGF					
	130	140	150	160	170	180
	190	200	210	219		
a012-1.pep	LRFG	RFLP	TLQL	FLCF	GRFL	FLFLFLFLMFCLFPAX
m012-1	LRFG	RFLP	TLQL	FLCF	GRFL	FLFLFLFLMFCLFPAX
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 87>:

g013.seq

```

1  aTgcctttga ccatgctgtg cagcaGGAcg tGCGGTTtgt tcataataca
51  gtCcgaccGG AAAagcggAG GAAaCGCAGT GCCGCGCCCT TCCCCTTTCT
101 TGCCGTGGCA GCGATGCag tTgGATTCTGT AACTTTTGT CCCTTTtGtc

```


g013.pcp

m013.seq

m013.pcp

a013.seq

a013.pap

```

              10      20      30      40      50      60
m013.pep    MPLTMLCSSTCGFFMMKSERXSGGNMVP RPSPFLPWQATQLDSYTFCPFVMMLLSAAEEA
            |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a013         MPLTMLCSSTCGFFMMKSERXSGGNMVP RPSPFLPWQATQLDSYTFCPFVMMLLSAAEEA
              10      20      30      40      50      60

              70      80      90     100
m013.pep    AQQQPKTRAVGSRVVFIGVSEFMFETLLLLILRSGXKIFLPNQX
            ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a013         AQRQPKTRAVGSRVVFIGVSLMFETLLLLILRSGXKIFLPNRX
              70      80      90     100

```

ORF 013 shows 73.3% identity over a 101 aa overlap with a predicted ORF (ORF 013.ng) from *N. gonorrhoeae*:

198

m013/g013

	10	20	30	40	50	60
m013.pep	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
	: : : : :					
g013	MPLTMLCSRTCGLFIIQSDRKSGGNAVPRPSPFLPWQAMQLDSYTFCPFVMMLLSAAEAA					
	10	20	30	40	50	60
	70	80	90	100		
m013.pep	AQKQPKTRAVGSRVVFIVGSF-MFETLLLLILR-SGXKIFLPNQX					
	: : : : : : :					
g013	AQRQHMKMAVGSRVVFIVGSPNVLKPCLFLPLRGEKFFWPKSGIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 93>:

g015.seq

```

1  ATGCAGTATC TGATTGTCAA ATACAGCCAT CAAATCTTCG TTACCATCAC
51  CATTTTGGTA TTCAACATCC GTTTTTTCCT ACTTTGGAAA AATCCAGAAA
101 AGCCCTTGGT CGGCTTTTGG AAAGCACTGC CCCACCTCAA CGACACGATG
151 CTGCTGTTTA CGGGATTGTG GCTGATGAAG ATTACCCATT TCTCCCCGTT
201 CAACGCGCCT TGGCTCGGCA CAAAAATCCT GCTCCTGTTC GCCTACATCG
251 CACTGGGCAT GGTAATGATG CGCGCCCGTC CGCGTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTCGCTAT GTGTTGCATC GCCTGCATCG TTTACCTTGC
351 CAAAACCAAA GTCCTGCCAT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 94; ORF 015.ng>:

g015.pep

```

1  MQYLIVKYSH QIFVTITILV FNIRFFLLWK NPEKPLVGFV KALPHLNDTM
51  LLFTGLWLMK ITHFSPFNAP WLGTKILLLF AYIALGMVMM RARPRSTKFY
101 TVYLLAMCCI ACIVYLAKTK VLPF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 95>:

m015.seq (partial)

```

1  ..AAAATCAGAA AAGCCTTGGC GGGCTTTTGG AAGGCACTGC CCCACCTTAA
51  CGACACCATG CTGCTGTTTA CGGGATTGTG GCTGATGAAA ATTACCCATT
101 TCTCCCCGTT CAACGCGCCT TGGCTCGGTA CAAAAATCCT GCTTCTGCTC
151 GCCTATATCG CATTGGGTAT GATGATGATG CGCGCCCGTC CGCGTTCGAC
201 CAAGTTCTAC ACCGTTTACC TGCTCGCCAT GTGTTGCGTC GCCTGCATCG
251 TTTACCTTGC CAAAACCAAA GTCCTGCCTT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 96; ORF 015>:

m015.pep (partial)

```

1  ..KIRKALAGFW KALPHLNDTM LLFTGLWLMK ITHFSPFNAP WLGTKILLLL
51  AYIALGMMM RARPRSTKFY TVYLLAMCCV ACIVYLAKTK VLPF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 97>:

a015.seq

```

1  ATGCAGTATC TGATTGTCAA ATACAGCCAT CAAATCTTCG TTACCATCAC
51  CATTTTGGTA TTCAACATCC GTGTTTTCNT ACTTTGGAAA AATCCAGAAA
101 AGCCCTTGGC GGGCTTTTGG AAGGCACTGC CCCACCTTAA CGACACCATG
151 CTGCTGTTTA CGGGATTGTG GCTGATGAAA ATTACCCATT TCTCCCCGTT
201 CAACGCGCCT TGGCTCGGTA CAAAAATCCT GCTTCTGCTC GCCTATATCG
251 CATTGGGTAT GATGATGATG CGCGCCCGTC CGCGTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTCGCCAT GTGTTGCCTC ACCTGCATCG TTTACCTTGC
351 CAAAACCAAA GTCCTGCCTT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 98; ORF 015.a>:

a015.pep

```

1  MQYLIVKYSH QIFVTITILV FNIRVFXLWK NPEKPLAGFW KALPHLNDTM
51 LLFTGLWLMK ITHFSPFNAP WLGTKILLLL AYIALGMMM RARPRSTKFY
101 TVYLLAMCCL TCIVYLAKTK VLPF*

```

m015/a015 96.7% identity over a 91 aa overlap

```

                                10      20      30
m015.pep                      KIRKALAGFWKALPHLNDTMLLFTGLWLMKITH
                                | | | | | | | | | | | | | | | | | |
a015      LIVKYSHQIFVTITILVFNIRVFXLWKNPEKPLAGFWKALPHLNDTMLLFTGLWLMKITH
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m015.pep      FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTKFYTVYLLAMCCVACIVYLAKTKVLP
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a015      FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTKFYTVYLLAMCCLTCIVYLAKTKVLP
                                70      80      90      100     110     120

m015.pep      FX
               ||
a015          FX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 015 shows 94.5% identity over a 91 aa overlap with a predicted ORF (ORF 015.ng) from *N. gonorrhoeae*:

m015/g015

```

                                10      20      30
m015.pep                      KIRKALAGFWKALPHLNDTMLLFTGLWLMKITH
                                | | | | | | | | | | | | | | | | | |
g015      LIVKYSHQIFVTITILVFNIRFFLLWKNPEKPLVGFVKALPHLNDTMLLFTGLWLMKITH
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m015.pep      FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTKFYTVYLLAMCCVACIVYLAKTKVLP
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g015      FSPFNAPWLGTKILLLLFAYIALGMVMMRRARPRSTKFYTVYLLAMCCVACIVYLAKTKVLP
                                70      80      90      100     110     120

m015.pep      FX
               ||
g015          FX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 99>:

g018.seq

```

1  atGCAGCAGG GGCagttggt tggacgcgtc gcccgcaata AAGATATGCG
51 GAATgctggt CTGCATggtC AGCGGATCGG CAACGGGtac gccgcgcgcg
101 tctttgTCGA TATTGATGTT TTCCAAACCG ATATtgTCAA CGTTCGGACG
151 GCgACCTACG GCTGCCAACA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT tctACATTGC CGTCTGCGTC GAGTTTGACC
251 TCGGTTTTAG CATCCAGATG CAGTTTCAAT tctTCTCCGA ACACGGCTTT
301 CGCCTCGTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 100; ORF 018.ng>:

g018.pep

```

1  MQQGQLVGRV ARNKDMRNAG LHGQRIGNGY AARVFVDIDV FQTDIVNVRT
51 ATYGCQHIFG NKYAFAILL PMDFYIAVCV EFDLGFSIQM QQFFSEHGF

```

101 RLV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 101>:

```
m018.seq
1  ATGCAGCAGA GGCAGTTGGT TGGACGCATC GCCTGCGATG AAGATATGCG
51 GAATACTGGT CTGCATGGTC AGCGGGTCGG CAACAGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATATT TTCCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCCACG GCTGCCAGCA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCATC GAGTTTGACC
251 TCGGTTTTAG CATCCAGATG CAGTTTCAAT TCTTCGCCGA ACACGGCGTT
301 CGCCTCGTCT GA
```

This corresponds to the amino acid sequence <SEQ ID 102; ORF 018>:

```
m018.pep
1  MQQRQLVGRI ACDEDMRNTG LHGQRVGNRY AARIFFDIDI FQTDIVNVRT
51 AAHGCGHIFG NKYAFAFAIL PMDFYIAVCI EFDLGFSIQM QFQFFAEHGV
101 RLV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 103>:

```
a018.seq
1  ATGCAGCAGG GGCAGTTGGT TGGACGCGTC GCCCGCAATA AAGATATGCG
51 GAATACTGGT CTGCATAGTC AGCGGATCGG CAACGGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATGTT TTCCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCCTACG GCTGCCAGCA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCGTC GAGTTTGGCC
251 TCGGTTTTAG CATCCAAATG CAGTTTCAAT TCTTCACCGA ACACGGCTTT
301 CGCCTCGTCT GA
```

This corresponds to the amino acid sequence <SEQ ID 104; ORF 018.a>:

```
a018.pep
1  MQQGQLVGRV ARNKDMRNTG LHSQRIGNGY AARIFFDIDV FQTDIVNVRT
51 AAYGCGHIFG NKYAFAFAIL PMDFYIAVCV EFDLGFSIQM QFQFFTEHGF
101 RLV*
```

m018/a018 86.4% identity over a 103 aa overlap

	10	20	30	40	50	60
m018.pep	MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCGHIFG					
	10	20	30	40	50	60
a018	MQQGQLVGRVARNKDMRNTGLHSQRIGNGYAARIFFDIDVFQTDIVNVRTAAYGCGHIFG					
	70	80	90	100		
m018.pep	NKYAFAFAILPMDFYIAVCI EFDLGFSIQMQFQFFAEHGVRLVX					
	70	80	90	100		
a018	NKYAFAFAILPMDFYIAVCV EFDLGFSIQMQFQFFTEHGFRLVX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 018 shows 84.5% identity over a 103 aa overlap with a predicted ORF (ORF 018.ng) from *N. gonorrhoeae*:

```
m018/g018

10      20      30      40      50      60
m018.pep  MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCGHIFG
||| |||||:| ::|||:|||||:| |||||:| |||:|||||:|||||:|||||
g018      MQQGQLVGRVARNKDMRNAGLHGQRVGNRYAARVFDIDVFQTDIVNVRTATYGCQHIFG
10      20      30      40      50      60
```

	70	80	90	100
m018.pep	NKYAFFAILLPMDFYIAVCIEFDLGFSIQMQFQFFAEHGVRLVX			
	: : :			
g018	NKYAFFAILLPMDFYIAVCVEFDLGFSIQMQFQFFSEHGFRVLX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 105>:

```
g019.seq (partial)
1  ..ctgctggcgg ccctggtgct tgccgcgtgt tcttcgACAA ACacactGCC
51  AGCCGGCAAG ACCCCGGCAG ACAATATAGA AActgcCgAC CTTTCGGCAA
101 GCGTTCCCAC ccgcCCTGCC GAACCGGAAG GAAAAACGCT GGCAGATTAC
151 GGCGGCTACC CGTCCGCACT GGATGCAGTG AAACAGAACA ACGATGCGGC
201 AGCCGCCGCC TATTTGGAAA Acgcaggaga cagCGcgatg gcGGAAAtg
251 tccgcaagga gtgGCTGa
```

This corresponds to the amino acid sequence <SEQ ID 106; ORF 019.ng>:

```
g019.pep (partial)
1  ..LLAALVLAAC SSTNTLPAGK TPADNIETAD LSASVPTRPA EPEGKTLADY
51  GGYPSALDAV KQNNDAAAAA YLENAGDSAM AENVRKEWL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 107>:

```
m019.seq (partial)
1  ATGTACCTAC CCTCTATGAA GCATTCCCTG CCGCTGCTGG CGGCCCTGGT
51  GCTTGCCGCG TGTTCCTCGA CAAACACACT GCCAGCCGGC AAGACCCCGG
101 CAGACAATAT AGAAACTGCC GACCTTTCGG CAAGCGTTCC CACCCGCCCT
151 GCCGAACCCG AAAGAAAAAC GCTGGCAGAT TACGGCGGCT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTTGG
251 AAAACGCCGG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301 AAGTCTTTGG GCGCACGCAG ACAGTGGACG CTGTTTGCAC AGGAATACGC
351 CAAACTCGAA CCGGCAGGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCGCTG AACTGGTCAA AAATACGGGC
451 AAAGTGCCTT CGGGCTGCAC CAAACTGTTG GAACAGGCAG CCGCATCCCG
501 CTTGTTGGAC GGCAACGACG CCTGGAGGCG CGTGC GCGGA CTGCTGGCCG
551 GCCGCCAAAC CACAGACGCA CGCAACCTTG CCGCCGATT GGGCAGCCCG
601 TTTGACGGCG GTACACAAGG TTCGCGCGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAAGAA GCACGCAAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGGAAAGCGG TTTAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATTG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CTGCGCCCT TGGCATATTA
801 CGGCAAGGTT GCCGACCGCC GCCAACTGAC CGACGACCAA ATCAGTGGT
851 ACGCCCGCGC CGCCTTGCGC GCCGACGTT GGGACGAGCT GGCCTCCGTT
901 ATCTCGCATA TGCCCGAAAA ACTGCAAAAA AGCCCGACCT GGCTCTACTG
951 GCTGGCACGC AGCCGCGCCG CAACGGGCAA CACGCAAGAG GCGGAAAAAC
1001 TTTACAAACA GGCGGCAGCG ACGGGCAGGA ATTTTATGC GGTGCTGGCA
1051 GGGGAAGAAT TGGGTCGGAA AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAAAC AGCGTCCGCC GCATGGCGGA AGACGGTGCA GTCAACGCGC
1151 CACTGGTACT GTTCCAAAAC AGCCAATCTG CCGGTGATGC AAAAATGCGC
1201 CGTCAGGCTC AGGCGGAATG GCGTTTGGC ACACGCGGCT TTGACGAAGA
1251 CAAGCTGCTG ACCGCGCGC AAACCGCGTT CGACCACGGT TTTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCGACC GCAAACCTCA CTACACCTTG
1351 CGCTATATTT CGCGGTTTAA AGACACGGTA ATCCGCCACG CGCAAAATGT
1401 TAATGTCGAT CCGGCTTGGG TTTATGGGCT GATTCTGTCAG GAAAGCCGCT
1451 TCGTTATAGG CGCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGTT
1501 ATGCCTGCCA CCGCGCGCGA AATCGCCGGC AAAATCGGTA TGGATGCCGC
1551 ACAACTTTAC ACCGCCGACG GG...
```

This corresponds to the amino acid sequence <SEQ ID 108; ORF 019>:

```
m019.pep (partial)
1  MYLPSMKHSL PLLAALVLAA CSSTNTLPAG KTPADNIETA DLSASVPTRP
```

```

51  AEPERKTLAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARRQWT LFAQEYAKLE PAGRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGLV
251 GHYQSQNLNV PAALDYYGKV ADRRQLTDDQ IEWYARAALR ARRWDELASV
301 ISHMPEKLQK SPTWLYWLAR SRAATGNTQE AEKLYKQAAA TGRNFYAVLA
351 GEELGRKIDT RNNVPDAGKN SVRRMAEDGA VKRALVLFQV SQSAGDAKMR
401 RQAQAEWRFA TRGFDEDKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNYTL
451 RYISPFKDTV IRHAQNVNVD PAWVYGLIRQ ESRFVIGAQS RVGAQGLMQV
501 MPATAREIAG KIGMDAAQLY TADG...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 109>:

```

a019.seq
1  ATGTACCCAC CCTCTCTGAA GCATTCCCTG CCGCTGCTGG TGGNCTGGT
51  GCTTGCCGCG TGTTCTTNGA CAAACACACT GTCAGCCGAC AAGACCCCGG
101 CAGACAATAT AGAAACTGCC GACCTTTCGG CAAGCGTTCC CACCNGCCCT
151 CCCGAACCCG AANGAAAAAC GTNGGCAGAT TACGGCGGCT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTGG
251 AAAACGCCGG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301 AAGTCTTTGG GCGCGCGCAG ACAGTGGACG CTGTNTGCAC ANGAATATGC
351 NAAACTCGAA CCGGCANGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCGCCG AACTGGTCAA AAATACGGGC
451 AACTGCCTT CCGGCTGCAC CAAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTTGTTGGAC GGCAACGACG CCTGGAGGCG CGTGC CGGA CTGCTGGCCG
551 GCCGCCAAAC CACAGACGCA CGCAACCTTG CCGCCGCATT GGGCAGCCCG
601 TTTGACGGCG GTACACAAGG TTCGCGCGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAAGAA GCACGCAAAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGGAAAGCGG TTTAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATTG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CCTGCCGCT TGGACTATTA
801 NGGCAGGTT GCCGACCGCC GCGCAACTGAC CGACGACCAA ATCGAGTGGT
851 ACGCCCGCGC CGCNNTNNGC NNNCGNNGTT NGNANGANNT GGCNNCCGN
901 ANCNCGNNNN TGCNNGANAA ACNNNNNNAN AGNCNNANNT NGNTNNANTG
951 NNTGGCAGCG AGCCGCGCCG CNACGGGCAA CACGCAANAN GCGGANAAAC
1001 TNTACAAACA GGCGGCAGCA NCGGGCANGA ATTTTATGCT NGTGCTGNCN
1051 GGGGAAGAGT TGGGGCGCAN AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAANC AGCGTCTCC GTATGGCGGA AGACGGCGCG ATTAAGCGCG
1151 CGCTGGTGCT GTTCCGAAAC AGCCGAACCG CCGCGATGC GAAAAATGCGC
1201 CGTCNGGCTC AGGCGGAATG GCGTTTCGCC ACACGCGGCT TCGATGAAGA
1251 CAAGCTGCTG ACCGCCGCGC AAACCGCGTT CGACCACGGT TTTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCGACC GCAAACCTCA CTACACCTTG
1351 CGTACATTT CGNNNNNTNA NGACACGGTA ATCCGCCACG CGCAAAATGT
1401 TAATGTCGAT CCGGCGTGGG TTTACGGGCT GATTCGTCAG GAAAGCCGCT
1451 TCGTTATGGG CGCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGTT
1501 ATGCCTGCCA CCGCGCGCGA AATCGCCGGC AAAATCGGTA TGGATGCCGC
1551 ACAACTTTAC ACCGCCGACG GCAATATCCG TATGGGGACG TGGTATATGG
1601 CGGACACCAA ACGCGCCTG CAAAACAACG AAGTCCTCGC CACCGCAGGC
1651 TATAACGCCG GTCCCGGCAG GGCGCGCCGA TGGCAGGCGG ACACGCCCTT
1701 CGAAGGCGCG GTATATGCCG AAACCATCCC GTTTTCCGAA ACGCGCGACT
1751 ATGTCAAAAA AGTGATGGCC AATGCCGCCT ACTACGCCTC CCTCTTCGGC
1801 CGCCCGCACA TCCCGCTCAA ACAGCGTATG GGCATTGTCC CCGCCGCTG
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 019.a>:

```

a019.pep
1  MYPPSLKHSL PLLVLVLAA CSXTNTLSAD KTPADNIETA DLSASVPTXP
51  AEPEXKTXAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARRQWT LXAXEYAKLE PAXRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGLV
251 GHYQSQNLNV PAALDYXGKV ADRRQLTDDQ IEWYARAAXX XRXXXXXXAXX
301 XXXXXXXXXX XXXXXXXXXAR SRAATGNTQX AXKLYKQAAA XGXFYAVLX
351 GEELGRXIDT RNNVPDAGKX SVLRMAEDGA IKRALVLFVN SRTAGDAKMR
401 RXAQAEWRFA TRGFDEDKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNYTL

```

203

451 RYISXXXTDV IRHAQNVNVD PAWVYGLIRQ ESRFVMAQS RVGAQGLMQV
501 MPATAREIAG KIGMDAAQLY TADGNIRMGW WYMADTKRRL QNNEVLATAG
551 YNAGPGRARR WQADTPLEGA VYAETIPFSE TRDYVKKVMA NAAYYASLFG
601 APHIPLKQRM GIVPAR*

m019/a019 88.9% identity over a 524 aa overlap

m019.pep	10	20	30	40	50	60
	MYLPSMKHSLPLLAALVLAACSSNTLTPAGKTPADNIETADLSASVPTRPAPERKTLD					
a019	MYPPSLKHSLPLLVXLVLAACSXTNTLSADKTPADNIETADLSASVPTXPAEPEXKTXAD					
	10	20	30	40	50	60
m019.pep	70	80	90	100	110	120
	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKSLGARQWTLFAQEYAKLE					
a019	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKSLGARQWTLXAXEYAKLE					
	70	80	90	100	110	120
m019.pep	130	140	150	160	170	180
	PAGRAQEVECYADSSRNDYTRAAELVKNTGKLPSTGCTKLEQAAASGLLDGNDAWRRVRG					
a019	PAXRAQEVECYADSSRNDYTRAAELVKNTGKLPSTGCTKLEQAAASGLLDGNDAWRRVRG					
	130	140	150	160	170	180
m019.pep	190	200	210	220	230	240
	LLAGRQTTDARNLAAALGSPFDGGTQGSREYALLNVIGKEARKSPNAAALLSEMESGLSL					
a019	LLAGRQTTDARNLAAALGSPFDGGTQGSREYALLNVIGKEARKSPNAAALLSEMESGLSL					
	190	200	210	220	230	240
m019.pep	250	260	270	280	290	300
	EQRSAFAGVLGHYQSQNLNVPAALDYGKQVADRRQLTDDQIEWYARAALRARRWDELASV					
a019	EQRSAFAGVLGHYQSQNLNVPAALDYGKQVADRRQLTDDQIEWYARAAXXXRXXXAXX					
	250	260	270	280	290	300
m019.pep	310	320	330	340	350	360
	ISHMPEKLQKSPTWLYWLARSRAATGNTQEAELKLYQAAATGRNFYAVLAGEELGRKIDT					
a019	XXXXXXXXXXXXXXXXXARSRAATGNTQXAXKLYQAAAXGXNFYAVLXGEELGRKIDT					
	310	320	330	340	350	360
m019.pep	370	380	390	400	410	420
	RNNVPDAGKNSVRRMAEDGAVKRALVLFQNSQSAGDAKMRRQAQAEWRFATRGFDEDKLL					
a019	RNNVPDAGKXSVLRMAEDGAIKRALVLFNRNRTAGDAKMRRXAQAEWRFATRGFDEDKLL					
	370	380	390	400	410	420
m019.pep	430	440	450	460	470	480
	TAAQTAFDHGFYDMAVNSAERTDRKLNITLRYISPFKDTVIRHAQNVNVDPAWVYGLIRQ					
a019	TAAQTAFDHGFYDMAVNSAERTDRKLNITLRYISXXXTDVIRHAQNVNVDPAWVYGLIRQ					
	430	440	450	460	470	480
m019.pep	490	500	510	520		
	ESRFVIGAQSRSVGAQGLMQVMPATAREIAGKIGMDAAQLYTADG					
a019	ESRFVIGAQSRSVGAQGLMQVMPATAREIAGKIGMDAAQLYTADGNIRMGWYMAADTKRRL					
	490	500	510	520	530	540
a019	QNNEVLATAGYNAGPGRARRWQADTPLEGA VYAETIPFSETRDYVKKVMA NAAYYASLFG					
	550	560	570	580	590	600

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 019 shows 95.5% identity over a 89 aa overlap with a predicted ORF (ORF 019.ng) from *N. gonorrhoeae*:

g019/m019

		10	20	30	40	49
g019.pep		LLAALVLAACSSTNTLPAGKTPADNIETADLSASVPTRPAPPEGKTLAD				
m019	MYLP	SMKHS	PLLAALVLAACSSTNTLPAGKTPADNIETADLSASVPTRPAPPERKTLAD			
		10	20	30	40	50
	50	60	70	80	89	
g019.pep	YGGYPSALDAVKQNNDAAAAYLENAGDSAMAENVRKEWL					
m019	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKSLGARROWTLFAQEYAKLE					
		70	80	90	100	110
						120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 111>:

g023.seq

```

1   ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GCGATTGGGT
51  AATGCAGCGT GCGACTGCGG TTATTATGTT GATTTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTGCCCTG CCTAAAGAAT ATCCGGCATG GCAGGCATTT
151 TTTAGTCAAG CTTGGGTAAA AGTATTTACC CAAGTGAGCT TTATCGCCGT
201 ATTCTTGAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATCA
251 AACCCCTTCG CGTGCGTTTG TTTTTCAGG TTGCCACCAT TGtctGGCTG
301 GTCGGCTGCC TCGTGTATTC AGTTAAAGTG ATTTGGGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 023.ng>:

g023.pep

```

1   MVERKLGAH YGLRDWVMQR ATAVIMLIYT VALLVVLFA PKEYPAWQAF
51  FSQAWVKVFT QVSFIQVFLH AWVGIRDLWM DYIKPFGVRL FLQVATIVWL
101 VGCLVYSVKV IWG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 113>:

m023.seq

```

1   ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GCGATTGGGT
51  GATGCAACGT GCGACTGCGG TTATTATGTT GATTTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTCCCTG CCTAAAGAAT ATTCGGCATG GCAGGCATTT
151 TTTAGTCAAA CTTGGGTAAA AGTATTTACC CAAGTGAGCT TCATCGCCGT
201 ATTCTTGAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATCA
251 AACCCCTTCG CGTGCGTTTG TTTTTCAGG TTGCCACCAT CGTTTGGCTG
301 GTCGGCTGTC TCGTGTATTC AGTTAAAGTG ATTTGGGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 114; ORF 023>:

m023.pep

```

1   MVERKLGAH YGLRDWVMQR ATAVIMLIYT VALLVVLFS PKEYSAWQAF
51  FSQTVWKVFT QVSFIQVFLH AWVGIRDLWM DYIKPFGVRL FLQVATIVWL
101 VGCLVYSVKV IWG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

a023.seq

```

1   ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GGGATTGGGC
51  GATGCAACGT GCGACCGCGG TTATTATGTT GATTTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTGCTCTG CCTAAAGAAT ATTCGGCATG GCAGGCATTT
151 TTTAGTCAAA CTTGGGTAAA AGTATTTACC CAAGTGAGCT TCATCGCCGT

```


205

201 ATTCTTGAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATNA
 251 AACCCCTTCGG CGTGCGTTTG TTTTTCAGG TTGCCACCAT CGTCTGGCTG
 301 GTCGGCTGCT TGGTGTATTC AATTAAAGTA ATTTGGGGGT AA

This corresponds to the amino acid sequence <SEQ ID 116; ORF 023.a>:

a023.pep
 1 MVERKLTGAH YGLRDWAMQR ATAVIMLIYT VALLVVL FAL PKEYSAWQAF
 51 FSQTWVKVFT QVSFIAVFLH AWVGIRDLWM DYXKPFVRL FLQVATIVWL
 101 VGCLVYSIKV IWG*

m023/a023 96.5% identity over a 113 aa overlap

	10	20	30	40	50	60
m023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFSLPKEYSAWQAFFSQTWVKVFT					
a023	MVERKLTGAHYGLRDWAMQRATAVIMLIYTVALLVVLFALPKEYSAWQAFFSQTWVKVFT					
	10	20	30	40	50	60
	70	80	90	100	110	
m023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
a023	QVSFIAVFLHAWVGIRDLWMDYXKPFVRLFLQVATIVWLVGCLVYSIKVIWGX					
	70	80	90	100	110	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 023 shows 97.3% identity over a 113 aa overlap with a predicted ORF (ORF 023.ng) from *N. gonorrhoeae*:

g023/m023

	10	20	30	40	50	60
g023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFALPKEYPAWQAFFSQAWVKVFT					
m023	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFSLPKEYSAWQAFFSQTWVKVFT					
	10	20	30	40	50	60
	70	80	90	100	110	
g023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
m023	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 117>:

g025.seq
 1 ATGTTGAAAC AAACgACACT TTTGGCAGCT TGTACCGCCG TTGCCGCTCT
 51 GTTGGGCGGT TGcgCCACCC AACAGCCTGC TccTGTcATT GCAGGCAATT
 101 CAGGTATGCA GACCGTATCG TCTGCGCCGG TTTACAATCC TTATGGCGCA
 151 ACGCCGTACA ATGCCGCTCC TGCCGCCAac gatgcGCCgT ATGTGCCGCC
 201 CGTGCAAact gcgcccgttT ATTGCGCTCC TGCTTATGTT CCGCcgTCTG
 251 CACCTGCCGT TTCGGgtaca tatgtTCCTT CTTACGCACC CgtcgACATC
 301 aacgCGGCGa cgCataCTAT TGTGCGTGCG GACACgGtgt acaACATTTc
 351 caaAcgCtac CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA
 401 CCGACAATAC GTTGAGCATC GGTGAGATTG TTAAAGTCAA ACCGGCaggA
 451 TATGCCGCAC CGAAAACCGC AGCCGTAGAA AGCAGGCCCG CCGTACCGGC
 501 TGCCGCGCAA ACCCTGTGA AACCCGCCGc gcaACCGCCC GTTCAGTCCG
 551 CGCCGCAACC TGCCGCGCCC GCTGCGGAAA ATAAAGCGGT TCCCGCCCCC
 601 GCGCCCGCCC CGCAATCTCC TGCCGCTTCG CCTTCCGGCA CGCGTTCGGT
 651 CGGCGGCATT GTTGGCAGC GTCCGACCCA AGGTAAAGTG GTTGCCGATT

```

701 TCGGCGGCGG CAACAAGGGT GTCGATATTG CCGGCAATGC CGGACAACCC
751 GTTTTGGCGG CGGCTGACGG CAAAGTGGTT TATGCCGGTT CAGGTTTGAG
801 GGGATACGGA AACTTGGTCA TCATCCAGCA CAATTCCTCT TTCCTGACCG
851 CGTACGGGCA CAACCAAAAA TTGCTGGTCG GCGAAGGTCA GCAGGTCAAA
901 CGCGGTCAGC AGGTGCTTTT GATGGGTAAT ACCGATGCTT CCAGAACGCA
951 GCTTCATTTC GAGTGCGTC AAAACGGCAA ACCGGTTAAC CCGAACAGCT
1001 ATATCGCGTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 025.ng>:

g025.pep

```

1  MLKQTTLLAA CTAAVALLGG CATQQPAPVI AGNSGMQTVS SAPVYNPYGA
51  TPYNAAPAAAN DAPYVPPVQT APVYSPPAYV PPSAPAVSGT YVPSYAPVDI
101 NAATHTIVRG DTVYNISKRY HISQDDFRW NGMTDNTLSI GQIVKVKPAG
151 YAAPKTAAVE SRPAVPAAQ TPVKPAAQPP VQSAPQPAAP AAENKAVPAP
201 APAPQSPAAS PSGTRSVGGI VWQRPTQGV VADFGGNGK VDIAGNAGQP
251 VLAAADGKVV YAGSGLRGY NLVIIQHNS FLTAYGHNQK LLVGEGQQVK
301 RGQQVALMGN TDASRTQLHF EVRQNGKPVN PNSYIAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

m025.seq (partial)

```

1  ..GTGCCGCCG TGCAAAGCGC GCCGGTTTAT ACGCCTCCTG CTTATGTTCC
51  GCCGTCTGCA CCTGCCGTTT CGGGTACATA CGTTCCTTCT TACGCACCCG
101 TCGACATCAA CGCGGCGACG CATACTATTG TGCGCGGCGA CACGGTGTAC
151 AACATTTCCA AACGCTACCA TATCTCTCAA GACGATTTCC GTGCGTGGAA
201 CGGCATGACC GACAATACGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC
251 CGGCAGGATA TGCCGCACCG AAAGCCGCAG CCGTAAAAAG CAGGCCCGCC
301 GTACCGGCTG CCGCGCAACC GCCCGTACAG TCCGCACCCG TCGACATTAA
351 CGCGGCGACG CATACTATTG TGCGCGGCGA CACGGTGTAC AACATTTCCA
401 AACGCTACCA TATCTCTCAA GACGATTTCC GTGCGTGGAA CGGCATGACC
451 GACAATATGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC CGGCAGGATA
501 TGCCGCACCG AAAACCGCAG CCGTAGAAAG CAGGCCCGCC GTACCGGCTG
551 CCGTGCAAAC CCCTGTGAAA CCCGCCGCGC AACCGCCTGT GCAGTCCGCG
601 CCGCAACCTG CCGCGCCCCG TGCGGAAAAT AAAGCGGTTT CCGCGCCCCG
651 CCCGCAATCT CCTGCCGCTT CGCCTTCCGG CACGCGTTCT GTCGGCGGCA
701 TTGTTTGGCA GCGTCCGACG CAAGGTAAAG TGGTTGCCGA TTTCCGCGGC
751 AACAACAAGG GTGTCGATAT TGCCGGTAAT GCGGGACAGC CCGTTTTGGC
801 GGCGGCTGAC GGCAAAGTGG TTTATGCCGG TTCAGGTTTG AGGGGATACG
851 GAAACTTGGT CATCATCCAG CATAATTCTT CTTTCCTGAC CGCATACGGG
901 CACAACCAA AATTGCTGGT CGGCGAGGGG CAGCAGGTCA AACCGGTCA
951 GCAGGTGCT TTGATGGGCA ATACCGATGC TTCCAGAACG CAGCTTCATT
1001 TCGAGTGCG TCAAAACGGC AAACCGGTTA ACCCGAACAG CTATATCGCG
1051 TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 025>:

m025.pep (partial)

```

1  ..VPPVQSAPVY TPPAYVPPSA PAVSGTYVPS YAPVDINAAT HTIVRGDTVY
51  NISKRYHISQ DDFRAWNGMT DNTLSIGQIV KVKPAGYAAP KAAAVKSRPA
101 VPAAQPPVQ SAPVDINAAT HTIVRGDTVY NISKRYHISQ DDFRAWNGMT
151 DNLSIGQIV KVKPAGYAAP KTAAVESRPA VPAAVQTPVK PAAQPPVQSA
201 PQPAAPAAEN KAVPAPAPQS PAASPSGTRS VGGIVWQRPT QGKVVADFGG
251 NNKGVDIAGN AGQPVLAAD GKVYAGSGL RGYGNLVIIQ HNSSFLLTAYG
301 HNQKLLVGEG QQVKRQQQVA LMGNTDASRT QLHFEVRQNG KPVNPNSYIA
351 F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

a025.seq

```

1  ATGTTGACAC CAACAACACT TTAGGTAGCT TGTACCGCCC TTGCCGCTCA
51  GTTGGGCGGA TGCCCCACCC AACACCTTC TCCTGTCATT GCAGGCAATT
101 CAGGTATGCA GACCGTACCG TCTGCGCCGG TTTACAATCC TTATGGCGCA

```

```

151  ACGCCGTACA ATGCCGCTCC TGCCGCCAAC GATGCGCCGT ATGTGCCGCC
201  GGTGCAAAGC GCGCCGGTTT ATANGCCTCC TGCTTATGTT CCGCCGTCTG
251  CACCTGCCGT TTCGGGTACA TACGTTCCTT CTTACGCANC CGTCGACATC
301  AACCGGGCGA CCCATACTAT TGTGCGCGGC GACACCGTGT ACAAGATTTC
351  CAAATGCTAC CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA
401  CCGACAATAC GTTGAGCATC GGTCAGATTG TTAAAGTCAA ACCGGCAGGA
451  TATGCCGCAC CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC
501  TGCCGCGCAA CCGCTCGTAC AGTCCGCACC CGTCGACATC AACGCGGCGA
551  CGCATACTAT TGTGCGCGGC GACACGGTGT ACAACATTTC CAAACGCTAC
601  CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA CCGACAATAC
651  GTTGAGCATC GGTCAGATTG TTAAAGTCAA ACCGGCAGGA TATGCCGCAC
701  CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC TGCCGTGCAA
751  ACCCCTGTGA AACCCGCCGC GCAACCGCCT GTGCAGTCCG CGCCGCAACC
801  TGCCGCGCCC GCTGCGGAAA ATAAAGCGGT TCCCGCGCCC GCCCGCAAT
851  CTCCTGCCGC TTCGCCTTCC GGCACGCGTT CGGTGCGCGG CATTGTTTGG
901  CAGCGTCCGA CGCAAGGTAA AGTGGTTGCC GATTTCGGCG GCAACAACAA
951  GGGTGTGAT ATTGCAGGAA ATGCGGGACA GCCCGTTTGT GCGGCGGCTG
1001 ACGGCAAAGT GGTTTATGCA GGTTCGGTT TGAGGGGATA CGGCAATTG
1051 GTCATCATCC AGCATAATTC TTCCTTCTG ACCGCATACG GGCACAACCA
1101 AAAATTGCTG GTCGGCGAAG GCCAGCAGGT CAAACGCGGG CAGCAGGTCG
1151 CTTTGATGGG CAATACCGAG GCTTCTAGAA CGCAGCTTCA TTTCGAGGTG
1201 CGGCAAAACG GCAAACCGGT TAATCCGAAC AGCTATATCG CGTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 025.a>:

```

a025.pep
  1  MLTP TTL*VA CTALAAQLGG CPTQHPSPIV AGNSGMQTVP SAPVYNPYGA
 51  TPYNAA PAAN DAPYVPPVQS APVYXPPAYV PPSAPAVSGT YVPSYAXVDI
101  NAATH TIVRG DTVYKISKCY HISQDD FRAW NGMTDNTLSI GQIVKVKPAG
151  YAAPK AAVK SRPAVPAAQ PLVQSAPVDI NAATH TIVRG DTVYNISKRY
201  HISQDD FRAW NGMTDNTLSI GQIVKVKPAG YAAPK AAVK SRPAVPAAVQ
251  TPVKP AAQPP VQSAPQPAAP AAENKAVPAP APQSPAASPS GTRSVGGIVW
301  QRPTQ GKVVA DFGGNNKGVD IAGNAGQPV LAAADGKVVA GSGLRGYGNL
351  VIIQH NSSFL TAYGHNQKLL VEGEQQVKRG QQVALMGNTE ASRTQLHFEV
401  RQNGK PNVNPN SYIAF*

```

m025/a025 97.4% identity over a 351 aa overlap

```

                                     10      20      30
m025.pep                                VPPVQSAPVYTPPAYVPPSAPAVSGTYVPS
                                     |||||:|||||
a025      GMQTVPSAPVYNPYGATPYNAAPAANDAPYVPPVQSAPVYXPPAYVPPSAPAVSGTYVPS
               40      50      60      70      80      90

               40      50      60      70      80      90
m025.pep      YAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMTDNTLSIGQIVKVKPAGYAAP
               || |||||:|||||
a025      YAXVDINAATH TIVRGDTVYKISKCYHISQDD FRAWNGMTDNTLSIGQIVKVKPAGYAAP
               100     110     120     130     140     150

               100     110     120     130     140     150
m025.pep      KAAAVKSRPAVPAAQPPVQSAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMT
               |||||:|||||
a025      KAAAVKSRPAVPAAQPLVQSAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMT
               160     170     180     190     200     210

               160     170     180     190     200     210
m025.pep      DNMLSIGQIVKVKPAGYAAPKTA AVESRPAVPAAVQTPVKPAAQPPVQSAPQPAAPAAEN
               || |||||:|||||
a025      DNTLSIGQIVKVKPAGYAAPKAAAVKSRPAVPAAVQTPVKPAAQPPVQSAPQPAAPAAEN
               220     230     240     250     260     270

               220     230     240     250     260     270
m025.pep      KAVPAPAPQSPAASPSGTRSVGGIVWQRPTQ GKVVADFGGNNKGVDIAGNAGQPVLAAD
               |||||:|||||

```

```

m025.pep                                10          20          30
                                VPPVQSAPVYTTPPAYVPPSAPAVSGTYVPS
                                |||||:||||:|||||
g025    GMQTVSSAPVYNPYGATPYNAAPAANDAPYVPPVQTAPVYSPPAYVPPSAPAVSGTYVPS
          40          50          60          70          80          90

m025.pep          40          50          60          70          80          90
YAPVDINAATHTIVRGDTVYNISKRYHISQDDFRANGMTDNTLSIGQIVKVKPAGYAAP
|||||
g025    YAPVDINAATHTIVRGDTVYNISKRYHISQDDFRANGMTDNTLSIGQIVKVKPAGYAAP
          100         110         120         130         140         150

m025.pep          100         110         120         130         140         150
KAAAVKSRPAVPAAAQPPVQSAPVDINAATHTIVRGDTVYNISKRYHISQDDFRANGMT
|
g025    K-----

m025.pep          160         170         180         190         200         210
DNMLSIGQIVKVKPAGYAAPKTAAVESRPAPVPAAVQTPVKPAAQPPVQSAPQPAAPAAEN
|||||
g025    -----TAAVESRPAPVPAAAQTPVKPAAQPPVQSAPQPAAPAAEN
          160         170         180         190

m025.pep          220         230         240         250         260
KAVPAPAP--QSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
|||||
g025    KAVPAPAPAPQSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
          200         210         220         230         240         250

m025.pep          270         280         290         300         310         320
ADGKVYVYAGSGLRGYGNLVI IQHNSSFLTAYGHNQKLLVGEQQVVKRQQVALMGNTDAS
|||||
g025    ADGKVYVYAGSGLRGYGNLVI IQHNSSFLTAYGHNQKLLVGEQQVVKRQQVALMGNTDAS
          260         270         280         290         300         310

m025.pep          330         340         350
RTOLHFEVRONGKPVNPNSYIAFX

```

g025 |||||
 RTQLHFEVRQNGKPVNPNSYIAFX
 320 330

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 113>:

g031.seq
 1 ATGGTGTCCC TCCGCTTCAG ATTCGGCAAC CACTTTAAAC GCCGACATTC
 51 TGACAATTTT CTTTTCCGCC AGCCAAATAT CATGCGTATC TTTCGGTTTCG
 101 GGCTTGTTGG GCATGGCAAC CTTCAACAGC CGCGCCATCA CAGGAATCGT
 151 CGTTCCCTGA ATCAGCAGCG ACAGCACCAC CACGGCAAAC GCCACATCAA
 201 ACAGCAGGTG CGAATTGGGA ACGCCCATCA CCAGCGGCAT CATCGCCAGC
 251 GAAATCGGTA CGGCTCCTCG CAAGCCCAAC CAACTGATAT ACGCCTTTTC
 301 ACGCAGGCTG TAATTGAATT TCCACAAACC GCCGAACACT GCCAGCGGAC
 351 GCGCGACCAG CATCAGGAAC GCCGCAATCG CCAAGGCTTC CGCCGCCCTG
 401 TCCAACACGC CGGCGGGAGA AACCAGCAGA CCGAGCATGA CGAACAAAGT
 451 TGCCTGCGCC AGCCAAGCCA AACCGTCCAT CACACGCAA ACCTGTTCG
 501 TcgCACGGTT GCGCTGGTTA CCGACAATGA TGCCGGCAAG GTAAACCGCC
 551 AAAAAGCCGC TGCCGCCTAT GGTATTGGTA AACGCAACA CAAGCAGCCC
 601 GCCCGACACA ATCATCAGCG CGTACAGACC TTCCGtacac acctccaatt
 651 cccaatcaac gtcataagctg tctcccggtg taaaatgttc ttcacttcag
 701 aatccccccc ttcttcccag cccgaaacct tcatgtgtta naccctgggg
 751 tgccccaacg gatttagtaa cctcccaatg actctgcttg tcgccccctt
 801 cgcccgcttt ctccttcgag gaaaacttgt tgccccgctc ttacattaa

This corresponds to the amino acid sequence <SEQ ID 114; ORF 031.ng>:

g031.pep
 1 MVSLRFRFGN HFKRRHSDNF LFRQPNIMRI FRFGLVGHGN LQQRHHRNR
 51 RSLNQQRQHH HGKRHIKQV RIGNAHQHRH HRQRNRYGSS QAQPTDIRLF
 101 TQAVIEFPQT AEHCQRTDQ HQERRNRQGF RRPVQHAGGR NQQTTEHDEQS
 151 CLRQPSQTVH HTQNVFRRTV ALVTDNDAGK VNRQKAAAAY GIGKRKHKQP
 201 ARHNHQRVQT FRTHLQFPIN VIAVSRVKMF FTSESPPSSQ PETFCMXTLG
 251 CPNGFSNLPM TLLVAPFARF LLPGKLVVPV LH*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

m031.seq (partial)
 1 ...CGCCTGAAGC ACGGTGTCGG ACTGCATTTT TATTCGGCTA TACGCCTTTT
 51 CACGCAGGCT GTAATTGAAT TTCCACAAAC CGCCGAACAC TGCCGACGGA
 101 CGCGCGACCA GCATCAGGAA CGCCGCAATC GCCAAGGCTT CCGCCGCCCT
 151 GTCCAACACG TTGGCAGGAG AAACCAGCAG CAAAGGCATT CCCAAACGTG
 201 CGGACAAAGT GGTGCAAAAC ACGCTCAGAA ACAACAGTGC GCCACCCGGC
 251 AG....

This corresponds to the amino acid sequence <SEQ ID 116; ORF 031>:

m031.pep (partial)
 1 ...RLKHGVGLHF YSAIRLFTQA VIEFPQTAEH CRRTRDQHQE RRRNRQGFRRP
 51 VQHVGRRNQQ QRHSQTCGQS GRNHAQKQQC ATRQ....

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

a031.seq
 1 ATACGCCTTT TCACGCAGGC TGTAATTGAA TTTCCACAAA CCGCCGAACA
 51 CTGCCGGCGG ACGCGCGACC AGCATCAGGA ACGCCGCAAT CGCCAAGGCT
 101 TCCGCCGCCG CGTCCAACAC GTTGGCAGGA GAAACCAGCA GCAAAGGCAT
 151 TCCCAAACGT GCGGACAAAG TGGTCGAAAC CACGCTCAGA AACAACAGTG
 201 CGCCACCCGG CAG

This corresponds to the amino acid sequence <SEQ ID 118; ORF 031.a>:

a031.pep (partial)
 1 IRLFTQAVIE FPQTAEHCRH TRDQHQRERN RQGFRRPVQH VGRRNQQQRH
 51 SQTGQSGRN HAQKQQCATR Q

210

m031/a031 100.0% identity over a 71 aa overlap

	10	20	30	40	50	60
m031.pep	RLKHGVLH	FYSAIRLFTQ	AVIEFPQTAEH	CRRTDQHQ	ERRNRQGFRR	PVQHVGRNQ
a031		IRLFTQAVIEFPQTAEH	CRRTDQHQ	ERRNRQGFRR	PVQHVGRNQ	
		10	20	30	40	
	70	80				
m031.pep	QRHSQTCGQSGRNHAQKQ	QCATRQ				
a031	QRHSQTCGQSGRNHAQKQ	QCATRQ				
	50	60	70			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 031 shows 60.0% identity over a 85 aa overlap with a predicted ORF (ORF 031.ng) from *N. gonorrhoeae*:

m031/g031

				10	20	30
m031.pep				RLKHGVLH	FYSAIRLFTQ	AVIEFPQTAEH
g031	NQQRQHHHGKRHIKQ	QVRIGNAHHQ	RHRQRNRYGSSQAQ	PTDIRLFTQ	AVIEFPQTAEH	
	60	70	80	90	100	110
	40	50	60	70	80	
m031.pep	CRRTDQHQ	ERRNRQGFRR	PVQHVGRNQ	QRHS-QTCGQSGRNHAQKQ	QCATRQ	
g031	CQRTDQHQ	ERRNRQGFRR	PVQHAGGRNQ	TEHDEQSCLRQPSQ	TVHHTQNVFRRTVALV	
	120	130	140	150	160	170
g031	TDNDAGKVN	RQKAAAYGIGK	RKHQPARHNNH	QVRVQTFRTHLQ	FPINVIASRVK	MFFTS
	180	190	200	210	220	230

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 119>:

g032.seq

```

1  ATGCGGCGAA  ACGTGCCTGC  CGTCGCCGTA  TTGCGCCGCC  CACGATTCTGA
51  GGCGTTTTTG  GATTGGCGGT  TGCGTCAGGC  GCGTGCCGTT  CCTGCCGGTA
101 AACAGGGCTT  TGCCGTCCGA  TGCCGTCTGA  CGCAGCGGCA  GATAGTTTTT
151 CAAGGCTTCC  ACGCTTTTGC  CGGTCAGCGG  AACCTGACGC  TGCTTGCGCC
201 CTTTGCCGGT  AACGTGTACC  CACGCTTCGT  CCAAATATAC  ATCATCTGCA
251 TTCAAGCCGT  GTATCTCGCT  CACGCGCAAA  CCGCTGCCGT  ACATCAGCTC
301 GAACAGCGCG  TGGTCGCGCA  CCGCCAGCGG  GTCGCGCCCG  TCCACGGGCA
351 AATCCAACAT  CCGGTTTCTG  CATTCCTGCG  GCAGGGCTTT  GGGTACGCGC
401 TCGGGCTGCT  TCGGCGGTTT  GATGTCGGCG  GTCGGGTCGG  CGCGCATCAG
451 CCGCGGTTTG  ACCAGCCAGG  CGCAATACTG  CCGCCACGCC  GACAGCTTGC
501 GCGCCAGCGT  CCGACCGTCC  AAACCGCGCT  GCGACAGCCG  CCGCAACGCC
551 GccgTAAAA  CGCGCCGCGA  CAAGTCCTGC  GGCACGCgc  ctgcaTCTTC
601 AGACGGCAT  TGTGCCAACA  GTGCAAACAG  TTCTTCCAAA  TCGCGCCGGT
651 ATGCCGCAAC  CGTGTGCTCC  GACTTGCCCT  CGCGCACGAT  GTTTTCCAAA
701 TAAGCGTCAA  AATAcgcgc  AAACccgTCC  AAAACCATAA  CCGTCCCACA
751 CAAATATCAA  AAAACCACTG  A

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 032.ng>:

g032.pep

```

1  MRRNVPVAV  LRRPRFEAF  L  DLALAAQARAV  PAGKQGFVAV  CRLTQRQIVF
51  QGFHAFAGQ  R  NLTLAPFAG  N  NVYPRFVQIY  IICIQAVYLA  HAQTAAVHQL

```

m032.seq (partial)

m032.pep (partial)

a032.seq

a032.pcp

```

      10      20      30      40      50      60
m032.pep  MRRNVXAVAVXRRPLRQTFLDLALAAQARAVPAGKQGFVRCRLTQRQIVFQGFHAFADQR
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a032      MRRNVPAVAVLRRPLRQTFLDLALAAQARAVPAGKQGFVRCRLTQRQIVFQGFHAFAGQR
          10      20      30      40      50      60

```

212

	70	80	90	100	110	120
m032.pep	HLPLXAPFADNVYPRXVQIDIICIQAVYLAHAQTAAVHQFEQGVVAHRQ RVA AVHGQIQH					
a032	NLPLLASFAGNVYPRVQIYIICIQAVYLAHAQTAAVHQFEQRVIAHRQ RVA AVHGQIQH					
	70	80	90	100	110	120
	130	140	150	160	170	
m032.pep	PVQPFLRQGFYALGLLRRFDVGGRVGVHQAALYQPNAILPPRRKLASQRPFPPQTA					
a032	PVQPFLRQGFYALGLLRRFDVGGRVGMQQTAFDQPGAILPPRRQLARQRPRIQTALRQP					
	130	140	150	160	170	180
a032	PQRRRKIALRQALRHAACIFRRHLCQQRKQFFQIAPVCRHRVLRRLALAHDFVQISVKMRR					
	190	200	210	220	230	240

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 032 shows 86.4% identity over a 176 aa overlap with a predicted ORF (ORF 032.ng) from *N. gonorrhoeae*:

m032/g032

	10	20	30	40	50	60
m032.pep	MRRNVXAVAVXRRPLRQTFLDLALAQAARAVPAGKQGFVAVRCRLTQRQIVFQGFHAFADQR					
g032	MRRNVPAVAVLRRPRFEAFDLDLALAQAARAVPAGKQGFVAVRCRLTQRQIVFQGFHAFAGQR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m032.pep	HLPLXAPFADNVYPRXVQIDIICIQAVYLAHAQTAAVHQFEQGVVAHRQ RVA AVHGQIQH					
g032	NLTLAPFAGNVYPRFVQIYIICIQAVYLAHAQTAAVHQFEQRVVAHRQ RVA AVHGQIQH					
	70	80	90	100	110	120
	130	140	150	160	170	
m032.pep	PVQPFLRQGFYALGLLRRFDVGGRVGVHQAALYQPNAILPPRRKLASQRPFPPQTA					
g032	PVQPFLRQGFYALGLLRRFDVGGRVGAHQPAFDQPGAILPPRRQLARQRPPTVQTALRQP					
	130	140	150	160	170	180
g032	PQRRRKIAPRQVLRHAACIFRRHLCQCKQFFQIAPVCRNRVLRRLALAHDFVQISVKIRR					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 115>:

g033.seq

```

1  ATGGCGGCGG CGGACAAACT CTGGGCGGC GACCGCCGA GCGTCGCCAT
51  CATCGGAGAC GCGCGATGA CGGCGGGCA GCGGTTTGA GCCTTGAATT
101 GCGCGGGCGA TATGGATGT GATTGCTGG TCGTCCTCA CGACAACGAA
151 ATGTCGATTT CCCCAACGT CGGCGCGTT CCCAAATAT TTGCCAGCAA
201 CGTCGTGCGC GATATGCAC GACTGTTGAG TACCGTCAA GCGCAAAcgg
251 GCAAGGTATT AGACAAATA CCCGGCGCG TGGagtTTG CCAAAAAGTC
301 GAACAcaaa TCAAAACCCT TGCCGAAGAA GCCGAACAC CCAAACAGTC
351 GCTGTCGCTG TTTGAAATT TCGGCTTCC CTACACCGG CCCGTGGACG
401 GACACAACGT CGAGAATCT GTGGACGTAT TGAAAGACT GCGCAGCCGC
451 AAAGGCCCTC AGTTGCTGA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGACCCc tcaAATACCA CGCCGTCGc aACCTGCcta
551 AAGAAGGCGG GCGCAAATg ccGTCTGAAA AAGAACCCAA GCCCGCCgCc
601 aaaccgACCT ATACCCAAGT ATTCGGCAA TGGCTGTGCG ACCGGGCGGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG

```



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701  GACTGGTGGA  GTTTGAACAA  CGATTCCCCG  ACCGCTATTT  CGATGTCGGC
751  ATCGCCGAGC  AGCACGCCGT  tacCTTTGCC  GGCGGTTTGG  CGTGCGAAGG
801  CATGAAGCCC  GTCGTGGCGA  TTTATTCCAC  CTTTTTACAA  CGCGCCTACG
851  ACCAACTGGT  GCACGACATC  GCCCTGCAAA  ACCTGCCCGT  TTTGTTTGCC
901  GTCGACCGTG  CGGGCATCGT  CGGCGCGGAC  GGTCCGACCC  ATGCCGGCTT
951  GTACGATTTG  AGCTTCTTGC  GCTGTGTGCC  GAACATGATT  GTTGCCGCGC
1001 CGAGCGATGA  AAACGAATGC  CGCCTGCTGC  TTTCGACCTG  CTATCAGGCG
1051 GATGCGCCCG  CCGCCGTCCG  CTATCCGCGC  GGCACGGGTA  CGGGCGCGCC
1101 GGTTTCAGAC  GGCATGGAAA  CCGTGGAAT  CGGCAAGGGC  ATTATCCGCC
1151 GCGAAGGTGA  GAAAACCGCC  TTcatTGCCT  TCGGCAGTAT  GGTGCGCCAC
1201 GCATTGGCGG  TTGCCGAAAA  ACTGAACGCC  ACCGTCGCCG  ATATGCGCTt
1251 cgtcaaacCG  ATAGACGAAG  AGTTGATTGT  CCGCCTTGCC  CGAAGCCAcy
1301 accGCATCGT  TACCCTTGAA  GAAAACGCCG  AACAGGGCGG  CGCAGGCGGC
1351 CCGGTCTTGG  AAGTGTGCG  GAAACACGGC  ATCTGCAAA  CCGTTTTGCT
1401 TTTGGGCGTT  GCCGATACCG  TAACCGAACA  CGGCGATCCG  AAAAACTTT
1451 TGGACGATTT  GGGTTTGAGT  GCCGAAGCGG  TGAACGCCG  GGTGCGCGAG
1501 TGGCTGCCGG  ACCGTGATGC  GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 116; ORF 033.ng>:

g033.pep

```

1  MAAADKLLGG  DRRSVAII  GD  GAMTAGQAFE  ALNCAGDMDV  DLLVVLNDNE
51  MSISPNVGAL  PKYLASN  VVR  DMHGLLSTVK  AQTGKVLDKI  PGAMEFAQKV
101 EHKIKTLAEE  AEHAKQSL  SL  FENFGFRYTG  PVDGHNVENL  VDVCLKDLRSR
151 KGPQLLHVIT  KKGNGYKL  AE  NDPVKYHAVA  NLPKEGGAQM  PSEKEPKPAA
201 KPTYTQVFGK  WLCDRAA  ADS  RLVAITPAMR  EGSGLVEFEQ  RFPDRYFDVG
251 IAEQHAVTFA  GGLACEGM  KP  VVAIYSTFLQ  RAYDQLVHDI  ALQNLPLVLF
301 VDRAGIVGAD  GPTHAGLY  DL  SFLRCVPNMI  VAAPSDENEC  RLLLSTCYQA
351 DAPAAVRYPR  GTGTGAPV  SD  GMETVEIGKG  IIRREGEKTA  FIAFGSMVAT
401 ALAVAEKLNA  TVADMRFV  KP  IDEELIVRLA  RSHDRIVTLE  ENAEQGGAGG
451 AVLEVLAKHG  ICKPVLL  LGV  ADTVTEHGDP  KKLLDDLGLS  AEAVERRVRE
501 WLPDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

m033.seq

```

1  ATGGCGGCGG  CAGACAA  ACT  CTTGGGCAGC  GACCGCCGCA  GCGTCGCCAT
51  CATCGGCGAC  GGC GCGATGA  CGGCGGGGCA  GGCGTTTGAA  GCCTTGAATT
101 GCGCaG.CGA  TATGGATG  Tr  GATTTGCTrG  TCGTCCTCAA  CGACAACGAA
151 ATGTGCGATTT  CCCCCAAC  GT  CGGCGCGCTG  CCGAAATACC  TTGCCAGCAA
201 CGTCGTGCGC  GATATGCA  CG  GCCTGTTGAG  TACCGTCAAA  GCGCAAAACGG
251 GCAAGGTATT  AGACAAA  ATA  CCCGGCGCGA  TGGAGTTTGC  CCAAAAAGTC
301 GAACACAAAA  TCAAAACC  CT  TGCCGAAGAA  GCCGAACACG  CCAAAACAGTC
351 GCTGTCTTTG  TTTGAAA  ACT  TCGGCTTCCG  CTACACCGGC  CCCGTGGACG
401 GACACAACGT  CGAAAAT  CTG  GTGGACGTAT  TGAAAGACTT  GCGCAGCCGC
451 AAAGGCCCTC  AGTTGCT  GCA  CGTCATCACC  AAAAAGGGCA  ACGGCTACAA
501 ACTCGCCGAA  AACGACCC  CG  TCAAATACCA  CGCCGTCGCC  AACCTGCCTA
551 AAGAAAGCGC  GGC GCAAATG  CCGTCTGAAA  AAGAACCCAA  GCCGCGCGCC
601 AAACCGACCT  ATACCCA  AGT  GTTCGGCAAA  TGGCTGTGCG  ACCGGGCGGC
651 GGCAGATTCC  CGACTGG  TTG  CGATTACCCC  CGCCATGCGC  GAGGGCAGCG
701 GCTTGTTTGA  GTTTGAAC  AA  CGATTCCCCG  ACCGCTATTT  CGATGTCGGC
751 ATCGCCGAGC  AGCACGCC  GT  TACCTTTGCC  GGCGGTTTGG  CTTGCGAAGG
801 GATGAAGCCC  GTCGTGG  CGA  TTTATTCCAC  CTTTTTACAA  CGCGCCTACG
851 ACCAACTGGT  GCACGACA  TC  GCCCTGCAAA  ACCTACCCGT  TTTGTTTGCC
901 GTCGACCGCG  CGGGCAT  CGT  CGGCGCGGAC  GGCCCGACCC  ATGCCGGTCT
951 GTACGATTTG  AGCTTTT  TGC  GCTGCGTGCC  GAACATGATT  GTCGCCGCGC
1001 CGAGCGATGA  AAACGAAT  GC  CGCCTGTTGC  TTTTCGACCTG  CTATCAGGCA
1051 GACGCGCCCG  CCGCCGT  CCG  CTATCCGCGC  GGCACGGGTA  CGGGCGCGCC
1101 GGTTTCAGAC  GGCATGG  AAA  CCGTGGAAT  CGGCAAGGGC  ATTATCCGCC
1151 GCGAAGGTGA  GAAAACCG  CA  TTCATTGCCT  TCGGCAGTAT  GGTGCGCCCC
1201 GCATTGGCGG  TTGCCGAA  AA  ACTGAACGCC  ACCGTCGCCG  ATATGCGCTT
1251 CGTCAAACCG  ATAGACGA  AG  AGTTGATTGT  CCGCCTTGCC  CGAAGCCACG

```

```

1301 ACCGCATCGT TACCCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCGGC
1351 GCGGTGCTGG AAGTATTGGC GAAACACGGC ATCTGCAAAC CCGTTTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATTT GGGCTTGAGT GCCGAAGCGG TGAACGGCG TGTGCGCGCG
1501 TGGCTGTCGG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 033>:

m033.pep

```

1 MAAADKLLGS DRRSVAIIGD GAMTAGQAFE ALNCAXDMDV DLLVVLNDNE
51 MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTAAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDVLLKDLRSR
151 KGPQLLHVIT KKGNGYKLA E NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRAAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA
301 VDRAGIVGAD GPTHAGLYDL SFLRCVPNMI VAAPSDENEC RLLLSTCYQA
351 DAPAAVRYPR GTGTGAPVSD GMETVEIGKG IIRREGEKTA FIAFGSMVAP
401 ALAVA EKLNA TVADMR FVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGG
451 AVLEVLAKHG ICKPVLLLG V ADTVTGHGDP KKLLDDLGLS ABAVERRVRA
501 WLSDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

a033.seq

```

1 ATGGCGGCGG CGGACAAACA GTTGGGCAGC GACCGCCGCA GCGTCGCCAT
51 CATCGGCGAC GCGCGATGA CGGCGGTCA GCGGTTTGA GCCTTGAAC
101 GCGCGGCGA TATGGATGTG GATTGCTGG TCGTCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAAGT CGGTGCGTTG CCCAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GACTGTTGAG TACCGTCAA GCGCAAACGG
251 GCAAGGTATT AGACAAAATA CCCGGCGCGA TGGAGTTTGC CCAAAAAGTC
301 GAACATAAAA TCAAACCCCT TGCCGAAGAA GCCGAACACG CCAAACAGTC
351 ACTGCTTTTG TTTGAAAACT TCGGCTTCCG CTATACCGGC CCCGTGGACG
401 GACACAACGT CGAAAATCTG GTCGATGTAT TGAAGACCT GCGCGGACGC
451 AAGGCGCCGC AGCTTCTGCA CGTCATCAC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGATCCCG TCAAATACCA CGCCGTCGCC AACCTGCCTA
551 AAGAAAGCGC GGCGCAAATG CCGTCTGAAA AAGAACCCTA GCCCGCCGCC
601 AAACCGACCT ATACCCAAGT GTTCGGCAA TGGCTGTGCG ACCGGGCGCG
651 GGCAGATTCC CGACTGTTTG CGATTACCC CGCATGCGC GAGGCGAGCG
701 GCTTGGTTGA GTTTGAACAA CGATTCCCG ACCGCTATT CGATGTCGGC
751 ATCGCCGAGC AGCACGCCGT TACCTTTGCC GCGGTTTGG CTTGCGAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTACAA CGCGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAA ACCTGCCCGT TTTGTTTGGC
901 GTCGACCGCG CGGCATCGT CGGCGCGGAC GGCCCGACCC ATGCGGTTT
951 GTACGATTTA AGCTTTTTC GCTGCATTCC GAATATGATT GTCGCGCGC
1001 CGAGCGATGA AAATGAATGC CGCTGCTGC TTTGACCTG CTATCAGGCA
1051 GACGCGCCCG CCGCGTCCG CTATCCGCG GGCACGGGTA CGGGCGTGCC
1101 GGTTCAGAC GGCATGAAA CCGTGAAAT CGGCAAGGGC ATTATCCGCC
1151 CGAAGGTGA GAAAACCGCA TTCATTGCCT TCGGCAGTAT GGTCGCCCTT
1201 GCATTGGCGG TCGCCGAAA ACTGAACGCC ACCGTCGCC ATATGCGCTT
1251 CGTCAAACCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCACG
1301 ACCGCATCGT TACCCTTGAA GAAAACGCC AACAGGGCGG CGCAGGCAGC
1351 GCGGTGCTGG AAGTGTTGGC GAAACACGGC ATCTGCAAAC CCGTCTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATTT GGGCTTGAGT GCCGAAGCGG TGAACGGCG TGTGCGCGCG
1501 TGGCTGTCGG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 120; ORF 033.a>:

a033.pep

```

1 MAAADKQLGS DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVVLNDNE
51 MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTAAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDVLEDLGR
151 KGPQLLHVIT KKGNGYKLA E NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRAAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA

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301 VDRAGIVGAD GPTHAGLYDL SFLRCIPNMI VAAPSDENEC RLLSTCYQA
351 DAPAAVRYPR GTGTGVPVSD GMETVEIGKG IIRREG EKTA FIAFGSMVAP
401 ALAVAGK LNA TVADMR FVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGS
451 AVLEVLAKHG ICKPVLLLG V ADTVTGHGDP KKLLDDLGLS AEAVERRVRA
501 WLSDRDAAN*

```

m033/a033 98.4% identity over a 509 aa overlap

	10	20	30	40	50	60
m033.pep	MAAADKLLGSDRRSVAIIGDGAMTAGQAFEALNCAXDMDVDLLVVLNDNEMSISP NVGAL					
a033	MAAADKQLGSDRRSVAIIGDGAMTAGQAFEALNCAGDMDVDLLVVLNDNEMSISP NVGAL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m033.pep	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL					
a033	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m033.pep	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKG PQLLHVITKKNGYKLAENDPVKYHAVA					
a033	FENFGFRYTGPVDGHNVENLVDVLEDLRGRKG PQLLHVITKKNGYKLAENDPVKYHAVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m033.pep	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSR LVAITPAMREGSGLVEFEQ					
a033	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSR LVAITPAMREGSGLVEFEQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m033.pep	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNL PVLFA					
a033	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNL PVLFA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m033.pep	VDRAGIVGADGPTHAGLYDLSFLRCVPNMIVAAPSDENECRLLSTCYQADAPAAVRYPR					
a033	VDRAGIVGADGPTHAGLYDLSFLRCIPNMIVAAPSDENECRLLSTCYQADAPAAVRYPR					
	310	320	330	340	350	360
	370	380	390	400	410	420
m033.pep	GTGTGAPVSDGMETVEIGKGIIRREG EKTA FIAFGSMVAPALAVAEKLNATVADMR FVKP					
a033	GTGTGVPVSDGMETVEIGKGIIRREG EKTA FIAFGSMVAPALAVAGKLNATVADMR FVKP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m033.pep	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLG VADTVTGHGDP					
a033	IDEELIVRLARSHDRIVTLEENAEQGGAGSAVLEVLAKHGICKPVLLLG VADTVTGHGDP					
	430	440	450	460	470	480
	490	500	510			
m033.pep	KKLLDDLGLSAEAVERRVRAWLSDRDAANX					
a033	KKLLDDLGLSAEAVERRVRAWLSDRDAANX					
	490	500	510			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 033 shows 98.4% identity over a 509 aa overlap with a predicted ORF (ORF 033.ng) from *N. gonorrhoeae*:

m033/g033

m033 . pep	MAAADKLLGSDRRSVAIIGDGAMTAGQAFEALNCAXDMDVDLLVVLNDNEMSI SPNVGAL	60
g033	MAAADKLLGGDRRSVAIIGDGAMTAGQAFEALNCAGDMDVDLLVVLNDNEMSI SPNVGAL	60
m033 . pep	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL	120
g033	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL	120
m033 . pep	FENFGFRYTGPDVGHNVENLVDVLKDLRSRKG PQLLHVITKKGNGYKLAENDPVKYHAVA	180
g033	FENFGFRYTGPDVGHNVENLVDVLKDLRSRKG PQLLHVITKKGNGYKLAENDPVKYHAVA	180
m033 . pep	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAADSRLVAITPAMREGSGLVEFEQ	240
g033	NLPKEGGAQMPSEKEPKPAAKPTYTQVFGKWLCDRAADSRLVAITPAMREGSGLVEFEQ	240
m033 . pep	RFPDRYFDVGIAEQHAVTFAGGLACEGMPVVAIYSTFLQRAYDQLVHDIALQNL PVLFA	300
g033	RFPDRYFDVGIAEQHAVTFAGGLACEGMPVVAIYSTFLQRAYDQLVHDIALQNL PVLFA	300
m033 . pep	VDRAGIVGADGPTHAGLYDLSFLRCVPMIVAAPSDENECRLLLSTCYQADAPAAVRYPR	360
g033	VDRAGIVGADGPTHAGLYDLSFLRCVPMIVAAPSDENECRLLLSTCYQADAPAAVRYPR	360
m033 . pep	GTGTGAPVSDGMETVEIGKGIIRREGEKTAFIAFGSMVAPALAVA EKL NATVADMR FVKP	420
g033	GTGTGAPVSDGMETVEIGKGIIRREGEKTAFIAFGSMVATALAVA EKL NATVADMR FVKP	420
m033 . pep	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGI CKP VLLLGVADTVTG H GDP	480
g033	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGI CKP VLLLGVADTVTEH GDP	480
m033 . pep	KKLLDDLGLSAEAVERRVRAWLSDRDAANX	510
g033	KKLLDDLGLSAEAVERRVREWLPDRDAANX	510

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 121>:

g034 . seq

1	ATGAGCCGTT	TATGGTTTTT	TGCCGTAAAA	AACATTATAA	TCCGCTTAT
51	TTACCTATTG	CCCAAGGAGA	CACAAATGGC	ACTCGTATCC	ATGCGCCAAC
101	TGCTTGACCA	CGCCGCCGAA	AACAGCTACG	GCCTGCCCGC	GTTCAACGTC
151	AACAACCTCG	AACAAATGCG	CGCCATTATG	GAAGCCGCCG	ACCAAGTCAA
201	CGCGCCCGTC	ATCGTACAGG	CGAGCGCAGG	TGCGCGCAAA	TACGcgggCG
251	CGCCGTTTTT	GCGCCACCTG	ATTCTGGCGG	CAGTCGAAGA	ATTTCCGCAC
301	ATCCCCGTCG	TGATGCACCA	AGACCACGGC	GCATCGCCCG	ACGTgtgCCA
351	ACGCTCCATC	CAACTGGGCT	TCTCCTCCGT	GATGATGGAC	GGCTCTTTGC
401	TCGAAGACGG	CAAAACCCCT	TCTTCTTACG	AATACAACGT	CAACGCCACC
451	CGTACCGTCG	TCAACTTCTC	CCACGCCTGC	GGCGTGTCGG	TCGAAGGCGA
501	AATCGGCGTA	TTGGGCAACC	TCGAAACCGG	CGAAGCAGGC	GAAGAAGACG
551	GAGTGGGCGC	GGCAGGCAAA	CTCTCACACG	ACCAAATGCT	CACCAGCGTT
601	GAAGATGCCG	TGCGTTTCGT	TAAAGATACC	GGCGTTGACG	CATTGGCGAT
651	TGCCGTCGGC	ACCAGCCACG	GCGCATACAA	ATTACCCCGT	CCGCCACACG

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701 GCGACGTATT GCGTATCGAC CGCATCAAGG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CGgctCCAGC TCCGTTCCGC AAGAatgGCT
801 GAAAGTCATC AACGAATACG GCGGCAATAT CGGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGCG CAAAGTCAAC
901 ATCGATACCG ACCTGCGCCT CGCTTCCACC GCGCGGTAC GCCGCTACCT
951 TGCCGAAAAC CCGTCCGACT TTGATCCGCG CAAATACTTG GGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCCTCGACC GTTATCTTGC GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAAT CAAACCTGTT TCGTTGGAAA AAATGGCAAG
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 122; ORF 034.ng>:

g034.pep

```

1 MSRLWFFAVK NIIIRLIYLL PKETQMALVS MRQLLDHAAE NSYGLPAFNV
51 NNLEQMRAIM EAADQVNPV IVQASAGARK YAGAPFLRHL ILAAVEEFPF
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLLEDGKTP SSYEYNVNAT
151 RTVVNFHSHAC GVSVEGEIGV LGNLETGEAG EEDGVGAAGK LSHDQMLTSV
201 EDAVRVFKDT GVDALAI AVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKV I NEYGNIGET YGVPVEEIVE GIKHGVRKVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPRKYL GKTIEAMKQI CLDRYLAFGC
351 EGQAGKIKPV SLEKMASRYA KGELNQIVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 123>:

m034.seq (partial)

```

1 ATGAGCTGTT TATGGTTTTT TGCTGTAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA WACAGCTACG GCyTGCCGGC GTTCAACGTC
151 AACAACTCG WACAGATGCG CGCCATCATG GAGGCTGCAG ACCAAGTCGA
201 CGCCCCGTC ATCGTACAGG CGAGTGCCGG TGCGCGCAA TATGCGGGTG
251 CGCCGTTTTT ACGCCACCTG ATTTTGCGCG CTGTCGAAGT ATTTCCACAC
301 ATCCCGTCG TCATGCACCA AGACCACGGC GCATCACCCG ACGTGTGCCA
351 ACGTCCATC CAACTGGGCT TCTCCTCTGT AATGATGGAC GGCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTACG AATACAACGT CAACGCCACA
451 CGTACCGTGG TTAACCTCTC CCACGCTTGC GCGGTATCCG TTGAAGGCGA
501 AATCGCGTA TTGGGCAACC TCGAAACCGG CGATGCAGGC GAAGAAGACG
551 GTGTAGGCGC AGTGGCAAAA CTTTCCACG ACCAAATGCT GACCAGCGTC
601 GAAGATGCCG TATGTTTCGT TAAAGATACC GCGGTTGACG CATTGGCTAT
651 TGCGTCCGCG ACCAGCCACG GCGCATACAA ATTCACCCGT CCGCCCACAG
701 GCGATGTATT ACGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA C...

```

This corresponds to the amino acid sequence <SEQ ID 124; ORF 034>:

m034.pep (partial)

```

1 MSCLWFFAVK NIIIRLIYLL PKETQMALVS MRQLLDHAAE XSYGLPAFNV
51 NNLXQMRAIM EAADQVDAPV IVQASAGARK YAGAPFLRHL ILAAVEVFPF
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFHSHAC GVSVEGEIGV LGNLETGDAG EEDGVGAVGK LSHDQMLTSV
201 EDAVCFVKDT GVDALAI AVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMH...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 125>:

a034.seq

```

1 ATGAGCCGTT TATGGTTTTT TGCCGCAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA AACAGCTACG GCCTGCCCGC GTTCAACGTC
151 AACAACTCG AACAAATGCG CGCCATTATG GAAGCCGCCG ACCAAGTCAA
201 CGCGCCCGTC ATCGTACAGG CGAGCGCAGG TGCGCGCAA TACGCGGGCG
251 CGCCGTTTTT GCGCCACCTG ATTTTGCGCG CTGTCGAAGA ATTTCCGCAC
301 ATCCCGTCG TGATGCACCA AGACCACGGC GCATCGCCCG ACGTGTGCCA
351 ACGTCCATC CAACTGGGCT TTTCTCCGT GATGATGGAC GGCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTATG AATACAACGT CAACGCCACC

```

```

451 CGTACCGTGG TTAATTTCTC CCACGCCTGC GCGGTATCCG TTGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAACTGG CGAAGCCGGC GAAGAAGACG
551 GTGTAGGCGC AGTGGGCAAA CTTTCCACG ACCAAATGCT CACCAGCGTC
601 GAAGATGCCG TGC GTTTCGT TAAAGATACC GCGGTGACG CATTGGCGAT
651 TGCCGTCGGC ACCAGCCACG GCGGTACAA ATTCACCCGT CCGCCACAG
701 GCGACGTGTT GCGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CGGCTCCAGC TCCGTCCGC AAGAATGGCT
801 GAAAGTCATC AACGAATACG GCGCAATAT CGGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGCG TAAAGTCAAC
901 ATCGATACCG ACTTGCGCCT TGCTCCACC GCGCGGTAC GCCGTACCT
951 TGCCGAAAAC CCGTCCGACT TCGATCCGCG CAAATATTG AGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCCTCGACC GCTACCTCG GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAT CAAACCGGTT TCCTTGAAA AAATGGCAAA
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 126; ORF 034.a>:

```

a034.pep
1  MSRLWFFAAK NIIIRLIYLL PKETQMALVS MRQLLDHAAE NSYGLPAFNV
51 NNLEQMRAIM EAADQVNAPV IVQASAGARK YAGAPFLRHL ILAAVEEFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFHAC GVSVEGEIGV LGNLETGEAG EEDGVGAVGK LSHDQMLTSV
201 EDAVRVFKDT GVDALAIAGV TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKV NEYGGNIGET YGVPVEEIVE GIKHGVRKVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPRKYL SKTIEAMKQI CLDRYLAFGC
351 EGQAGKIKPV SLEKMANRYA KGELNQIVK*

```

m034/a034 96.9% identity over a 257 aa overlap

```

          10      20      30      40      50      60
m034.pep  MSCLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNNLXQMRAIM
          ||  |||||:|||||
a034      MSRLWFFAAKNIIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNNLEQMRAIM
          10      20      30      40      50      60

          70      80      90      100     110     120
m034.pep  EAADQVDAPVIVQASAGARKYAGAPFLRHLILAAVEVFPHIPVVMHQDHGASPDVCQRSI
          |||||:|||||
a034      EAADQVNAPVIVQASAGARKYAGAPFLRHLILAAVEEFPHPVVMHQDHGASPDVCQRSI
          70      80      90      100     110     120

          130     140     150     160     170     180
m034.pep  QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVNFHACGVSVEGEIGVLGNLETGDAG
          |||||:|||||
a034      QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVNFHACGVSVEGEIGVLGNLETGEAG
          130     140     150     160     170     180

          190     200     210     220     230     240
m034.pep  EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAIAGVTSHGAYKFTRPPTGDVLRID
          |||||:|||||
a034      EEDGVGAVGKLSHDQMLTSVEDAVRFVKDTGVDALAIAGVTSHGAYKFTRPPTGDVLRID
          190     200     210     220     230     240

          250
m034.pep  RIKEIHQALPNTHIVMH
          |||||
a034      RIKEIHQALPNTHIVMHGSSSVPQEWLKVINEYGGNIGETYGVPVEEIVEGIKHGVRKVN
          250     260     270     280     290     300

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 034 shows 96.5% identity over a 257 aa overlap with a predicted ORF (ORF 034.ng) from *N. gonorrhoeae*:

m034/g034

m034 . pep	MSCLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNNLXQMRAIM	60
g034	MSRLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNNLEQMRAIM	60
m034 . pep	EAADQVDAPVIVQASAGARKYAGAPFLRHLILA AVEVFPHIPVVMHQDHGASPDVCQRSI	120
g034	EAADQVNAPVIVQASAGARKYAGAPFLRHLILA AVEEFPHIPVVMHQDHGASPDVCQRSI	120
m034 . pep	QLGFSSVMMDGSLMEDGKTPSSYEYNVNATRTVNVNFSHACGVSVEGEIGVLGNLETGDAG	180
g034	QLGFSSVMMDGSLLEDGKTPSSYEYNVNATRTVNVNFSHACGVSVEGEIGVLGNLETGEAG	180
m034 . pep	EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAI AVGTSHGAYKFTRPPTGDVLRID	240
g034	EEDGVGAAGKLSHDQMLTSVEDAVRFVKDTGVDALAI AVGTSHGAYKFTRPPTGDVLRID	240
m034 . pep	RIKEIHQALPNTHIVMH	257
g034	RIKEIHQALPNTHIVMHGSSSVPOEWLKVINEYGGNIGETYGVPVEEIVEGIKHGVRKVN	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 127>:

g036 . seq

1	ATGCTGAAGC	CGTGTTTGGT	ATACAGTGCC	TGTGCGGCGG	cgttg cCTGC
51	GCGGACTTCG	AGCAGCAGGC	GTTGCGTGCC	TTCGGGCAGA	TGTGCGTACC
101	AATATTCGAG	CAGGGCGGAC	GCAACGCCCC	GTCGGCGGCA	TTCGGGCGCG
151	GTGGCAATCA	GGTGCAGTTC	GGATTTCGTC	GGCAGGTTCT	GCCAAACGAT
201	AAAGGCGGCA	ATCCTGCCGT	CTTTTCCGC	AAGGAAAACC	TGTTCCGACG
251	GCGAAACAAG	CGCGGACTCA	AATTGGCGTT	GCGTCCACGC	GGACGGGTTG
301	CAGACGGTAT	CGAGCGCGGC	CAGTGC GGCG	CAGTCGGACG	GTGAGGCTGG
351	GCGGATGTTT	ATGTTTCGTG	CTTCCGTTCC	GCCTGTTCTT	TGGCAGTCAG
401	GGCGATTTTG	TTGCGGACGT	AGAGCAGTTC	GGCGTGTGCC	GCGCCAGTTG
451	CGGGATAGCC	GCCGCCGAGG	GCGAGCGCGA	GAAAATCGGC	GGCGGTCCGC
501	ATATCGGGTT	TGCCTGAGAA	GGGCGGACGG	TTTTCAGTG	CGAACGCACT
551	CGCGATGCCG	TCTGAAAAGA	CGTACCCCTC	GGGGAGGGCA	ATGTCTGCCG
601	CCCTACCGAC	TTGATAATCG	CTCAAACGGC	GGCGGTTTCA	CGTGTGGAAC
651	CACGCATAAA	ACACTTCGCC	CATACGCGCG	TCCGAGCGCG	CGAGTATGCA
701	GCTTTGCGGC	GGCGGCAGCG	AGGCGGCGGC	ATCGAGCGTG	GGGATGCCGA
751	TTAAAGGCGT	GTCGAACGGC	GTTGCCAAAC	CTTGCGCCAC	GCCGATGCCG
801	ATACGCAGTC	CGGTAA			

This corresponds to the amino acid sequence <SEQ ID 128; ORF 036.ng>:

g036 . pep

1	MLKPCLVYSA	CAAALPARTS	SSRRCVPSGR	CAYQYSSRAD	ATPRRRHSGA
51	VAIRCSSDSS	GRFCQTIKAA	ILPSFSARKT	CSDGETSADS	NWRCVHADGL
101	QTVSSAASAA	QSDGEAGRMF	MFVPSVPPVL	WQSGRFCCGR	RAVRRVPRQL
151	RDSRRRGRAR	ENRRRSAYRV	CLRRADGFPV	RTHCRCRLKR	RTPRGGQCLP
201	PYRLDNRSNG	GSACRTTHK	TLRPYARPQR	RVCSFAAAAA	RRRHRAWGCR
251	LKACRTALPN	LAPRRCRYAV	R*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 129>:

m036 . seq

1	ATGCTGAAGC	CGTGCGCCGT	GTACAGTGCC	TGTGCGGCGG	TGTTGCCTGC
51	ACGGACTTCG	AGCAGCAGGC	GTTGCGTGTC	TTCGGGCAGA	TGTGTGAACC
101	AATATTCGAG	CAGGGCGGAC	GCAATTCCTT	GGCGGCGGCA	TTCGGGCGCG
151	GTGGCAATCA	GGTGCAGTTC	GGATTTCGTC	GGCAGGTTCT	GCCAAACGAT
201	AAAGGCGGCA	ATCCCg . CGT	CTTTTCCGC	AAGGAAAACC	TGTTCCGACG
251	GCGAAACCAG	TGCGGACTCA	AATTGGCGTT	GCGTCCATGC	GGACGGGTTG
301	CAGACGGCAT	CGAGTGC GGC	CAGCTCCTCA	CAATCGGCAC	AAACGGCACG

220

```

351 GCGGATGTTT ACGGGCGCGC TCTCCGTTTC GCCTGTTCTT TGGCAGTCAG
401 GGGGATTTTG TTGCGGACGT AGAGCAAACC GCGTGTGCG GCATGGACGG
451 CAGGATAACC GCCCTTGGCT GCCAATGCGA GAAAGTCGGC GGCAGTCGGC
501 ATATCCGGTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551 GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601 CCCGCCCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651 CATGCATAAA ACACTTCGCC CATAAGAGCG TCCGTAGCG CAAGGATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAGGGGGT ATCAAACGGC GTTGCCAAAC CCTGAGCTAC ACCGATGCCG
801 ATACGCAGTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 130; ORF 036>:

m036.pep

```

1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPXSFSARKT CSDGETSADS NWRCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNRPWLPMR ESRRQSAYPV CLRTAELLPA RTRCLCRLKR RIPPAAGCLP
201 PARPDNRSNG GSSAYRTMHK TLRPYERP*R QGCSFAAAAA RRRHRARVRR
251 LRGYQTALPN PELHRCRYAV R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 131>:

a036.seq

```

1 ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTTCCTGC
51 ACGGACTTCG AGCAGCAGGC GTTGCGTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCCGCCGT CTTTTTCCGC AAGGAAAACC TGTTCGGACG
251 GCGAAACCAG TGCGGACTCA AATTGGCGTT GCGTCCACGC GGACGGGTTG
301 CAGACGGCAT CGAGCGCGGC GAGTGCGGCG CAATCGGCAT AAACGGCGCG
351 GCGGATGTTT ACAGGCGCGC CCTCCGTTCC GCCTGTTCTT TGGCAGTCAA
401 GCGGATTTTG TTGCGGACGT AGAGCAGCTC GCGTGTGCC GCAGCGACGG
451 CGGGAAAACC GCCTTCAGCC GCCAGATTGA GGAAGTCGGC GCGGTCGGC
501 ATATCGGGTT TGCTGAGAA GGGCGGACGG TTTTCCAGCG CGAACGCATT
551 GCGGATGCCG TCTGAAAAGG CGCATCCTTC CGGCAGCCGG ATGTCTGCCG
601 CCCGACCGAC CTGATAATCG CTCAAACGGC GCGGTTTCAG CGTGTGCAAC
651 CATGCATAAA ACACTTCGCC CATACTGCG TCCGAGCGG CAAGGATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAAGGAGT ATCAAACGGC GTTGCCAAAC CTTGCGCCAC GCCGATGCCG
801 ATACGCAGTC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 132; ORF 036.a>:

a036.pep

```

1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPPSFSARKT CSDGETSADS NWRCVHADGL
101 QTASSAASAA QSA*TARRMF TGAPSVPPVL WQSRRFCCGR RAARRVPQRR
151 RENRLQPPD* GSRRRSAYRV CLRRADGFPA RTHCRCLKR RILPAAGCLP
201 PDRPDNRSNG GGSACRTMHK TLRPYVRPQR QGCSFAAAAA RRRHRARVRR
251 LKEYQTALPN LAPRRCRYAV P*

```

m036/a036 85.6% identity over a 270 aa overlap

```

          10      20      30      40      50      60
m036.pep MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAI PWRRHSGAVAI RCSSDSS
          |||
a036      MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAI PWRRHSGAVAI RCSSDSS
          10      20      30      40      50      60

          70      80      90     100     110     120
m036.pep GRFCQTIKAAIPXSFSARKT CSDGETSADSNWRCVHADGLQTASSAASSS QSAQTARRMF
          |||
a036      GRFCQTIKAAIPXSFSARKT CSDGETSADSNWRCVHADGLQTASSAASAAQSAXTARRMF
          70      80      90     100     110     120

```


221

	130	140	150	160	170	180
m036.pep	TGALSVRPVLWQSGRFCCGRRANRRVRHGRQDNRPWLPMPRESRRQSAYPVCLRTAELLPA					
a036	: : : :					
	130	140	150	160	170	180
	TGAPSVPPVLWQSGRFCCGRRARRVPQRRRENRLQPPDXGSRRRSAYRVCLRRADGFPA					
	190	200	210	220	230	240
m036.pep	RTRCLCRLKRRIPPAAGCLPPARPDNRSNGGSSAYRTMHKTLRPYERXPXQGCSTFAAAAA					
a036	: :					
	190	200	210	220	230	240
	RTHCRCLKRRILPAAGCLPPDRPDNRSNGGGSACRTMHKTLRPYVRPQRQGCSTFAAAAA					
	250	260	270			
m036.pep	RRRHRARVRRLRGYQTALPNPELHRCRYAVRX					
a036	: :					
	250	260	270			
	RRRHRARVRRLKEYQTALPNLAPRRCRYAVPX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 036 shows 74.9% identity over a 271 aa overlap with a predicted ORF (ORF 036.ng) from *N. gonorrhoeae*:

m036/g036

	10	20	30	40	50	60
m036.pep	MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAI PWRHSGAVAIRCSSDSS					
g036	: :					
	10	20	30	40	50	60
	MLKPCLVYSACAAALPARTSSSRRCVPSGRCAYQYSSRADATPRRHSGAVAIRCSSDSS					
	70	80	90	100	110	120
m036.pep	GRFCQTIKAAIPXSFSARKTCS DGETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF					
g036	: :					
	70	80	90	100	110	120
	GRFCQTIKAAILPSFSARKTCS DGETSADSNWRCVHADGLQTVSSAASAAQSDGEAGRMF					
	130	140	150	160	170	180
m036.pep	TGALSVRPVLWQSGRFCCGRRANRRVRHGRQDNRPWLPMPRESRRQSAYPVCLRTAELLPA					
g036	: : : : :					
	130	140	150	160	170	180
	MFVPSVPPVLWQSGRFCCGRRARRVPRLRDSRRRGRARENRRRSAYRVCLRRADGFVP					
	190	200	210	220	230	240
m036.pep	RTRCLCRLKRRIPPAAGCLPPARPDNRSNGGSSAYRTMHKTLRPYERXPXQGCSTFAAAAA					
g036	: : : :					
	190	200	210	220	230	240
	RTHCRCLKRRTPRGGQCLPPYRLDNRSNGGGSACRTTHKTLRPYARPPRRVCSFAAAAA					
	250	260	270			
m036.pep	RRRHRARVRRLRGYQTALPNPELHRCRYAVRX					
g036	: : :					
	250	260	270			
	RRRHRAWGCRLKACRTALPNLAPRRCRYAVRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 133>:

m036-1.seq

```

1  ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTTCCTGTC
51  ACGGACTTCG AGCAGCAGGC GTTGC GTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCGCGCGT CTTTTCCTGC AAGGAAAACC TGTTCCGACG
251 GCGAAACAG TGCGGACTCA AATTGGCGTT GCGTCCATGC GGACGGGTTG
301 CAGACGGCAT CGAGTGC GCGC CAGCTCCTCA CAATCGGCAC AAACGGCACG

```

```

351  GCGGATGTTT ACGGGCGCGC TCTCCGTTTC GCCTGTTCTT TGGCAGTCAG
401  GGCGATTTTG TTGCGGACGT AGAGCAAACC GGCGTGTGCG GCATGGACGG
451  CAGGATAACC GCCCTTGGCT GCCAATGCGA GAAAGTCGGC GGCAGTCGGC
501  ATATCCGCTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551  GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601  CCCGCCCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651  CATGCATAAA AACTTCGCC CATAAGAGCG TCCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 134; ORF 0036-1>:

```

m036-1.pep
  1  MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
 51  VAIRCSSDSS GRFCQTIKAA IPPSFSARKT CSDGETSADS NWRCVHADGL
101  QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151  QDNRPWLPMR ESRRQSAYPV CLRTAELLPA RTRCLCRLKR RIPPAAGCLP
201  PARPDNRSNG GSSAYRTMHK TLRPYERP*

```

m036-1/g036 76.8% identity in 228 aa overlap

```

              10      20      30      40      50      60
m036-1.pep  MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAIIPWRRHSGAVAIIRCSSDSS
g036        MLKPCLVYSACAAALPARTSSSRRCVPSGRCAVYSSRADATPRRRHSGAVAIIRCSSDSS
              10      20      30      40      50      60

              70      80      90     100     110     120
m036-1.pep  GRFCQTIKAAIPPSFSARKTCS DGETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF
g036        GRFCQTIKAAILPSFSARKTCS DGETSADSNWRCVHADGLQTVSSAASAAQSDGEAGRMF
              70      80      90     100     110     120

              130     140     150     160     170     180
m036-1.pep  TGALSVRPVLWQSGRFCCGRRANRRVRHGRQDNRPWLPMRESRRQSAYPVCLRTAELLPA
g036        MFVPSVPPVLWQSGRFCCGRRARRVPRQLRDSRRRGRARENRRRSAYRVCLRRADGFPV
              130     140     150     160     170     180

              190     200     210     220     229
m036-1.pep  RTRCLCRLKRRIPPAAGCLPPARPDNRSNGGSSAYRTMHKTLRPYERPX
g036        RTHCRCLKRRTPRGQCLPPYRLDNRSNGGGSACRTTHKTLRPYARPPQRRVCSFAAAAA
              190     200     210     220     230     240

g036        RRRHRAWGCRLKACRTALPNLAPRRCRYAVRX
              250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 135>:

```

g038.seq
  1  ATGACTGATT TCCGCCAAGA TTTCCTCAAA TTCTCCCTCG CCCAAAATGT
 51  TTTGAAATTC GGCGAATTTA CCACCAAAGC CGGACGGCGG TCGCCCTATT
101  TCTTCAATGC CGGCCTCTTC AACGACGGCG CGTCCACGCT GCAACTGGCA
151  AAATTCTATG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201  GTTCGGCCCC GCCTACAAAG GCATTATTTT GGCGGCGGCA ACCGCGATGA
251  TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301  GCCAAAGACC GCGGCGAAGG CGGCGTGTG GTCGGCGCGC CGCTTAAAGG
351  GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401  AATCAATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGCG CGGTGTCGCC
451  ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTAAATTGT CCGCCGTTCA
501  GGAAGTGGAA AAACAATACG GCCTGCCCGT CGCCCCCATC GCCAGCCTGA
551  ACGATTGTGT TATCCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601  GAACCCGTCC GCACCTACCG CCGGCAGTAC GCGGTAGAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 136; ORF 038.ng>:

```
g038.pep
1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGASTLQLA
51  KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101 AKDRGEGGVL VGAPLKGRVL IIDDISAGT SVRESIKLIE AEGATPAGVA
151 IALDRMEKGT GKLSAVQEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201 EPVRTYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 137>:

```
m038.seq
1  ATGACCGATT TCCGCCAAGA TTTCTCTCAA TTCTCCCTCG CCCAAAATGT
51  TTTGAAATTC GCGGAATTCA CCACCAAGGC AGGACGGCGG TCGCCCTATT
101 TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151 AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201 GTTCGGTCCC GCCTACAAAG GCATTATTTT GCGCGCGGCA ACCGCGATGA
251 TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301 GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGCGCGCG CGCTTAAAGG
351 GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401 AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGC CGGTGTCGCC
451 ATCGCGCTCG ATCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501 GGAAGTGGAA AAACAATACG GCTGCCCCGT CGCCCCATC GCCAGCCTGA
551 ACGATTTGTT TATTCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601 GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 138; ORF 038>:

```
m038.pep
1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
51  KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101 AKDHGEGGVL VGAPLKGRVL IIDDISAGT SVRESIKLIE AEGATPAGVA
151 IALDRMEKGT GELSAVQEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201 EPVRAYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 139>:

```
a038.seq
1  ATGACCGATT TCCGCCAAGA TTTCTCTCAA TTCTCCCTCG CCCAAAATGT
51  TTTGAAATTC GCGGAATTCA CCACCAAGGC AGGACGGCGG TCGCCCTATT
101 TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151 AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201 GTTCGGCCCC GCCTACAAAG GCATTATTTT GCGCGCGGCA ACCGCGATGA
251 TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301 GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGCGCGCG CGCTTAAAGG
351 GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401 AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGC CGGTGTCGCC
451 ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501 GGAAGTGGAA AAACAATACG GCTGCCCCGT CGCCCCATC GCCAGCCTGA
551 ACGATTTGTT TATTCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601 GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 140; ORF 038.a>:

```
a038.pep
1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
51  KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101 AKDHGEGGVL VGAPLKGRVL IIDDISAGT SVRESIKLIE AEGATPAGVA
151 IALDRMEKGT GELSAVQEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201 EPVRAYRRQY GVE*
```

m038/a038 100.0% identity over a 213 aa overlap

```
10 20 30 40 50 60
m038.pep MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA KFYAQSIIES
```

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```

|||||
a038 MTDFRQDFLKFSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
      10      20      30      40      50      60

      70      80      90      100     110     120
m038.pep GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
|||||
a038 GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
      70      80      90      100     110     120

      130     140     150     160     170     180
m038.pep IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
|||||
a038 IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
      130     140     150     160     170     180

      190     200     210
m038.pep ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
|||||
a038 ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
      190     200     210

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 038 shows 98.1% identity over a 213 aa overlap with a predicted ORF (ORF 038.ng) from *N. gonorrhoeae*:

m038/g038

```

      10      20      30      40      50      60
m038.pep MTDFRQDFLKFSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
|||||
g038 MTDFRQDFLKFSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGASTLQLAKFYAQSIIES
      10      20      30      40      50      60

      70      80      90      100     110     120
m038.pep GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
|||||
g038 GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDRGEGGVLVGAPLKGRVL
      70      80      90      100     110     120

      130     140     150     160     170     180
m038.pep IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
|||||
g038 IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGKLSAVQEVEKQYGLPVAPI
      130     140     150     160     170     180

      190     200     210
m038.pep ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
|||||
g038 ASLNDLFILLQNNPEFGQFLEPVRTYRRQYGVEX
      190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 141>:

g039.seq

```

1  ATGCCGTC CG AACCACCTGC CGCTTCAGAC GGCATCAAAC CGACACACAC
51  CGAGAAAACA TCATGCCCGC CTGTTTCTGT CCGCACTGCA AAACCCGCTT
101 CTGGGTCAAA GAAAcccagC TCAAcgtCgC ccaagGCTTC GTCGTCTgcc
151 aaAAAtgcga agGGCTgttt aaAgccaaaG accAtctggc aaGcacGAAA
201 gaacctatat tcaacgattg gcccgaaagt gtttcgggat gTcaaaCTCG

```

225

```

251 TCcaccgcaT cggcacgcac gccattagca aGAaacagat gtcccgcgac
301 gaaatCgccg atatcctcaa cggcggtaca acCCTGCACG ATACGCCGCC
351 CGCAACCGCC GCTGCCGCac ctGCCGCCGC ACCGCaggTT TCCGTACCGC
401 CCGCCCGTCA GGAAGGGCTC AACTGGACTA TTGCAACCCT GTTCGCACTT
451 ATCGTCCTCA TTATGCAGCT TTCCTACCTC TTCATCCTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 142; ORF 039.ng>:

g039.pep

```

1 MPSEPPAASD GIKPTHTEKT SCPPVSVRTA KPASGSKKPS STSPKASSSA
51 KNAKGCLKPK TIWQARKNLY STIGPKLFRD VKLVHRIGTH AISKKQMSRD
101 EIADILNGGT TLHDTTPATA AAAPAAAPQV SVPPARQEGL NWTIATLFAL
151 IVLIMQLSYL FIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 143>:

m039.seq

```

1 ATGCCGTCCG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCACTGCA AAACCCGTCT
101 CTGGGTCAA GAAACCCAAC TCAATGTCGC CGnnnnnnnnn nnnnnnnnnn
151 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
201 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnCCC GAGGCTGTTT
251 CGGATGTCAA ACTCGTTCAC CGTATCGGCA CGCGCGCCAT CGGCAAGAAA
301 CAGATTTCCC GTGACGAAAT CGCCGGCATC CTCAACGCGG GTACAACCCA
351 GCCCATATT CCGCCCGCAA CCGCCGCCAC CCCTGCTGCC GCACCGCAGG
401 TTACCGTACC GCCCGCCGCG CCCGCCGTC AGGATGGGTT CAACTGGACG
451 ATTGCAACCC TGTTTGCCCT TATCGTCCTC ATTATGCAGC TTTCTACCT
501 CGTCATCCTA TGA

```

This corresponds to the amino acid sequence <SEQ ID 144; ORF 039>:

m039.pep

```

1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPPXXXXXX
51 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX EAVSDVKLVH RIGTRAIGKK
101 QISRDEIAGI LGGTTQPD I PPATAATPAA APQVTVPAA PARQDGFNWT
151 IATLFLIVL IMQLSYLVIL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 145>:

a039.seq

```

1 ATGCCGTCTG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCACTGCA AAACCCGTCT
101 CTGGGTCAA GAAACCCAAC TCAATGTCGC CCAAGCTTC GTCTCTGCC
151 AAAAATGCGA AGGAATGTTT AAAGCCAAAG ACCATCTGGC AAGCAGGAA
201 GAACCCATAT TCAACGATT. TGCCCGAAGC TGTTCGGAT GTCAAACCTCG
251 TTCACCGCAT CGGCACGAGC GCCATCGGCA AGAAACAGAT TTCCCGTGAC
301 GAAATCGCCG GCATCCTCAA CGGCGGCACA ACCCAGCCCG ATATTCGCC
351 CGCAACCGCC GCCACCCCTG CTGCCGCACC GCAGGTTACC GTACCGCCCG
401 CCGCGCCCGC CCGTCAGGAT GGGTTCAACT GGACGATTGC AACCTGTTT
451 GCCCTTATCG TCCTCATTAT GCAGCTTTC TACCTCGTCA TCCTATGA

```

This corresponds to the amino acid sequence <SEQ ID 146; ORF 039.a>:

a039.pep

```

1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPKASSSA
51 KNAKECLKPK TIWQARKNPY STIXPEAVSD VKLVHRIGTS AIGKKQISR
101 EIAGILNGGT TQPDIPPATA ATPAAAPQVT VPPAAPARQD GFNWTIATLF
151 ALIVLIMQLS YLVIL*

```

m039/a039 79.4% identity over a 170 aa overlap

```

              10      20      30      40      50      60
m039.pep      MPSEPPYASDGIKPDTHEEIPCPPVSAPTAKPVSGSKKPNMSMPXXXXXXXXXXXXXXXXXX
              |||
a039           MPSEPPYASDGIKPDTHEEIPCPPVSAPTAKPVSGSKKPNMSMPKASSSAKNAKECLKPK

```

```

              10              20              30              40              50              60
              70              80              90              100             110             120
m039.pep      XXXXXXXXXXXXXXXXXXXXPEAVSDVKLVHRIGTRIAIGKKQISRDEIAGILNGGTTQPDI
a039          :      : |      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
              70              80              90              100             110
TIWQARKNPYSTIX-----PEAVSDVKLVHRIGTSAIGKKQISRDEIAGILNGGTTQPDI

              130             140             150             160             170
m039.pep      PPATAATPAAAPQVTVPPAAPARQDGFNWTIATLFALIVLIMQLSYLVILX
a039          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
              120             130             140             150             160
PPATAATPAAAPQVTVPPAAPARQDGFNWTIATLFALIVLIMQLSYLVILX

```

m039/q039

	10	20	30	40	50	60
m039.pep	MPSEPPYASDG	IKPDTHEE	IPC	PPVSAPTAK	PVSGSKKPN	SMSPXXXXXXXXXXXXXXXXXXXX
			:	:	:	
g039	MPSEPPAASDG	IKPTHTEK	TSCPPVSV	RTAKPASG	SKKPSSTSP	KASSAKNAKGCLKPK
	10	20	30	40	50	60
	70	80	90	100	110	120
m039.pep	XXXXXXXXXXXXXXXXXXXX	PEAVSDVK	LVHRIGT	RAIGKKQ	ISRDEIAG	ILNGGTTQPD
	:	:	:		:	
g039	TIWQARKN	LYSTIG----	PKLFRDVK	LVHRIGT	HAISKKQ	MSRDEIADILNGGTTLHDT
	70	80	90	100	110	
	130	140	150	160	170	
m039.pep	PPATAAT-P	AAAPQVTV	PPAAPARQ	DGFNWTI	ATL	FALIVLIMQLSYLVILX
	:		:			
g039	PPATAAAAP	AAAPQVSV	PPA--RQ	EGLNWTI	ATL	FALIVLIMQLSYLFILX
	120	130	140	150	160	

q040.seq

1	ATGAACGCGC	CCGACAGCTT	TGTCGCCAC	TTCCGCGAAG	CCGCCCCCTA
51	CATCCGCCAA	ATGCGCGGCA	CGACACTGGT	CGCCGGCATA	GAcggCCGCC
101	TGCTCGAAGG	CGGCACCTTA	AATAAGCTCG	CCGCCGACAT	CGGGCTGTGT
151	TCGCAACTGG	GCATCCGACT	CGTCTCATC	CACGGCCGCT	ACCACTTCTT
201	CGAaccgCTC	GCGCGCGCGC	AAGgccGCAC	CGCGCATTAT	TGCCGgggtt
251	tGCGCGTTAC	CGACGaAAc	tcGctcgGAC	AGGCGCAGCA	GtttGCCGGC
301	AccgTCCGCA	GCCGTTTTGA	agcCGCATTG	tcggcagCG	ttcaggatt
351	cgcgCGCGCG	CCTTCCGTCC	CGTCTGTA	gggcaacttc	ctgacCGCCC
401	GTCCgatggg	cgtgatgac	ggaACCGata	tgaataacgc	gggggttttc
451	gcgaaaaccg	ACACCGCGCG	CCTCCGTTTC	CAGTTCGACG	CGGGCAATAT
501	CGTCTGGATG	CCGCCGCTCG	GGCATTCCTA	CGGCGGCAAA	ACCTTCAATC
551	TCGATATGGT	GCAGGCCGCC	GC'TTCCGTG	CGTCTCGCT	TCAGGCCGAA
601	AAACTCGTTT	ACCTGACCTT	TTCAGACGAG	ATTTCCCGCT	CCGACGGCAC
651	GCTCGCCGAA	ACCTCTCGG	CACAGGAAGC	GCAATCGCTG	GCGGAACACG
701	CCGCCACGCA	AACCCGACGA	CTGATTTCGT	CGCCGTTTGC	CGCGCTCGAA
751	GGCGGCGTGC	ATCGCGTCCA	AATCCTCAAC	GGGGCCGCCG	ACGGCAGCCT
801	GCTGCAAGAA	CTCTTCACCC	GCAACGGCAT	CGGCACGTCC	ATTGCCAAAG
851	AAGCCTTCGT	CTCCACCCGT	CAGGCGCACG	GCGGCGCAT	CCCGCACATC
901	GCCGCCCTCA	TCCGCCCCGG	GGAAGAACAG	GGCGTCCAT	TGCACCGCAG
951	CCGCGAATAC	CTCGAAAACC	ACATTTCCGA	ATTTTCCATC	CTGAACACG

```

1001  ACGGCGACCT  GTACGGCTGT  GCCGCACTCA  AAACCTTTGC  CGAAGCCGAT
1051  TCGGCGGAAA  TCGCCTGCCT  TGCCGTCTCG  CCGCAGGCAC  AGGACGGCGg
1101  ctACGGCGAA  CGCCTGCTTG  CCCACATTAT  CGATAAGGCG  CGCGGCATAG
1151  GCATAAGCAG  GCTGTTCGCA  CTGTCCACAA  ATACCGGCGA  ATGGTTTGCC
1201  GAACGCGGCT  TTCAGACGGC  ATCGGAAGAC  GAGCTGCCCC  AAACGCGGCG
1251  CAAAGACTAC  CGCAGCAACG  GACGAAACCC  GCATATTCTG  GTGCGTCGCC
1301  TGCACCGCTG  A

```

This corresponds to the amino acid sequence <SEQ ID 148; ORF 040.ng>:

g040.pep

```

1  MNAPDSFVAH  FREAAPYIRQ  MRGTTLVAGI  DGRLLGGTLL  NKLAADIGLL
51  SQLGIRLVLI  HGAYHFLDRL  AAAQGRTPHY  CRGLRVTDET  SLGQAQQFAG
101  TVRSRFEAAL  CGSVSGFARA  PSVPLVSGNF  LTARPMGVID  GTDMEYAGVI
151  RKTDTAALRF  QLDAGNIVWM  PPLGHSYGGK  TFNLDMVQAA  ASVAVSLQAE
201  KLVYLTLSDG  ISRPDGTLA  E  TLAQEAQSL  AEHAASETRR  LISSAVAAL
251  GGVHRVQILN  GAADGSLLQE  LFTRNGIGTS  IAKEAFVSIR  QAHSGLDIPHI
301  AALIRPLEEQ  GVLLHRSREY  LENHISEFSI  LEHDGDLYGC  AALKTFEAD
351  CGEIACLAVS  PQAQDGGYGE  RLLAHIIDKA  RGIGISRLFA  LSTNTGEWFA
401  ERGFQTASED  ELPETRRKDY  RSNGRNPHIL  VRRLLHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 149>:

m040.seq

```

1  ATGAGCGCGC  CCGACCTCTT  TGTCGCCCAC  TTCCGCGAAG  CCGTCCCCTA
51  CATCCGCCAA  ATGCGCGGCA  AAACGCTGGT  CGCCGGCATA  GACGACCGCC
101  TGCTCGAAGG  TGATACCTTA  AACAAGCTCG  CCGCCGACAT  CGGGCTGTTG
151  TCGCAACTGG  GCATCAGGCT  CGTCCTCATC  CACGGCGCGC  GCCACTTCCT
201  CGACCGCCAC  GCCGCCGCTC  AAGGCCGCAC  GCCGCATTAT  TGCCGGGGCT
251  TCGCGCTTAC  GCACGAAACC  TCGCTCGAAC  AGGCGCAGCA  GTTTGCCCGC
301  ACCGTCCGCA  GCCGTTTTGA  AGCCGCATTG  TGCGGCAGCG  TTTCCGGGTT
351  CGCGCGCGCG  CCTTCCGTCC  CGCTCGTATC  GGGCAACTTC  CTGACCGCCC
401  GTCCGATAGG  TGTGATTGAC  GGAACCGATA  TGAATACGCG  GGGCGTTATC
451  CGCAAAACCG  ACACCGCCGC  CCTCCGTTTC  CAACTCGACG  CGGGCAATAT
501  CGTCTGGCTG  CCGCCGCTCG  GACATTCCCTA  CAGCGGCAAG  ACCTTCTATC
551  TCGATATGCT  TCAAACCGCC  GCCTCCGCCG  CCGTCTCGCT  TCAGGCCGAA
601  AAACCTCGTT  ACCTGACCCT  TTCAGACGGC  ATTTCCCGCC  CCGACGGCAC
651  GCTCGCCGAA  ACCCTCTCGG  CACAGGAAGC  GCAATCGCTG  GCGGAACACG
701  CCGGCGGGCA  AACGCGACGG  CTGATTTCTG  CCGCCGAAC  CTTACCCCGC
751  AACGGCATCG  GCACGTCCAT  TGCCAAAGAA  GCCTTCGTCT  CCATCCGGCA
801  rGCGCAywgG  G. CGACATCC  CGCACATCGC  CGCCCTCATC  CGCCCGCTGG
851  AAGAACAGGG  CATCCTGCTG  CACCGCAs. c  GCGAATACCT  CGAAAACAC
901  ATTTCCGAAT  TTTCCATCCT  CGAACACGAC  GGCAACCTGT  ACGGTTGCGC
951  CGCCCTGAAA  ACCTTTGCCG  AAGCCGATTG  CGGCGAAATC  GCCTGCCTTG
1001  CCGTCTCGCC  GCag. cACAG  GACGGCGGCT  ACGGCGAAGC  CnTGCTTGCC
1051  CACATTATCG  ATAAGGCGCG  CGGCATAGGC  ATAAGCAGGC  TGTTCCGCACT
1101  GTCCACAAAT  ACCGGCGAAT  GGTTCGCCGA  ACGCGGCTTT  CAGACGGCAT
1151  CGGAAGACGA  GTTGCCCGAA  ACGCGGCGCA  AAGACTACCG  CAGCAACCGA
1201  CGGAACTCGC  ATATTCTGGT  ACGTCGCCCTG  CACCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 150; ORF 040>:

m040.pep

```

1  MSAPDLFVAH  FREAVPYIRQ  MRGKTLVAGI  DDRLLEGDTL  NKLAADIGLL
51  SQLGIRLVLI  HGARHFLDRH  AAAQGRTPHY  CRGLRVTDET  SLEQAQQFAG
101  TVRSRFEAAL  CGSVSGFARA  PSVPLVSGNF  LTARPIGVID  GTDMEYAGVI
151  RKTDTAALRF  QLDAGNIVWL  PPLGHSYSGK  TFYLDMLQTA  ASAAVSLQAE
201  KLVYLTLSDG  ISRPDGTLA  E  TLAQEAQSL  AEHAGGQTRR  LISSAELEFTR
251  NGIGTSIAKE  AFVSIRQAHX  XDIPHIAALI  RPLEEQGILL  HRXREYLENH
301  ISEFSILEHD  GNLYGCAALK  TFAEADCGEI  ACLAVSPQXQ  DGGYGERXLA
351  HIIDKARGIG  ISRLFALSTN  TGEWFAERGF  QTASEDELPE  TRRKDYRSNG
401  RNSHILVRRL  HR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 151>:

a040.seq

```
a040.pep
1  MIVPDLFVAH FREAAPYIRQ MRGKTLVAGI DDRLLEGDTL NKFAADIGLL
51  SQLGIRLVLI HGARHFLDRH AAQGRTPHY CRGLRVTDIT SLEQAQQFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPIGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIWVL PPLGHSYSGK TFHLDMLQTA ASDVAVSLQAE
201 KLVYLTLSDG ISRPDGT LAV TLSAQEAQSL AEHAGGETRR LISSAVAALE
251 GGVHRVQILN GAADGSLQEQ LFTRNGIGTS IAKEAFVSIR QAHSGDIPHI
301 AALIRPLEEQ GILLHRSREY LENHISEFSI LEHDGNLYGC AALKTFEAD
351 CGEIACLAWS PQAQDGRGGE RLLAHIIDKA RGIGISRLFA LSTNTGEWFA
401 ERGETOASED ELPETRRKDY RSNGRNSHIL VRGLHR*
```

	10	20	30	40	50	60
m040.pep	MSAPDLFVAHFREAVPYIRQMRGKTLVAGIDDRLLLEGDTLNKLAADIGLLSQLGIRLVLI					
a040	MIVPDLFVAHFREAAPYIRQMRGKTLVAGIDDRLLLEGDTLNKFADIGLLSQLGIRLVLI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m040.pep	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEEALCGSVSGFARA					
a040	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEEALCGSVSGFARA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m040.pep	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYS GK					
a040	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYS GK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m040.pep	TFYLDMLQTAASAASVLSQAEKLVLVLTSDGISRPDGT LAETLSAQEAQS LAEHAGGQTRR					
a040	TFHLDMLQTAASVASVLSQAEKLVLVLTSDGISRPDGT LAVTLSAOEAO SLAEHAGGETRR					

229

	190	200	210	220	230	240
m040.pep	LISSA-----					250
a040	LISSAVAAL					250
m040.pep	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLA					280
a040	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLA					280
m040.pep	PQXQDGGYGERXLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY					340
a040	PQXQDGGYGERXLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY					340
m040.pep	RSNGRNSHILVRRRLHRX					400
a040	RSNGRNSHILVRRRLHRX					400

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 040 shows 88.3% identity over a 436 aa overlap with a predicted ORF (ORF 040.ng) from *N. gonorrhoeae*:

m040/g040

m040.pep	MSAPDLFVAHFREAVPYIRQMRGKTLVAGIDDRLLEGDTLNKLAADIGLLSQLGIRLVLI	60
g040	MNAPDSFVAHFREAAPYIRQMRGKTLVAGIDGRLLLEGDTLNKLAADIGLLSQLGIRLVLI	60
m040.pep	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA	120
g040	HGAYHFLDRLAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA	120
m040.pep	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYSGK	180
g040	PSVPLVSGNFLTARPMGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWMPPLGHSYSGK	180
m040.pep	TFYLDMLQTAASAAVSLQAQKLVYLTLSDGISRPDGTLAETLSAQEAQSLAEHAGGQTRR	240
g040	TFNLDMLQTAASAAVSLQAQKLVYLTLSDGISRPDGTLAETLSAQEAQSLAEHAAQTRR	240
m040.pep	LISSA-----ELFTRNGIGTSIAKEAFVSIRQAHXXDIPHI	276
g040	LISSAVAAL	300
m040.pep	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLA	336
g040	AALIRPLEEQGVLLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLA	360
m040.pep	PQXQDGGYGERXLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY	396
g040	PQXQDGGYGERLLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY	420
m040.pep	RSNGRNSHILVRRRLHRX	413
g040	RSNGRNSHILVRRRLHRX	437

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 153>:

```
g041.seq
  1  ATGAGTTCGC CCAAACACAT CGGCTTGCAG GCGGCAGCA ACGGCGCCT
 51  GATTACCGCC GCCGCCTTCG TCGCGGAACC GCAAAGCATC GGTGCGCTGG
101  TGTGCGAAGT ACCGCTGACC GATATGATCC GTTATCCGCT GCTGTCCGCC
151  GGTTCAAGTT GGACGACGA ATACGGCAAT CCGCAGAAAT ACGAAGCCTG
201  CAAACGCCGG CTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251  TCGATTATCC GCCCGCACTC ATTACCACCA GCCTCAGCGA CGACCGCGTC
301  CATCCCGCCC ACGCGCTCAA ATTCTACGCC AAAGTGC GCG AAACCTCGCC
351  GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401  CCCAACGCGA ATCCGCCGAC AAAGTGCCT GCGTGTGCT GTTTTGTAAA
451  GAATTTTGG GATAA
```

This corresponds to the amino acid sequence <SEQ ID 154; ORF 041.ng>:

```
g041.pep
  1  MSSPKHIGLQ GSNNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
 51  GSSWTDEYGN PQKYEACKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101  HPAHALKFYA KLRETSPQSW LYSPDGGGHT GNGTQRESAD KLACVLLFLK
151  EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 155>:

```
m041.seq
  1  ATCAGTTCGC CCGAACACAT CGGCTTGCAG GCGGCAGCA ACGGCGGACT
 51  GATTACTGCC GCCGCCTTCG TCGCGGAACC GCAAAGCATC GGTGCGCTGG
101  TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151  GGTTCAAGCT GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201  CAAACGCCGG TTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251  TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301  CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAAGTGC GCG AAACCTCCGC
351  GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401  CCCAACGCGA ATCCGCCGAC GAACTCGCCT GCGTCTTGCT GTTTTGTAAA
451  GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 156; ORF 041>:

```
m041.pep
  1  ISSPEHIGLQ GSNNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
 51  GSSWTDEYGN PQKYEVCKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101  HPAHALKFYA KLRETSQSW LYSPDGGGHT GNGTQRESAD ELACVLLFLK
151  EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 157>:

```
a041.seq
  1  ATCAGTTCGC CCGAACACAT CGGCTTGCAG GCGGCAGCA ACGGCGGACT
 51  GATTACTGCC GCCGCCTTCG TCGCGGAACC GCAAAGCATA GGTGCGCTGG
101  TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151  GGTTCAAGCT GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201  CAAACGCCGG TTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251  TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301  CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAAGTGC GCG AAACCTCGCC
351  GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401  CGCAGCGCGA AGCCGCCGAC GAACTCGCCT GCGTGTGCT GTTTTGTAAA
451  GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 158; ORF 041.a>:

```
a041.pep
  1  ISSPEHIGLQ GSNNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
 51  GSSWTDEYGN PQKYEVCKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101  HPAHALKFYA KLRETSPQSW LYSPDGGGHT GNGTQREAAD ELACVLLFLK
```

231

151 EFLG*

m041/a041 98.7% identity over a 154 aa overlap

	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSNGGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
a041	ISSPEHIGLQGGSNGGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCRRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSAQSW					
a041	PQKYEVCRRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSPOQSW					
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGTQRESADELACVLLFLKEFLGX					
a041	LYSPDGGGHTGNGTQREAADELACVLLFLKEFLGX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 041 shows 96.8% identity over a 154 aa overlap with a predicted ORF (ORF 041.ng) from *N. gonorrhoeae*:

m041/g041

	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSNGGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	: :					
g041	MSSPKHIGLQGGSNGGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCRRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSAQSW					
	:					
g041	PQKYEACKRRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSPOQSW					
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGTQRESADELACVLLFLKEFLGX					
	:					
g041	LYSPDGGGHTGNGTQRESADKLACVLLFLKEFLGX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 159>:

g041-1.seq

1	ATGAAATCCT	ACCCCGACCC	CTACCGCCAT	TTTGAAAACC	TCGATTCCGC
51	CGAAACGCAA	AACCTCGCTG	CTGAAGCGAA	TGCCGAAACG	CGCGCGCGTT
101	TTTTAAACAA	CGACAAGGCG	CGCGCACTTT	CAGACGGCAT	TTTGAATCAA
151	ATGCAGGACA	CGCGGCAGAT	TCCGTTTTGT	CAGGAACACC	GCGCGCGGAT
201	GTACCATTTT	CATCAGAATG	CGGAATATCC	GAAGGGCGTG	TACCGCATGT
251	GTACGGCGGC	GACCTACCGT	TCCGGCTATC	CCGAGTGGAA	AATCCTGTTT
301	TCGGTGCGCG	ATTTTCGATGA	GTTGCTCGGC	GACGATGTGT	ATTTGGGCGG
351	CGTGTCGCAC	TTGGTGGAGC	AGCCCAACCG	CGCGCTGCTG	ACTTTGAACA
401	AATCGGGCGG	CGATACGGCG	TATACGCTGG	AAGTGGATTT	GGAAGCAGGG
451	GAATTGGTAG	AGGGCGGTTT	TCACTTTCCG	GCAGGCAAAA	ACCATGTGTC
501	GTGGCGCGAT	GAAAACAGCG	TGTGGGTGTG	TCCGGCTTGG	GACGAACGCC
551	AGTTGACCGA	ATCGGGCTAT	CCGCGCGAAG	TGTGGCTGGT	GGAACGCGCG

```

601 AAGAGTTTCG AGGAAAGCCT GCCGGCGTAC CAAATCGATA AAGGCGCGAT
651 GATGGTAAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTTCG CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AGACGTATTT GCAGGTGTCTG
751 TCCGAAGGCG GGGCGAAACC GTTGAACCTG CCTAATGATT GCGATGTGGT
801 CCGCTATCTG GCGGGACATC TTTTGTCTGAC GCTGCGCAAG GACTGGCACC
851 CCGCGAACCA AAGCTATCCG AGTGGCGCGT TGGTGGCGGT GAAACTGAAT
901 CGGGGCGAAC TCGGGGCGGC GCAGCTTTTG TTTGCGCCCG ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTGGTG GCAAGCCTGC
1001 TGGAGAATGT ACAAGGCCGT CTGAAAGCGT GCGCGTTTGC CGACAGCAAA
1051 TGGCAGGAAG CCGAGTTGCC GCACCTGCCC TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCG TGGGGCGGCG ACGTGGTTTA TCTTGCCGCC AGCGATTTC
1151 CCACGCCGCT GACGCTGTTT GCGCTGGATT TGAACGTGAT GGAACGTACC
1201 GTCATGCGCC TCCAGCCGCA GCAGTTTGTT TCAGACGGCA TCGAAGTGCG
1251 GCAGTTTTCG GCGGTGTCGT CCGACGCGCA ACGCATTCCT TATTTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACACGCCGA CCTTAGTCTA TGCTTACGGA
1351 GGTTCGGCA TTCCTGAATT GCCGCATTAT CTGGGCAGCG TCGGCAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTTGTATT GGCAAACATC CGCGGCGGCG
1451 GAGAATTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAACAC
1501 AAAAGCGTTG ATGATTGTGT GGCAGTCGTG CGTGATTTGT CCGAACGCGG
1551 CATGAGTTCG CCCAAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGCC
1601 TGATTACCGC CGCCGCCTTC GTGCGCGAAC CGCAAAGCAT CGGTGCGCTG
1651 GTGTGCGAAG TACCGCTGAC CGATATGATC CGTTATCCGC TGCTGTCCGC
1701 CGGTTCAAGT TGGACGGACG AATACGGCAA TCCGCAGAAA TACGAAGCCT
1751 GCAAACGCCG GCTGGGCGAA TTGTGCGCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCCGCACT CATTACCACC AGCCTCAGCG ACGACGCGT
1851 CCATCCCGCC CACGCGCTCA AATTCTACGC CAAACTGCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGCG
1951 ACCCAACGCG AATCCGCCGA CAAACTCGCC TCGGTGTTGC TGTTTTGTAA
2001 AGAATTTTTG GGATAA

```

This corresponds to the amino acid sequence <SEQ ID 160; ORF 041-1.ng>:

g041-1.pep

```

1  MKSYDPYRHH FENLDSAETQ NFAAEANAET RARFLNNDKA RALSDGILNQ
51  MQDTRQIPFC QEHRARMYHF HQNAEYPKGV YRMCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TLNKSGGDTA YTLEVDLEAG
151 ELVEGGFHFP AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVLVVERG
201 KSFEESLPAY QIDKGAMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
251 SEGGAAPLNL PNDGDVVGYL AGHLLLTLRK DWHRANQSYR SGALVAVKLN
301 RGELGAAQLL FAPDETQALE SVETTKRFV ASLLENVQGR LKAWRFADSK
351 WQEAELPHLP SGALEMTDQP WGGDVVYLAA SDETTPLTLF ALDLNVMELT
401 VMRLQPQFV SDGIEVRQFW AVSSDGERIP YFHVGNKNAAP DPTPLVYAYG
451 GFGIPELPHY LGSVQKYWLE EGNFVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLLAV RDLSEGMSS PKHIGLQGG NGGLITAAAF VREPQSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEACKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
651 TQRESADKLA CVLLFLKEFL G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 161>:

m041-1.seq

```

1  ATGAAATCCT ACCCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51  CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAGAAAA CGACAAGGCG CGCGCGCTTT CAGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGGCAGAT TCCGTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTC CATCAGGACG CGGAGTATCC GAAGGGCGTG TACCGCGTGT
251 GTACCGCGGC GACGTATCGT TCCGGCTATC CCGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTTCGACGA ATTGCTTGGC GACGATGTGT ATTTGGGCGG
351 CGTGTGCGAC TTGGTGGAAC AGCCCAACCG CGCGTTGTTA AACTGAGCA
401 AATTGGGCGC CGATACGGCG TACACGCTGG AAGTGGATTT GGAAGCAGGG
451 GAGTTGGTCG AAGGCGGTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG AACGAACGCC
551 AGTTGACCCA ATCGGGCTAT CCGCGCGAAG TATGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT GCCTGTGTAT CAAATCGGCG AAGACGGCAT
651 GATGGTGAAC GCGTGGCGTT ATCTCGATCC GCAGGGTTTC CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AAACCTATT GCGGGTCTCA

```

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```

751 GCCGAAGGCG AGGCGAAACC GTTAAACCTG CCCAACGATT GCGACGTGGT
801 CGGCTATCTG GCGGGGCATC TTTTGCTGAC GCTGCGCAAG GACTGGAACC
851 GCGCGAACCA AAGCTATCCG AGCGGCGCGC TGGTGGCGGT GAAGCTGAAT
901 CGGGGCGAAC TCGGGGCGGC GCAGCTTTTG TTGCGCCCG ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTGGTG GCGAGCCTGT
1001 TGGAGAACGT ACAAGGCCGT CTGAAAGCAT GGCGGTTTGC CGACGGCAAA
1051 TGGCAGGAAG TCGAATTGCC GCGCCTGCCT TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCT TGGGGCGCGC ACGTGTTTA CTTGCGGCC AGCGATTTCA
1151 CCACGCGCT GACGCTGTTT GCGCTGGATT TGAACGTGAT GGAAGTACC
1201 GTCATGCGCC GCCAGCGCA GCAGTTTGAT TCAGACGGCA TTAACGTGCA
1251 GCAGTTTGG ACGACTTCGG CTGACGGCGA GCGCATTCCT TATTTCCACG
1301 TCGGCAAAA CGCCGCGCCC GACATGCCGA CGCTGGTCTA TGCCTACGGC
1351 GGTTCGGCA TTCCGAATT GCCGCATTAT CTGGGCAGCA TTGGCAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTTGTATT GGCGAACATC CGCGGCGGCG
1451 GCGAGTTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAACAT
1501 AAAAGCGTTG ATGATTTATT GGCAGTCGTG CGCGATTTGT CCGAACGCGG
1551 TATCAGTTCG CCCGAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGAC
1601 TGATTACTGC CGCCGCCTTC GTGCGCGAAC CGCAAAGCAT CGGCGCGCTG
1651 GTGTGCGAAG TGCCGCTGAC CGACATGATC CGTTATCCGC TGCTCTCCGC
1701 CGGTTCAGC TGGACAGACG AATACGGCAA TCCGCAAAA TACGAAGTCT
1751 GCAAACGCG GTTGGGCGAA TTGTCGCGCT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCGCGCT CATTACCACC AGCCTGTCCG ACGATCGCGT
1851 CCATCCCGCC CACGCGCTCA AGTTCTACGC CAAACTGCGC GAAACCTCCG
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACCCAACGCG AATCCGCCGA CGAACTCGCC TCGCTCTTGC TGTTTTTGAA
2001 AGAGTTTTTG GGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 162; ORF 041-1>:

m041-1.pep

```

1 MKSYDPYRHFENLDSAETQ NFAAEANAET RARFLENDKA RALSDGILAQ
51 LQDTRQIPFC QEHRARMYHF HQDAEYPKGV YRVCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TSKLGSDDTA YTLEVDLEAG
151 ELVEGGFHFP AGKNHVSWRD ENSVWVCPAW NERQLTQSGY PREVWLVERG
201 KSFEESLPVY QIGEDGMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLRVS
251 AEGEAKPLNL PNDGDVVGYL AGHLLTLRK DWNRRANQSY SGALVAVKLN
301 RGELGAAQLL FAPDETQALE SVETTKRFV ASLLENVQGR LKAWRFADGK
351 WQVELPRLP SGALEMTDQP WGGDVVYLA SDFTTPTLTF ALDLNVMELT
401 VMRRQPQFD SDGINVQFW TTSADGERIP YFHVGNKNA DMPTLVYAYG
451 GFGIPELPHY LGSIGKYWLE EGNAFVLNI RGGGEFGPRW HQAAQGISKH
501 KSVDDLAVV RDLSEGISS PEHIGLQGS NGGLITAAAF VREPQSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEVCKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDRVHPA HALKFYAKLR ETSQSWLYS PDGGGHTGNG
651 TQRESADELA CVLLFLKEFL G*

```

m041-1/g041-1 94.6% identity in 671 aa overlap

	10	20	30	40	50	60
m041-1.pep	MKSYDPYRHFENLDSAETQNF AAEANAETRARFLENDKARALSDGILAQ LQDTRQIPFC					
g041-1	MKSYDPYRHFENLDSAETQNF AAEANAETRARFLNNDKARALSDGILNQMQDTRQIPFC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041-1.pep	QEHRARMYHFHQDAEYPKGVYRVCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH					
g041-1	QEHRARMYHFHQNAEYPKGVYRMCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m041-1.pep	LVEQPNRALLT LSKLGSDDTA YTLEVDLEAGELVEGGFHFPAGKNHVSWRDENS VVWVCPAW					
g041-1	LVEQPNRALLT LNKSGDDTA YTLEVDLEAGELVEGGFHFPAGKNHVSWRDENS VVWVCPAW					
	130	140	150	160	170	180
	190	200	210	220	230	240
m041-1.pep	NERQLTQSGYPREVWLVERGKSFEESLPVYQIGEDGMMVN AWRYLDPQGS PIDLIEASDG					
	: : : : : :					

```
g041-1      DERQLTESGYPREVWLVERGKSFEESLPAYQIDKGAMMVNAWRYLDPQGSPIDLIEASDG
              190      200      210      220      230      240

              250      260      270      280      290      300
m041-1.pep   FYTKTYLRVSAEGEAKPLNLPNDCDVVGYLAGHLLLTLRKDOWNRANQSYPSGALVAVKLN
              |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
g041-1      FYTKTYLQVSSEGGAKPLNLPNDCDVVGYLAGHLLLTLRKDWHRANQSYPSGALVAVKLN
              250      260      270      280      290      300

              310      320      330      340      350      360
m041-1.pep   RGELGAAQLLFAPDETQALESVETTKRFVVASLLENVQGRKAWRFADGKWQEVLPRLP
              |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
g041-1      RGELGAAQLLFAPDETQALESVETTKRFVVASLLENVQGRKAWRFADSKWQEAELPHLP
              310      320      330      340      350      360

              370      380      390      400      410      420
m041-1.pep   SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTMRRQPQQFSDGINVQQFW
              |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
g041-1      SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTMRLQPQQFVSDGIEVRQFW
              370      380      390      400      410      420

              430      440      450      460      470      480
m041-1.pep   TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI
              ::|:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
g041-1      AVSSDGERIPYFHVGNKNAAPDPTLVYAYGGFGIPELPHYLGSVGKYWLEEGNAFVLANI
              430      440      450      460      470      480

              490      500      510      520      530      540
m041-1.pep   RGGGEFGPRWHQAAQGISKHKSVDDLAVVRDLSESGISSPEHIGLQGGSNGLITAAAF
              |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
g041-1      RGGGEFGPRWHQAAQGISKHKSVDDLAVVRDLSESGMSSPKHIGLQGGSNGLITAAAF
              490      500      510      520      530      540

              550      560      570      580      590      600
m041-1.pep   VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRLGELSPYHNLSDG
              |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
g041-1      VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEACKRRLGELSPYHNLSDG
              550      560      570      580      590      600

              610      620      630      640      650      660
m041-1.pep   IDYPPALITTSLSDDRVPALHAKFYAKLRETSAQSWLYSPDGGGHTNGTQRESADELA
              |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
g041-1      IDYPPALITTSLSDDRVPALHAKFYAKLRETSFQSWLYSPDGGGHTNGTQRESADKLA
              610      620      630      640      650      660

              670
m041-1.pep   CVLLFLKEFLGX
              |||||:|||||
g041-1      CVLLFLKEFLGX
              670
```

m041-1/P55577

sp|P55577|Y4NA_RHISN PROBABLE PEPTIDASE Y4NA >gi|2182536 (AE000086) Y4na [Rhizobium sp.
NGR234] Length = 726

Score = 370 bits (940), Expect = e-101

Identities = 217/682 (31%), Positives = 331/682 (47%), Gaps = 22/682 (3%)

Query: 2 KSYDPYRHFENLDSAETQNFAAEANAETRARFLENDKARALSDGILAQLQDTRQIPFCQ 61
K DP + +D + + N T + ++ + L LQ T +I
Sbjct: 42 KDASDPRAYLNEIDGDKAMTWVEAHNLSVTDKLSKDPYSEYQADALTILQATDRIASPS 101

Query: 62 EHRARMY-HFHQDAEYPKGVYRVCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH 120
R M +F QD + +G++R T +YRSG P+W+ + V + G G
Sbjct: 102 FARDGMIDNFWQDGHVQGLWRRRTWESYRSGNPQWRITLDVDALSKAEGKTWVFEGGDC 161

Query: 121 LVEQPNRALLTSLKLGSDTAYTLEVDLEAGELVEGGFHFHPAGKNHVSWRDENSVMVCPAW 180
L N L+ LS G D E D+ GE V+ GF P GK V+W DEN+++V W

Sbjct: 162 LPPTSNLCLIRLSDDGGKDADVREFDIAKGEFVKEGFVLPEGKQSVTWVDENTIIYVTREW 221

Query: 181 NERQLTQSGYPREVWLVERGKSFEESLPVYQ-----IGEDGMM--VNAWRYLDPQGSPI 232
 ++T SGY +V+RG+S ++++ +++ E G++ ++ +D +

Sbjct: 222 TPGEVTSSGYAYVTKVVRKQSLDQAVEIFRGQKKDVSAERGVLRLDIDGKYVMDTSYRGL 281

Query: 233 DLIEASDGFYTKTYLRVSAEGEAKPLNLPNDCDVVGYLAGHLLTLRKDWNANQS-YPS 291
 D FY + + L LP GY G + L+ DW A + + +

Sbjct: 282 DFFNTELAIFYPNHG---PDTRKVVLPPLTTAVFSGYYKQAIYWLKSDWTSAGKTVFHN 337

Query: 292 GALVAVKLNREGELGAAQL---LFAPDETQALESVETTKRFVVASLLENVQGRKAWRFA 347
 GA++A L A++ LF P+E Q++ TK +V S+L NV ++++ F

Sbjct: 338 GAIIFDLKAALADPARVEPLVLFMPNEHQSVAGTTQTKNRLVLSILSNVTSEVRSFDFG 397

Query: 348 DGKWQEVLEPRLPSGALEMTDQPWGGDVVYLAASDFTTPTLTLFALDLNVMELTVMRRQPO 407
 G W +L + L +T D +++ + F P TLF D ++ + P

Sbjct: 398 KGGWSSFKLALPENSTLSLTSSDDESQLFVFESEGFLEPSTLFCADAATGQVEKITSTPA 457

Query: 408 QFDSGGINVQQFWTTSADGERIPYFHVKGNAAP---DMPTLVYAYGGFGIPELPHYLGSI 464
 +FD+ G+ QQFW TS DG ++PYF V + PT++YAYGGF IP P Y +

Sbjct: 458 RFDAGGLQAQQFWATSKDGTKVPYFLVARKDVKLDGNTPTILYAYGGFQIPMQPSYSAVL 517

Query: 465 GKYWLEEGNAFVLANIRGGGEFGPRWHQAAQGISKHKSVDDLAVVRDLSERGISSPEHI 524
 GK WLE+G A+ LANIRGGGEFGP+WH A ++ + DD AV +DL + ++S H+

Sbjct: 518 GKLWLEKGGAYALANIRGGGEFGPKWH DAGLKTNRQRYDDFQAVAQDLIAKKVTSTPHL 577

Query: 525 GLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEV 584
 G+ GGSNGGL+ ++ P A+V +VPL DM+ + +SAG+SW EYG+P V

Sbjct: 578 GIMGGSNGGLLMGVQMIQRPDLWNAVVIQVPLLDVMNFTMSAGASWQAEYGSPPD-PVE 636

Query: 585 KRRLGELSPYHNLSGDIDYPPALITTSLSDDRVRHPAHALKFYAKLRETSQSWLYSPDGG 644
 L +SPYHN+ G+ YP TS DDRV P HA K A + + Y G

Sbjct: 637 GAFILRSISPYHNKAGVAYPEPFETSTKDDRVPVHARKMAALFEDMGLPFYYENIEG 696

Query: 645 GHTNGTQRESADELACVLLFL 666
 GH +E A A +++

Sbjct: 697 GHAAAAANLQEHARRYALEYIYM 718

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 163>:

a041-1.seq

```

1 ATGAAATCCT ACCCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51 CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAAACAA CGACAAGGCA CGCGCATTGT CTGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGCAAAT TCCGTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTT CATCAAGATG CGGAATATCC GAAAGGCGTG TACCGCGTGT
251 GTACCGCGGC GACTTACCGT TCGGGCTATC CTGAGTGGAA AATCCTGTTT
301 TCGGTGCGCG ATTTGACGCA ATTGCTCGGT GACGATGTAT ATCTAGGCGG
351 CGTGTCGCAC CTGGTGGAA AGCCCAACCG CGCGTTGTTA AACTGAGCA
401 AATCGGCGCG CGATACCGCG TACACGCTGG AAGTGATTT GGAAGCAGGG
451 GAGTTGGTAG AAGGCGGTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG GACGAACGCC
551 AGTTGACCGA ATCGGGCTAT CCGCGCGAGG TGTGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT GCCGGTGTAC CAAATTGCTG AAGACGGCAT
651 GATGGTGAAC GCGTGGCGTT ACCTCGATCC GCAGGTTTCG CCGATTGATT
701 TGATTGAAGC GTCTGACGGT TTTTACACCA AAACCTATTT GCAGGTCTCA
751 GCCGAAGGCG AAGCGAAACC GTTAAACCTG CCCAACGATT GCGACGTAGT
801 CGGCTATCTG GCCGACATC TTTTGTCTGAC CTTGCGTAAA GACTGCGACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCAT TGGTAGCAGT AAAATTAAAC
901 CGCGGCGAAT TGGGCGCGGC GCAGCTTTTG TTTGCGCCCA ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTCTGT GCGAGCCTGC
1001 TGGAAAACGT ACAGGTCGT CTGAAAGCGT GCGGTTTAC TGATGGCAAA
1051 TGGCAGGAAA CCGAGTTGCC GCGCCTGCCT TCGGCGCGCT TGGAAATGAC
1101 CGACCAACCG TGGGGGGGCG ACGTAGTTTA CCTTGCCGCC AGCGATTTC A
1151 CCACGCCGCT GACGCTGTTT GCATTGGATT TGAACGTGAT GGAACGTGACC
1201 GTCATGCGCC GCCAGCCGCA GCAGTTTGAT TCAGACGGCA TTAACGTGCA
1251 GCAGTTTGG ACGACTTCGG CTGACGGCGA GCGCATTCCT TATTTCACG
1301 TCGGCAAAAA CGCCGCGCCC GACATGCCGA CGCTGGTCTA TGCCTACGGC
1351 GGTTCGGCA TTCCGAATT GCCGCATTAT CTGGGCAGCA TTGGCAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTTGTATT GCGGAACATC CGCGCGCGGC

```

```

1451 GCGAGTTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAACAT
1501 AAAAGCGTTG ATGATTATT GGCAGTCGTG AGCGATTGT CCGAACGCGG
1551 TATCAGTTCG CCCGAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGAC
1601 TGATTACTGC CGCCGCCTTC GTGCGCGAAC CGCAAAGCAT AGGCGCGCTG
1651 GTGTGCGAAG TGCCGCTGAC CGACATGATC CGTTATCCGC TGCTCTCCGC
1701 CGGTTCAAGC TGGACAGACG AATACGGCAA TCCGCAAAAA TACGAAGTCT
1751 GCAAACGCGG GTTGGGCGAA TTGTGCGCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCCGCGCT CATTACCACC AGCCTGTCCG ACGATCGCGT
1851 CCATCCCGCC CACGCGCTCA AGTTCTACGC CAAACTGCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACGCAGCGCG AAGCCGCCGA CGAACTCGCC TCGGTGTTGC TGTTTTTGAA
2001 AGAGTTTTTG GGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 164; ORF 041-1.a>:

a041-1.pep

```

1  MKSYDPYRH FENLDSAETQ NFAAEANAET RARFLNNDKA RALSDGILAQ
51  LQDTRQIPFC QEHRARMYHF HQDAEYPKG VYRVCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TLSKSGGDTA YTLEVDLEAG
151 ELVEGGFHFP AGKNHVS WRD ENSVWVCPAW DERQLTESGY PREVWLVERG
201 KSFEESLPVY QIAEDGMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
251 AEGEAKPLNL PNDCDVVGYL AGHLLTLRK DWHRANQSYPS GALVAVKLN
301 RGELGAAQLL FAPNETQALE SVETTKRFVV ASLLENVQGR LKAWRFTDGK
351 WQETELPRLP SGALEMTDQP WGGDVVYLAA SDFTTPTLTF ALDLNMELT
401 VMRRQPQQFD SDGINVQQFW TTSADGERIP YFHVGNKNAAP DMPTLVYAYG
451 GFGIPELPHY LGSIGKYWLE EGNAFVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLLAVV SDLSEGISS PEHIGLQGGG NGGLITAAAF VREPOSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEVCKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
651 TQREAADELA CVLFLKEFL G*

```

a041-1/m041-1 97.9% identity in 671 aa overlap

	10	20	30	40	50	60
a041-1.pep	MKSYDPYRHFENLDSAETQ	NFAAEANAETR	RARFLNNDKAR	ALSDGILAQ	LQDTRQIPFC	
m041-1	MKSYDPYRHFENLDSAETQ	NFAAEANAETR	RARFLNNDKAR	ALSDGILAQ	LQDTRQIPFC	
	10	20	30	40	50	60
	70	80	90	100	110	120
a041-1.pep	QEHRARMYHFHQDAEYPKG	VYRVCTAATYR	SGYPEWKILF	SVADFDELLG	DDVYLGGVSH	
m041-1	QEHRARMYHFHQDAEYPKG	VYRVCTAATYR	SGYPEWKILF	SVADFDELLG	DDVYLGGVSH	
	70	80	90	100	110	120
	130	140	150	160	170	180
a041-1.pep	LVEQPNRALLTLSKSGGDT	AYTLEVDLEAGEL	VEGGFHFPAG	KNHVS WRD	ENSVWVCPAW	
m041-1	LVEQPNRALLTLSKSGGDT	AYTLEVDLEAGEL	VEGGFHFPAG	KNHVS WRD	ENSVWVCPAW	
	130	140	150	160	170	180
	190	200	210	220	230	240
a041-1.pep	DERQLTESGYPREVWLVER	GKSFEESLPVYQ	IAEDGMMVN	AWRYLDPQGS	PIDLIEASDG	
m041-1	DERQLTESGYPREVWLVER	GKSFEESLPVYQ	IAEDGMMVN	AWRYLDPQGS	PIDLIEASDG	
	190	200	210	220	230	240
	250	260	270	280	290	300
a041-1.pep	FYTKTYLQVSAEGEAKPL	NLPNDCDVVGYL	AGHLLTLRK	DWHRANQSYPS	GALVAVKLN	
m041-1	FYTKTYLQVSAEGEAKPL	NLPNDCDVVGYL	AGHLLTLRK	DWHRANQSYPS	GALVAVKLN	
	250	260	270	280	290	300
	310	320	330	340	350	360
a041-1.pep	RGELGAAQLLFAPNETQAL	ESVETTKRFV	VASLLENVQGR	LKAWRFTDGK	WQETELPRLP	
m041-1	RGELGAAQLLFAPNETQAL	ESVETTKRFV	VASLLENVQGR	LKAWRFTDGK	WQETELPRLP	
	310	320	330	340	350	360

	370	380	390	400	410	420
a041-1.pep	SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTMRRQPQQFSDGINVQQFW					
m041-1	SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTMRRQPQQFSDGINVQQFW					
	370	380	390	400	410	420
	430	440	450	460	470	480
a041-1.pep	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
m041-1	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
	430	440	450	460	470	480
	490	500	510	520	530	540
a041-1.pep	RGGGEFGPRWHQAAQGISKHKSVDDLAVVSDLSESGISSPEHIGLQGGSNGLITAAAF					
m041-1	RGGGEFGPRWHQAAQGISKHKSVDDLAVVRDLSESGISSPEHIGLQGGSNGLITAAAF					
	490	500	510	520	530	540
	550	560	570	580	590	600
a041-1.pep	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRRLGELSPYHNLSDG					
m041-1	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRRLGELSPYHNLSDG					
	550	560	570	580	590	600
	610	620	630	640	650	660
a041-1.pep	IDYPPALITTSLSDDRVPALHAKFYAKLRETSQSWLYSPDGGGHTGNGTQRESADELA					
m041-1	IDYPPALITTSLSDDRVPALHAKFYAKLRETSQSWLYSPDGGGHTGNGTQRESADELA					
	610	620	630	640	650	660
	670					
a041-1.pep	CVLLFLKEFLGX					
m041-1	CVLLFLKEFLGX					
	670					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 165>:

g042.seq

```

1  ATGACGATGA TTTGCTTGCG CTTCCAagcG TTCGTGCCGC ATACCAGCGC
51  GTTATCCAAC ACTTCCACGG CAGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TGCGGTGCGAT GATGAAAATC CAGCCGGGGT TTTTCTCTTT GATGTATTCG
151 AAGGAAACGG GCTGCCCGTG CCCTTCGTTG CGTAAAGATT CGTCCACGGG
201 CGGCAGGCCG ATGTCGCCGT GTATCCAAC TGCACAACCG GATTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCTGTAACCG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG cggCTTCGCG CTTTGTGGCG AACAGCGCGT CAATCTGCGC
351 ATTCAATTCC GCCACGCGCG CTTCTTACC GAAAATCCGC GACAGGGTCT
401 CCATCTGCTT CTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAAA
451 TCTATGgtgG TCGCGTTTTT CGCCAACGTG TCATACGCTT CCGCACCCGG
501 CCCGCCGGTA ATGACAAACT GCGGATTGTG GCGGTGCAGG GATTGCAAT
551 CGGGCTCAAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAAA TGCAGGCTGC
601 AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 166; ORF 042.ng>:

g042.pep

```

1  MTMICLRFQA FVPHTSALSN TSTAAGPSCP MAAVRSMMKI QPGFFSLMYS
51  KETGCPGPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTGSTSPRP
101 LPLAASRFWA NSASICAFNS ATRASLPKIR DRVSICFSPL VRILPLSTVK
151 SMVVAFFANC SYASAPGPPV MTNCGLWRCR DSQSGSNSVP TVAALSNAAG
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 167>:

m042.seq

```

1   ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAmT ACTTCGACAG CCGcCGGCCy TTCyTGCCCG ATGGCGGCCG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCTG
151 AAGGAAACAG GCTGCCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCCCTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 168; ORF 042>:

m042.pep

```

1   MTMICLRFOA FVPRTSALSX TSTAAGXSCP MAAVRSMMKI QSGFFSLMYS
51  KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVT DSTSPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTSXGLXRRCR ASXSGSNSVP TVAALSNAAG
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 169>:

a042.seq

```

1   ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCG ATGGCGGCCG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCTG
151 AAGGAAACAG GCTGCCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCCCTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCCAACGTG TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 170; ORF 042.a>:

a042.pep

```

1   MTMICLRFOA FVPRTSALSX TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51  KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVT DSTSPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*GL*RCR AS*SGSNSVP TVAALSNAAG
201 K*

```

m042/a042 99.0% identity over a 201 aa overlap

	10	20	30	40	50	60
m042.pep	MTMICLRFOAFVFPRTSALSXTSTAAGXSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
a042	MTMICLRFOAFVFPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
	10	20	30	40	50	60
m042.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
a042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
m042.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
a042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
m042.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRRCR					
a042	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRRCR					

```

a042      |||||
          AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANCSYASAPGPPVMTSXGLXRCR
          130      140      150      160      170      180

          190      200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
          |||||
a042      ASXSGSNSVPTVAALSNAGCKX
          190      200

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 042 shows 93.0% identity over a 201 aa overlap with a predicted ORF (ORF 042.ng) from *N. gonorrhoeae*:

m042/g042

```

          10      20      30      40      50      60
m042.pep  MTMICLRFAQFVPRTSALSXTSTAAGXSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL
          |||||:|||||
g042      MTMICLRFAQFVPHTSALSNTSTAAGPSCPMAAVRSMMKIQPGFFSLMYSKETGCPCPSL
          10      20      30      40      50      60

          70      80      90      100     110     120
m042.pep  RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS
          |||||
g042      RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRFWANSASICAFNS
          70      80      90      100     110     120

          130     140     150     160     170     180
m042.pep  AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANCSYASAPGPPVMTSXGLXRCR
          |:|||||:|||||:|||||:|||||: || |||
g042      ATRASLPKIRDVSICFSPLVRILPLSTVKSMVVAFFANCSYASAPGPPVMTNCGLWRCR
          130     140     150     160     170     180

          190     200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
          | |||||
g042      DSQSGSNSVPTVAALSNAGCKX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 171>:

m042-1.seq

```

1  ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51 GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCTG
151 AAGGAAACAG GCTGCCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGCACAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTC AATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 172; ORF 042-1>:

m042-1.pep

```

1  MTMICLRFAQ FVPRTSALSN TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51 KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVT DSTSPR
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*

```

m042-1/g042 95.4% identity in 173 aa overlap

240

	10	20	30	40	50	60
m042-1.pep	MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
g042	MTMICLRFQAFVPHTSALSNTSTAAGPSCPMAAVRSMMKIQPGFFSLMYSKETGCPCPSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m042-1.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
g042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRFWANSASICAFNS					
	70	80	90	100	110	120
	130	140	150	160	170	
m042-1.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX					
g042	ATRASLPKIRD RVSICFSPLVRILPLSTVKSMVVAFFANC SYASAPGPPVMTNCGLWRCR					
	130	140	150	160	170	180
g042	DSQSGSNSVPTVAALSNAGCKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 173>:

a042-1.seq

1	ATGACGATGA	TTTGCTTGCG	CTTCCAAGCG	TTCGTGCCGC	GTACCAGCGC
51	GTTATCCAAT	ACTTCGACAG	CCGCCGGCCC	TTCCTGCCCG	ATGGCGGCGG
101	TACGGTCGAT	GATGAAAATC	CAATCGGGGT	TTTTCTCTTT	GATGTATTCG
151	AAGGAAACAG	GCTGCCCCGT	CCCCTCGTTG	CGTAAAGATT	CGTCTACAGG
201	CGGTAGGCCG	ATGTGCGCGT	GTATCCAAC	TGCCAACCGC	GACTGCGTGC
251	CGAAGGCGGA	CACCTTGTTG	CCCGTAACCG	ACAGCACCAG	CCGCGTCCT
301	TTGCCTTTGG	CGGCTTCGCG	CGTTTGGGCG	AACAGCGCGT	CAATCTGCGC
351	CTTCAATTCC	GCCGCGCGCG	CTTCCTTGCC	GAAAATCCGC	GCCAAGGTCT
401	CCATCTGCTT	TTCGCGCGTG	GTGCGGATAT	TGCCGTTGTC	CACCGTCAGA
451	TCTATGGTGG	TCGCGTTTTT	CGCCAACGTG	TCATACGCTT	CCGCGCCCCG
501	CCGCGCGGTA	A			

This corresponds to the amino acid sequence <SEQ ID 174; ORF 042-1.a>:

a042-1.pep

1	MTMICLRFQA	FVPRTSALS	N TSTAAGPSCP	MAAVRSMMKI	QSGFFSLMYS
51	KETGCPCPSL	RKDSSTGGRP	MSPCIQLANR	DCVPKADTLL	PVT DSTSPRP
101	LPLAASRVWA	NSASICAFNS	AARASLPKIR	AKVSICFSPL	VRILPLSTVR
151	SMVVAFFANC	SYASAPGPPV	MTS*		

m042-1/a042-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
m042-1.pep	MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
a042-1	MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m042-1.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
a042-1	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
	130	140	150	160	170	
m042-1.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX					
a042-1	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 175>:

```

g043.seq
  1  ATGGTTGTTT CAAATCAAAA TATCTATGCC GTCGGCCCAT CAGCACTTTT
 51  TCACATCCGA AGGCAAAAAT CCGTAATGCC GCCTGAACGC TTCgttgAAC
101  CGTCCCGCGT ggcggtagcc gcAAAAGTGC ATcGCGGCTT GGATGGTGCT
151  GCGCGATTTC ATGAGGGcga gcGCGTGTTC CAGCCGCAGG CGGCGCAGGC
201  GTCCGGCGAC GGTTCGCGG GTTTGCCTT TGAATAGCG TTTCAGGTAG
251  CATTCGTTCA GCGCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGGCG
301  GCGGAATTCG CTGTTCAAAA TATCGCGCGC TTCGTCTATG CGCCGGCGGC
351  GGTAGCCGTT GTCGTGGCGG CGGAAGGTGA AGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 176; ORF 043.ng>:

```

g043.pep
  1  MVVSNQNIYA VGPSALFHIR RQKSVMPER FVEPSRVAVA AKVHRGLDGA
 51  ARFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQPD AAGDFGDGQRA
101  GEFVQNIIGG FVYAPAAVAV VVAEEGEA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 177>:

```

m043.seq
  1  ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCCT CAGCACTTCT
 51  TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
101  CGTCCCGCGT GCGGGTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT
151  GCGGATTTCG ATGAGGGCGA GCGCGTGTTC CAGCCGCAGG CGGCGCAGGC
201  ATCCGGCGAC GGTTCGCGG GTTTGCCTT TGAATAGCG TTTCAGGTAG
251  CATTCGTTCA GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301  GCGGAATTCG TGTTCAGGA TGTGCGCGC TTCGTCTATG CGCCGACGGC
351  GGTAACCGTT GTCGTGGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 178; ORF 043>:

```

m043.pep
  1  MVVSNQNIYA AGPSALLHIR RQKSVMPER FVEPSRVAVA AKVHGGLDGA
 51  AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AAGDFGDGQRT
101  GEFVLQDVGG FVYAPTAVTV VVAEEGEAQ*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 043 shows 89.8% identity over a 128 aa overlap with a predicted ORF (ORF043.a) from *N. gonorrhoeae*:

m043/g043

	10	20	30	40	50	60
m043.pep	MVVSNQNIYAAGPSALLHIRRQKSVMPSEFVEPSRVAVAAKVHGGGLDGAAGFDEGERVF					
	: : : : : : : : : :					
g043	MVVSNQNIYAVGPSALFHIRRQKSVMPSEFVEPSRVAVAAKVHRRGLDGAARFDEGERVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
	: : : : : : : : :					
g043	QPQAAQASGDGFAGLRFEIAFQVAFVQPDAGDFGDGQRTGEFVQNIIGGFVYAPAAVAV					
	70	80	90	100	110	120
	130					
m043.pep	VVAEEGEAQX					
g043	VVAEEGEAXX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 179>:

```

a043.seq
  1  ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCCT CAGCACTTCT
 51  TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
101  CGTCCCGCGT GCGGGTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT

```

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```

151 GCCGATTTCG ATGAGGGCGA GCGCGTGTTT CAGCCGCAGG CGGCGCAGGC
201 ATCCGGCGAC GGTTCGCCG GTTTGCGCTT TGAAATAGCG TTTCAGGTAG
251 CATTCTGTTA GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301 GGCGAATTCG TGTTGCAGGA TGTCGGCGGC TTCGTCTATG CGCCGACGCG
351 GGTAACCGTT GTCGTGGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 180; ORF 043.a>:

```

a043.pep
  1 MVVSNQNIYA AGPSALLHIR RQKSVMPSEF FVEPSRVAVA AKVHGGLDGA
 51 AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AGDFGDGQRT
101 GEFVLQDVGG FVYAPTAVTV VVAAEGEAQ*

```

m043/a043 100.0% identity in 129 aa overlap

```

              10      20      30      40      50      60
m043.pep      MVVSNQNIYAAGPSALLHIRRQKSVMPSEFVEPSRVAVAAKVHGGLDGAAGFDEGERVF
              |||||
a043           MVVSNQNIYAAGPSALLHIRRQKSVMPSEFVEPSRVAVAAKVHGGLDGAAGFDEGERVF
              10      20      30      40      50      60

              70      80      90      100     110     120
m043.pep      QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV
              |||||
a043           QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV
              70      80      90      100     110     120

              130
m043.pep      VVAAEGEAQX
              |||||
a043           VVAAEGEAQX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 181>:

```

g044.seq
  1 ATGCTGCCCG ACCAGAGCGT CGAGTTCTTG CCACAAGTCG TCGTTTTTGA
 51 CGGGCTGTTT GGCGGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
101 CAGTTTTTCCA TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTTGAGCG ATTTTCAGCCC TTCGATAACG GCGGTCAGCT
201 CCATGCGGTT GTTGGTGGTT TCGCTTCGC CGCCGAAAAG TTCTTTTTCG
251 CGGCTGCCGT AGCGCATTA

```

This corresponds to the amino acid sequence <SEQ ID 182; ORF 044.ng>:

```

g044.pep
  1 MLPDQSVEFL PQVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
 51 GAAAFERFQP FDNGGQLHAV VGGLRFAAEK FFFAAVAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 183>:

```

m044.seq
  1 ATGCCGTCCG ACTAGAGCGT CGAGTTCTTT CCAGAAGTCG TCGTTTTTGA
 51 CGGGCTGTTT GGAGGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
101 CAGTTTTTCCA TGCCATTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTTGAGCG ATTTTCAGTCC TTCGATGACG GCAGTCAGTT
201 CCATGCGGTT GTTGGTGGTT TCGCTTCGC CGCCGAAAAG TTCTTTTTCG
251 TGGTACCGT AGCGCAyTAa

```

This corresponds to the amino acid sequence <SEQ ID 184; ORF 044>:

```

m044.pep
  1 MPSDXSVEFF PEVVFDGLF GGGFPAVALP TVYPVFHAI F DVLRVGADDD
 51 GAAAFERFQS FDDGSQFHAV VGGLRFAAEK FFFVATVAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 185>:

```
a044.seq
1  GTGCCGTCGG ACCAGCGCGT CGAGTCTTTT CCACAAGTCG TCGTTTTTGA
51  CGGGCTGTTT GCGGCGCGGT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
101 CAGTTTTCCA TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTTGAGCG ATTCAGTCC TCGATGACG GCGGTCAGTT
201 CCATACGGTT GTTGGTGGTT TCGCTTCGC CGCCGAAAAG TTCTTTTTCG
251 TGGCTGCCGT AGCGCATTA
```

This corresponds to the amino acid sequence <SEQ ID 186; ORF 044.a>:

```
a044.pep
1  VPSDQREFF PQVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
51  GAAAFERFQS FDDGGQFHTV VGGLRFAAEK FFFVAVAH*
```

m044/a044 91.0% identity over a 89 aa overlap

```

      10      20      30      40      50      60
m044.pep  MPSDXSVEFFPEVVFDGLFGGGFPAVALPTVYPVFHAFDVLRVGADDDGAAAFERFQS
          :||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a044      VPSDQREFFPQVVFDGLFGGGFPAVALPTVYPVFHAVFDVLRVGADDDGAAAFERFQS
          10      20      30      40      50      60

      70      80      90
m044.pep  FDDGSQFHAVVGGLRFAAEKFFFVATVAHX
          |||:||||:|||||:|||||:|||||:|||||
a044      FDDGGQFHTVVGGLRFAAEKFFFVAVAHX
          70      80      90
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 044 shows 86.5% identity over a 89 aa overlap with a predicted ORF (ORF 044.ng) from *N. gonorrhoeae*:

```
m044/g044

      10      20      30      40      50      60
m044.pep  MPSDXSVEFFPEVVFDGLFGGGFPAVALPTVYPVFHAFDVLRVGADDDGAAAFERFQS
          | | |||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g044      MLPDQSVEFLPQVVFDGLFGGGFPAVALPTVYPVFHAVFDVLRVGADDDGAAAFERFQP
          10      20      30      40      50      60

      70      80      90
m044.pep  FDDGSQFHAVVGGLRFAAEKFFFVATVAHX
          ||:|:|:|||||:|||||:|||||:|||||
g044      FDNGGQLHAVVGGLRFAAEKFFFAAFAHX
          70      80      90
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 187>:

```
g046.seq
1  ATGTCGGCAA TGCTGCGTCC GACAAGCAGC CCGCCGcgcc gCGCCTGTAT
51  GATGACCATC CGCACGCGGT CGTCTGCAA ACGTAAAACC TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCGGGG
151 CTGATGTTT CGGTATGCC gaATATGGAA AGGCTGCCgt TTtCGTTGTT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TtcgctGGAA CGGACGCGCG
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG
301 ATGTTGGTTT CGTCGCTGCG GGagaGCGCG AGcagcaagt cggcatcttC
351 CgcgccggcG Cgttataatg tgAAGGGGGA TGCGccgttg ccgaAAACGG
401 TTTGGacatc gaggcggtcg CCTGTTTCCT GCAATGCTTT TTCGTCGATG
451 TCGATAAcgg TTACGTCGTT GTTGGTGATG GCGGCAAGGT TTTGCGCGAC
```

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501 GGTAGAACCT ACCTGCCCCGT TGCCTAAAAT GAGGATTTTC ACGGTATGGG
 551 TCGCCGGGTG A

This corresponds to the amino acid sequence <SEQ ID 188; ORF 046.ng>:

g046.pep
 1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
 51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
 101 MLVSSLRESA SSKSASSAPA RYNVKGDAPL PKTVWTSRRL PVSCNAFSSM
 151 SITVTSLLVM AARFCATVEP TCPLPKMRIF TVWVAG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 189>:

m046.seq
 1 ATGTCGGCAA TGCTGCGTCC GACAAGCAst CCGC.r.sGC gCGcCTGTAT
 51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC
 101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
 151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTCGTTGTT
 201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG
 251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG
 301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC
 351 CGCGCCGCG CGTTCTAATG TGAAGGGGGA TCGCCCGTTG CCGAAAACGG
 401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG
 451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC
 501 GGTAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG
 551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 190; ORF 046>:

m046.pep
 1 MSAMLRPTSX PXXRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
 51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
 101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM
 151 SITVTSLLGM AARFCATVEP TCPLPKMRIF TVWVAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 191>:

a046.seq
 1 ATGTCGGCAA TGCTGCGTCC GACAAGCAGT CCGCCGCGCC GCGCCTGTAT
 51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC
 101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
 151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTCGTTGTT
 201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG
 251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG
 301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC
 351 CGCGCCGCG CGTTCTAATG TGAAGGGGGA TCGCCCGTTG CCGAAAACGG
 401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG
 451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC
 501 GGTAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG
 551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 192; ORF 046.a>:

a046.pep
 1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
 51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
 101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM
 151 SITVTSLLGM AARFCATVEP TCPLPKMRIF TVWVAE*

m046/a046 98.4% identity over a 186 aa overlap

	10	20	30	40	50	60
m046.pep	MSAMLRPTSXPXXRACMMTIIRTRSSAKRKT CNAPGQSIRPASCSVTSCSGLMVSVMPNME					
a046	MSAMLRPTSSPPRRACMMTIIRTRSSAKRKT CNAPGQSIRPASCSVTSCSGLMVSVMPNME					

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	10	20	30	40	50	60
m046.pep	70	80	90	100	110	120
	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
a046	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
m046.pep	130	140	150	160	170	180
	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
a046	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
a046	TVWVAEX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 046 shows 97.3% identity over a 185 aa overlap with a predicted ORF (ORF 046.ng) from *N. gonorrhoeae*:

m046/g046

	10	20	30	40	50	60
m046.pep	MSAMLRPTSXPPXRACMMTIRTRSSAKRKTGNAPGQSIRPASC SVTSCSGLMVSVMPNME					
g046	MSAMLRPTSSPPRRACMMTIRTRSSAKRKTGNAPGQSIRPASC SVTSCSGLMVSVMPNME					
	10	20	30	40	50	60
m046.pep	70	80	90	100	110	120
	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
g046	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
m046.pep	130	140	150	160	170	180
	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
g046	RYNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLVMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
g046	TVWVAGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 193>:

g047.seq

```

1  ATGGTCATCA TACAGGCGcg gcGCGGCGGG CTGCTTGTCG GACGCAGCAT
51  TGCCGACATC GCCCAAGATT TGCCCGACGG GGCCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTCATCGTCC CCGCGCCGCA AACCCTCATC
151 ATCGAAGGCG ACGAAATCCT GTTTGCCGCC GCCGCCGAAA ACATCGGGGC
201 GGTCATACCc gaATTGCGCC CCAAAGAAAC CAGCACCCGC CGCATCATGA
251 TTGCCGCGCG CGGCAACATc tgctACCGCC TCGCCAAGCA GCTCGAACAC

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```

301 GCATAcacG TCAAAATCAT CGAATGCCGG CCGCGCcggtg ccgaATGGAT
351 AGCCGAAAAAC ctcgAcaaCA CCCTCGTCCT GCAAGGTTCG Gcaaccgacg
401 aAaccctgct cgAcaacgaa tacatcgacg aaatcgaCGT ATTCTGCGCC
451 CTGACCAACG ACGACGAAAG CAACATTAtg tCCGCCCTTT TGGCGAAAAA
501 CCTcggcgCG AAGCgcggtca tcggCATCGT CAACCGCTCA AGCTACGTCG
551 ATTTGCTCGA AGGCAACAAA ATCGACATCG TCGTCTCCCC CCACCTCATC
601 ACCATCGGCT CGATACTCGC CCACATCCGG CGCGGCGACA TCGTTGCCGT
651 CCACCCCATC CGGCGCGGCA CGGCGGAAGC CATCGAAGTC GTCGCGCAGC
701 GCGACAAAAA AACTTCCGCC ATCATCGGCA GGCGCATCAG CGGCATCAAA
751 TGGCCCGAAG GCTGCCACAT TGCCGCCGTC GTCCGCGCCG GAACCGGCGA
801 AACCATTATG GGACACCATA CCGAAACCGT CATCCAAGAC GGTGACCACA
851 TCATCTTTTT CGTCTCGCGC CGGCGCATCC TGAACGAACT GGAGAAACTC
901 ATCCAAGTCA AAATGGGCTT TTTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 194; ORF 047.ng>:

g047.pep

```

1 MVIIQARRGG LLVGRSIADI AQDLPDGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETSTR RIMIAGGGNI CYRLAKQLEH
101 AYNVKIIECR PRRAEWIAEN LDNTLVLQGS ATDETLLDNE YIDEIDVFCA
151 LTNDDESIM SALLAKNLGA KRVIGIVNRS SYVDLLEGNK IDIVVSPHLI
201 TIGSILAHIR RGDIVAVHPI RRGTAEAIEV VAHGDKKTS AIIGRISGIK
251 WPEGCHIAAV VRAGTGETIM GHHTETVIQD GDHIIFFVSR RRILNELEKL
301 IQVKMGFFG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 195>:

m047.seq

```

1 ATGGTCATCA TACAGgCGcG C. .syGCGGA sTGCTTGTCTG GACGCAGCAT
51 TGCCGACATC GCCCAAGATT TGCCCGACGG GGCCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTCATCGTCC CCGCGCCGCA AACCGTCATC
151 ATCGAAGGCG ACGAAATCCT ATTTGCCGCC GCCGCCGAAA ACATCGGCGC
201 GGTACATCCC GAATTGCGCC CCAAAGAAAC CCAAAGAAAC CAGCcCmgmm
251 GcATCATGAT TkCCGGCGGC GGCAACATCG GCTACCGTCT CGCCAAGCAG
301 CTGAACACG CATAACAAGT yAAAATCATC GAATGCCGGC CGCGCCGTGC
351 CGAATGGATA GCCGAAAACC TCGACAACAC CCTCGTCyTG CAAGGTTCGG
401 CAACCGACGA AACCTGCTC GACAACGAAT ACATCGACGA AATCGACGTA
451 TTCTGCGCCC TGACCAACGA CGACGAAAGC AACATTATGT CCGCCCTTTT
501 GCGGaaAAAC CTCGGCGCGA AGCGCGTCAT CGGCATCGTC AACCGTCAA
551 GCTACGTCGA TTTGCTCGAA GGCAACAAA TCGACATCGT CGTCTCCCCC
601 CACTCATCA CCATCGGCTC GATACTCGCC CACATCCGGC GCGCGACAT
651 CGTTGCCGTC CACCCCATCC GGCGCGGCAC GGCGGAAGCC ATCGAAGTCG
701 TCGCACACGG CGACAAAAA ACTTCCGCCA TCATCGGCAG GCGCATCAGC
751 GGATCAAAT GGCCCGAAGG CTGCCACATT GCCGCCGTCG TCCGCGCCGG
801 AACCGGCGAA ACCATTATGG GACACCATAC CGAAACCGTC ATCCAAGACG
851 GCGACCACAT CATCTTTTTC GTCTCGCGCC GGCGCATCCT GAACGAACTG
901 GAAAACTCA TCCAGGTCAA AATGGGCTT TTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 196; ORF 047>:

m047.pep

```

1 MVIIQARXXG XLVGRSIADI AQDLPDGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETQRN QPXXIMIXGG GNIGYRLAKQ
101 LEHAYNVKII ECRPRRAEWI AENLDNTLV LQGSATDETL DNEYIDEIDV
151 FCALTNDDES NIMSALLAKN LGAKRVIGIV NRSSYVDLLE GNKIDIVVSP
201 HLITIGSILA HIRRGDIVAV HPIRRGTAE AIEVVAHGDKK TSAIIGRRIS
251 GIKWPEGCHI AAVVRAGTGE TIMGHHTETV IQDGDHIIFF VSRRRILNEL
301 EKLIQVKMGF FG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 197>:

a047.seq

```

1 ATGGTCATCA TACAGGCGCG GCGCGGCGGA CTGCTTGTCTG GACGCAGCAT

```

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```
51  TGCCGACATC GCCCAAGATT TGCCCGACGG GGCCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTCATCGTCC CCGCGCCGCA AACCGTCATC
151 ATCGAAGGCG ACGAAATCCT ATTTGCCGCC GCCGCCGAAA ACATCGGCGC
201 GGTACATACC GAATTGCGCC CCAAAGAAAC CAGCACCCGC CGCATCATGA
251 TTGCCGGCGG CGGCAACATC GGCTACCGTC TCGCCAAGCA GCTCGAACAC
301 GCATACAACG TCAAAATCAT CGAATGCCGG CCGCGCCGTG CCGAATGGAT
351 AGCCGAAAAC CTCGACAACA CCCTCGTCCT GCAAGGTTCT GCAACCGACG
401 AAACCCTGCT CGACAACGAA TACATCGACG AAATCGACGT ATTCTGCGCC
451 CTGACCAACG ACGACGAAAG CAACATTATG TCCGCCCTTT TGGCGAAAAA
501 CCTCGGCGCG AAGCGCGTCA TCGGCATCGT CAACCGCTCA AGCTACGTCG
551 ATTTGCTCGA AGGCAACAAA ATCGACATCG TCGTCTCCCC CCACCTCATC
601 ACCATCGGCT CGATACTCGC CCACATCCGG CGCGGCGACA TCGTTGCCGT
651 CCACCCATC CGGCGCGGCA CGGCGGAAGC CATCGAAGTC GTCGCACACG
701 GCGCAAAAAA AACTTCCGCC ATCATCGGCA GGCGCATCAG CGGCATCAAA
751 TGGCCCGAAG GCTGCCACAT TGCCGCCGTC GTCCGCGCCG GAACCGGCGA
801 AACCATTATG GGACACCATA CCGAAACCGT CATCCAAGAC GGCGACCACA
851 TCATCTTTTT CGTCTCGCGC CGGCGCATCC TGAACGAACT GGA AAAA ACTC
901 ATCCAAGTCA AAATGGGCTT TTTCGGATAA
```

This corresponds to the amino acid sequence <SEQ ID 198; ORF 047.a>:

```
a047.pep
1  MVIIQARRGG LLVGRSIADI AQDLPGADC QICAVYRNNR LIVPAPQTVI
51  IEGDEILFAA AAENIGAVIP ELRPKETSTR RIMIAGGGNI GYRLAKQLEH
101 AYNVKIIECR PRRAEWIAEN LDNTLVLQGS ATDETLTLDNE YIDEIDVFCA
151 LTNDDES NIM SALLAKNLGA KRVIGIVNRS SYVDLLEGNK IDIVVSEPHLI
201 TIGSILAHIR RGDIVAVHPI RRGTAEAIEV VAHGDKKTS A IIGRRISGIK
251 WPEGCHIAAV VRAGTGETIM GHHTETVIQD GDHIIFFVSR RRILNELEKL
301 IQVKMGFFG*
```

m047/a047 96.5% identity over a 312 aa overlap

```

      10      20      30      40      50      60
m047.pep  MVIIQARXXGXLVGRSIADIAQDLPGADCQICAVYRNNRLIVPAPQTVIIIEGDEILFAA
          ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a047      MVIIQARRGGLLVGRSIADIAQDLPGADCQICAVYRNNRLIVPAPQTVIIIEGDEILFAA
          10      20      30      40      50      60

      70      80      90     100     110     120
m047.pep  AAENIGAVIPELRPKETQRNPXXIMIXGGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI
          ||||| : ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a047      AAENIGAVIPELRPKETSTRR---IMIAGGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI
          70      80      90     100     110

      130     140     150     160     170     180
m047.pep  AENLDNTLVLQGSATDETLTLDNEYIDEIDVFCALTNDDES NIMSALLAKNLGAKRVIGIV
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a047      AENLDNTLVLQGSATDETLTLDNEYIDEIDVFCALTNDDES NIMSALLAKNLGAKRVIGIV
          120     130     140     150     160     170

      190     200     210     220     230     240
m047.pep  NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEIVVAHGDKK
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a047      NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEIVVAHGDKK
          180     190     200     210     220     230

      250     260     270     280     290     300
m047.pep  TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRRILNEL
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a047      TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRRILNEL
          240     250     260     270     280     290

      310
m047.pep  EKLIQVKMGFFGX
          |||||
```

a047 EKLIQVKMGFFGX
 300 310

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 047 shows 96.2% identity over a 312 aa overlap with a predicted ORF (ORF 047.ng) from *N. gonorrhoeae*:

m047/g045

m047.pep	MVIIQARXXGLVGRSIADIAQDLDPGADCQICAVYRNNRLIVPAPQTVIIIEGDEILFAA	60
g047	MVIIQARRGGLLVGRSIADIAQDLDPGADCQICAVYRNNRLIVPAPQTVIIIEGDEILFAA	60
m047.pep	AAENIGAVIPELRPKETQRNQXXIMIXGGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI	120
g047	AAENIGAVIPELRPKETSTR--IMIAGGGNICYRLAKQLEHAYNVKIIIECRPRRAEWI	117
m047.pep	AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV	180
g047	AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV	177
m047.pep	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK	240
g047	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK	237
m047.pep	TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRRILNEL	300
g047	TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRRILNEL	297
m047.pep	EKLIQVKMGFFGX 313	
g047	EKLIQVKMGFFGX 310	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 199>:

g048.seq

```

1   ATGCTCGACA AAGGCGAGGA GTTGCCCGTC GATTTCACCA ACCGCCTGAT
51  TTACTACGTc ggcCCcgTCG ATCCGGTCCG CGATGAAGTC GTCGGTCCCG
101 CAGGTCCGAC CACAGCCACC CGCATGGACA AATTTACCCG CCAAATGCTC
151 AAACAAACCG GCCTCTTGGG CATGATCGGC AAATCCGagc gcgGcgcggc
201 cacctGCGAA GCcatCGCCG ACAACAAGGC CGTGTACCTC ATGGCAGTCG
251 GCGGCGCGGC ATACCTCGTG GCAAAAAGCCA TCAAATCTTC CAAAGTCTTG
301 GCGTTCCCCG AATTGGGTAT GGAAGCCGTT TACGAATTG AAGTCAAAGA
351 TATGCCCGTA ACCGTCGCCG TGGACAGCAA AGGCGAATCC ATCCACGCCA
401 CCGCCCCGCG CAAATGGCAG GCGAAAATCG GCATCATCCC CGTCGAGTCT
451 TGA

```

This corresponds to the amino acid sequence <SEQ ID 200; ORF 048.ng>:

g048.pep

```

1   MLDKGEELPV DFTNRLIYYV GPVDPVGDEV VGPAGPTTAT RMDKFTRQML
51  KQTGLGMIG KSERGAATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 AFPELGMEAV YEFEVKMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 201>:

m048.seq

```

1   ATGCTCAACA AAGGCGAAGA ATTGCCCGTC GATTTCACCA ACCGCCTGAT
51  TTACTACGTC GGCCCCGTCG ATCCGGTCCG CGATGAAGTC GTCGGTCCCG

```

```
m048.pep
  1  MLNKGELPV DFTNRLIYYV GPVDPVGDEV VGPAGPTTAT RMDKFTRQML
51  EQTDLLGMIG KSERGVATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 AFPELGMEAI YFEVVKDMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151 *
```

```
a048.seq
1  ATGCTCGACA AAGGCGAAGA ATTGCCCGTC GATTTCACCA ACCGCTTGAT
51  TTTACTACGTC GGCCCCCGTCG ATCCGGTCCGG CGACGAAATC GTCGGCCCCAG
101 CAGGTCCTGAC CACCGCCACC CGCATGGACA AATTCAACCG CCAAATGCTC
151 GAACAAACCG ACCTCTTGGG CATGATCGGC AAATCCGAGC CGGGCGCGCG
201 CACCTGCGAA GCCATCGCCG ACAACAAAGC CGTGTACCTC ATGGCAGTCG
251 GCGGCGCGCG GTATCTCGTG GCAAAGCCA TCAAATCTTC CAAAGTCTTG
301 GCGTTCCCGG AATTGGGCAT GGAAGCCATT TACGAATTTC AAGTCAAAGA
351 CATGCCCGTA ACCGTCGCGG TAGACAGCAA AGGCGAATCC ATCCACGCCA
401 CCGCCCCGCC CCAATGGCAG GCGAAAATCG GCATCATCCC CGTCAAATCT
451 TGA
```

```
a048.pep
1  MLDKGEELPV DFTNRLIYYV GPVDPVGDEI VGPAGPTTAT RMDKFTRQML
51  EQTDLLGMIG KSERGAATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 APFELGMEAI YEFEVKDMPV TVAVDSKGES IHATAPPQWQ AKIGIIPVKS
151 *
```

	10	20	30	40	50	60
m048.pep	MLNKGEELPVDF	TNRLIYYVGP	VPDVPVGDE	VVGPA	PTTATAT	MDKFTRQMLEQTDL
	:					
a048	MLDKGEELPVDF	TNRLIYYVGP	VPDVPVGDE	VVGPA	PTTATAT	MDKFTRQMLEQTDL
	10	20	30	40	50	60
	70	80	90	100	110	120
m048.pep	KSERGVATCEAI	ADNKAVYLM	AVGGAAYLV	AKAIKSSK	VLAFPELG	MEAIYEF
	:					
a048	KSERGAATCEAI	ADNKAVYLM	AVGGAAYLV	AKAIKSSK	VLAFPELG	MEAIYEF
	70	80	90	100	110	120
	130	140	150			
m048.pep	TVAVDSKGESI	HATAPRKWQ	AKIGIIP	VESX		
	:					
a048	TVAVDSKGESI	HATAPPQWQ	AKIGIIP	VKSX		
	130	140	150			

ORF 048 shows 96.4% identity over a 150 aa overlap with a predicted ORF (ORF 048.ng) from *N. gonorrhoeae*:

250

m048/g048

	10	20	30	40	50	60
m048.pep	MLNKGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTRQMLEQTDLLGMIG					
	:					
g048	MLDKGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTRQMLKQTGLLGMIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m048.pep	KSERGVATCEAIADNKAVYLMVGGAAAYLVAKAIKSSKVLAFPELGMEAIYEFVVKDMPV					
	:					
g048	KSERGAATCEAIADNKAVYLMVGGAAAYLVAKAIKSSKVLAFPELGMEAVYEFVVKDMPV					
	70	80	90	100	110	120
	130	140	150			
m048.pep	TVAVDSKGESIHATAPRKWQAKIGIIPVESX					
g048	TVAVDSKGESIHATAPRKWQAKIGIIPVESX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 205>:

g049.seq

```

1   ATGCGGGCGC AGGCGTTTGA TCAACCGTTC GGTCAGCTCC TGTTCCGACA
51  GGCAGAACAC TTCGCGCCGG TTGACGGCTT TCGGGTTCAG GATATTGATT
101 TGGACGGGCA TCAACGCCTC TTCCGCACCG CCTTCGCCGT TTTCCGCAAC
151 CCCGTCTGCC GCCGTACCGG ATTCTGCCGC ATCGGCGTTT TCCCGCCCT
201 CAATCTGTGC GGTTCAAAT TCGGCACTGT CTTTTTTGGC ATCGAACCGG
251 ATTCTCCGCC GCGATTCGAT GTGTTTTTCC GAAAccggca tTTGCAGGGA
301 AGCCTgcgcg TTGAGCCAGT TTTCTGAAG GACGATCATC GGGTCGGTTT
351 CGACTTCCTC GCCGCAATCG GCAACGGCgc tGTTGTGTTC TTCCTGCCAT
401 TTCTTCAGAT ACGCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 206; ORF 049.ng>:

g049.pep

```

1   MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ DIDLDGHQRL FRTAFVAVFRN
51  PVCRRTGFCR IGVFPALNLC GFKFGTVFFG IEPDSPPRFD VFFRNRHLQG
101 SLRVEPVFLK DDHRVGFDL AAIGNGAVVF FLPFQIRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 207>:

m049.seq (partial)

```

1   ATGCGGGCGC AGGCGTTTGA TCAGCCGTTC GGTCAGCTCC TGTTCCGACA
51  GGCAGAACAC TTCGCGCCGG TTGACGGCTT TCGGGTTCAG GATATTGATT
101 TGGACGGGCA TCAACGTTTC TTCCGCATCG TTTTCCCGGT TTTCCGAAAC
151 CGCCGGCTCA TTCGTGCCGG ATTCTGCCTC GTCGGCGTTT TCCCGCTTT
201 CAATCTGTCC GGTTCAAAT TCGACACTGT CTTTTTTGGT ATCAAACCGG
251 ATTCTCCGCC GCGATTCGAT GTGTTTTTCC GAAACCGACA TTTGCAGGGA
301 AGCCTGCGCG TTGAGCCAGT TTTCTGAAG GACGATCATC GGGTCGGTTT
351 CGACTTCCTC GCCGCAATCG GCAACGGCGG CATTGTGTTC CTCCTGCCAT
401 TTTTTCAGAT ACGCCTT...

```

This corresponds to the amino acid sequence <SEQ ID 208; ORF 049>:

m049.pep (partial)

```

1   MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ DIDLDGHQRF FRIVFPVFRN
51  RRLIRAGFCL VGVFPFNLS GFKFDTVFFG IKPDSPPRFD VFFRNRHLQG
101 SLRVEPVFLK DDHRVGFDL AAIGNGGIVF LLPFFQIRL...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 209>:

a049.seq

251

```

1   ATGCGGGCGC AGGCGTTTGA TCAGCCGTTT GGTGAGCTCC TGTTCCGACA
51  GGCAGAACAC TTCGCGCCGG TTGACGGCTT TCGGGTTCAG AATATTGATT
101 TGGACGGGCA TCAACGCTTC TTCCGCACCG CCTTCGCCGT TTTCCGCAAC
151 CCCGTCTGCC GCCGTACCCG ATTCTGCCGC ATCGGCGTTT TCCCCGCCTT
201 CAATCTGTCC GGTTTCAAAT TCGGCACTGT CTTTTTTGGC ATCAAACCGG
251 ATTCTCCGCC GCGATTGAT GTGTTTTTCC GAAACCGACA TTTGCAGGGA
301 AGCCTGCGCG TTGAGCCAGT TTTCTGAAG GACGATCATC GGGTCGGTTT
351 CGACTTCCTC GCCGCAATCG GCAACGGCGG CATTGTGTTC CTCCTGCCAT
401 TTTTTCAGAT ACGCCTT

```

This corresponds to the amino acid sequence <SEQ ID 210; ORF 049.a>:

```

a049.pep
1   MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ NIDLDGHQRF FRTAFAVERN
51  PVCRRTRFCR IGVFFAFNLS GFKFGTVFFG IKPDSPPRFD VFFRNRHLQG
101 SLRVEPVFLK DDHRVGFDL AAIGNGGIVF LLPFFQIRL

```

m049/a049 90.6% identity over a 139 aa overlap

```

              10      20      30      40      50      60
m049.pep      MRAQAFDQPFQQLLFGQAEHFAPVDGFRVQDIDLDGHQRFRRIVFPVFRNRRLIRAGFCL
              |||||:|||||:|||||:|||||:|||||:|||||
a049           MRAQAFDQPFQQLLFGQAEHFAPVDGFRVQDIDLDGHQRFRTAFAVERNPVCRTRFCR
              10      20      30      40      50      60

              70      80      90     100     110     120
m049.pep      VGVFFAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRHLQGSRLRVEPVFLKDDHRVGFDL
              :|||||:|||||:|||||:|||||:|||||:|||||
a049           IGVFFAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRHLQGSRLRVEPVFLKDDHRVGFDL
              70      80      90     100     110     120

              130     139
m049.pep      AAIGNGGIVFLLPFFQIRL
              |||||:|||||
a049           AAIGNGGIVFLLPFFQIRL
              130

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 049 shows 86.3% identity over a 139 aa overlap with a predicted ORF (ORF 049.ng) from *N. gonorrhoeae*:

```

m049/g049
              10      20      30      40      50      60
m049.pep      MRAQAFDQPFQQLLFGQAEHFAPVDGFRVQDIDLDGHQRFRRIVFPVFRNRRLIRAGFCL
              |||||:|||||:|||||:|||||:|||||:|||||
g049           MRAQAFDQPFQQLLFGQAEHFAPVDGFRVQDIDLDGHQRLFRRTAFAVERNPVCRRTGFCR
              10      20      30      40      50      60

              70      80      90     100     110     120
m049.pep      VGVFFAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRHLQGSRLRVEPVFLKDDHRVGFDL
              :|||||:|||||:|||||:|||||:|||||:|||||
g049           IGVFFAFNLSGFKFDTVFFGIEPDSPPRFDVFFRNRHLQGSRLRVEPVFLKDDHRVGFDL
              70      80      90     100     110     120

              130     139
m049.pep      AAIGNGGIVFLLPFFQIRL
              |||||:|||||
g049           AAIGNGAVVFFLPFLQIRLX
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 211>:

```
g050.seq
  1 atgggCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGG
 51 cagccccGAA AAAGccgtgt TGATGGcaaa AGAATCCCTG ATGAGCCACA
101 TCGAcatCca aGaATTGCAG GAAAAGCCG CGTccggggc ggaattgtcc
151 accaccgaAG ccCTGCGCCT cGAACTCTTT GAAAAGGTCA ACGCGCTGGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAT GCCGCCTCCA AACCGATTGC CATGATTCCC
301 AACTGTGCcg ccacCCGcca cgtcgAATTT GAATTGgACG GCTCAGGtcc
351 TGTCGAactc acgccGCcgc gtgtCGAAGA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 212; ORF 050.ng>:

```
g050.pep
  1 MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
 51 TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVED*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 213>:

```
m050.seq
  1 ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGTATCG GCATCGGCGG
 51 C..agCCgAA AAAGCCGTGC TGATGGCAAA AGAGTCCCTG ATGAGCCACA
101 TCGACATTCA AGAATTGCAG GAAAAGCCG CGTCCGGCGC GgAATTGTCC
151 ACCACCGAAG CCCTGCGCCT CGAACTCTTT GAAAAGTCA ACGCGCTGGG
201 CATCGGCGCA CAAGGCTTGG GCGGACTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA TCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCCC
351 TGTCGAACTC ACGCCGCCGC GCGTCGAAGA TGGCCCATT TGA
```

This corresponds to the amino acid sequence <SEQ ID 214; ORF 050>:

```
m050.pep
  1 MGAGWCPPGI LGIGIGGXAE KAVLMAKESL MSHIDIQELQ EKAASGAELS
 51 TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDGPI *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 215>:

```
a050.seq
  1 ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGG
 51 TACGCCGAA AAAGCCGTGT TGATGGCGAA AGAATCCCTG ATGAGCCACA
101 TCGACATCCA AGAATTGCAG GAAAAGCCG CGTCCGGCGC GGAATTGTCC
151 ACCACCGAAG CCCTGCGCCT CGAACTCTTT GAAAAGTCA ACGCGCTAGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCCC
351 TGTCGAACTC ACGCCGCCGC GCGTCGAAGA CTGGCCC
```

This corresponds to the amino acid sequence <SEQ ID 216; ORF 050.a>:

```
a050.pep
  1 MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
 51 TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDWP
```

m050/a050 97.7% identity over a 129 aa overlap

```

          10      20      30      40      50      60
m050.pep  MGAGWCPPGILGIGIGGXAEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF
          |||||
a050      MGAGWCPPGILGIGIGGTPEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF
```


253

	10	20	30	40	50	60
	70	80	90	100	110	120
m050.pep	EKVNALGIGAQGLGGLTTVLDVKILDYPHTHAASKPIAMIPNCAATRHVEFELDGS GPVEL					
a050	EKVNALGIGAQGLGGLTTVLDVKILDYPHTHAASKPIAMIPNCAATRHVEFELDGS GPVEL					
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
a050	TPPRVEDWP					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 050 shows 98.4% identity over a 127 aa overlap with a predicted ORF (ORF 050.ng) from *N. gonorrhoeae*:

m050/g050

	10	20	30	40	50	60
m050.pep	MGAGWCPPGILGIGIGGXAEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF					
g050	MGAGWCPPGILGIGIGGTPEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m050.pep	EKVNALGIGAQGLGGLTTVLDVKILDYPHTHAASKPIAMIPNCAATRHVEFELDGS GPVEL					
g050	EKVNALGIGAQGLGGLTTVLDVKILDYPHTHAASKPIAMIPNCAATRHVEFELDGS GPVEL					
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
g050	TPPRVEDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 217>:

g050-1.seq

```

1  ATGACCGTTA TCAAGCAAGA AGACTTTATT CAAAGTATCT GCGATGCCTT
51  CCAATTCATC AGCTACTACC ATCCAAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AATCCCGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGTAT GTGTGCCGAA AACAACCGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCCTCAA AGTCGGTATG GATGTGCAAT
251 GGGATGCGGA CATGAGCGTG GAAAAGATGG TTAACGAAGG CGTACGCCGC
301 GCCTACACTT GGGAAGGCAA CACCCTGCGC GCTTCCTCC TCGCCGATCC
351 GGCCGCAAAA CGCCAAAACA CCAAAGACAA CACCCCGGCC GTCATCCACA
401 TGAGCATCGT GCCGGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GGCGGCTCTG AAAACAATC CAAACTCGCT ATGCTCAACC CTTCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATCCC GACGATGGGC GCGGGCTGGT
551 GTCCTCCCGG CATCTGGGCG ATCGGCATCG GCGGCACgC CGAAAAAGCC
601 GTGTTGATGG cgaAAGAATC CCTGATGAGC CACATCGACA TCCAAGAATT
651 GCAGGAAAAA GCCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTTGAAGAAG GTCAACGCGC TGGGCATCGG CGCGCAAGGC
751 TTGGGCGGTC TGACCACCGT GTTGGACGTG AAAATCCTCG ATTACCCGAC
801 CCATGCCGCG TCCAAACCGA TTGCCATGAT TCCCAACTGT GCCGCCACCC
851 GCCACGTCGA ATTTGAATTG GACGGCTCAG GTCCTGTCGA ACTCACGCCG
901 CCGCGCGTCG AAGACTGACC CGATCTGACT TACAGCCCCG ACAACGGCAA
951 ACGGTCGAT GTCGATAAGC TGACCAAAGA AGAAGTGGA AGCTGGAAAA
1001 CCGCGACGAT ATTGCTGTTG AACGGCAAAA TCCTCACC GGCGCATGCC
1051 GCGCACAAAC GCCTCGTCAA TATGCTCGAC AAAGCGGAGG AGTTGCCCGT
1101 CGATTTACAC AACCCGCTGA TTTACTACGT CGGCCCGGTC GATCCGGTCG
1151 CCGATGAAGT CGTCGGTCCC GCAGGTCCGA CCACAGCCAC CCGCATGGAC
1201 AAATTTACCC GCCAAATGCT CAAACAAACC GGCCTCTTGG GCATGATCGG

```

```

1251 CAAATCCGAG CGCGGCGCGG CCACCTGCGA AGCCATCGCC GACAACAAGG
1301 CCGTGACCT CATGGCAGTC GGCGGCGCGG CACACCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GGCGTTCCCC GAATGGGTA TGGGAAGCCGT
1401 TTACGAATTT GAAGTCAAAG ATATGCCCCG AACCGTCGCC GTGGACAGCA
1451 AAGGCGAATC CATCCACGCC ACCGCCCGC GCAAATGGCA GGCGAAAATC
1501 GGCATCATCC CCGTCGAGTC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 218; ORF 050-1.ng>:

g050-1.pep

```

1  MTVIKQEDFI QSIDAFQFI SYHPKDYID ALYKAWQKEE NPAAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVM DVQWDADMSV EKMVNEGVRR
101 AYTWEENTLR ASVLADPAGK RQNTKDNTPA VIHMSIVPGG KVEVTCAAKG
151 GGSSENKSLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMAKESLMS HIDIQELQEK AASGAELSTT EALRLELFEK VNALGIGAQG
251 LGLLTTVLVDV KILDYPTTHA SKPIAMIPNC AATRHVEFEL DSGGPVELTP
301 PRVED*PDLT YSPDNCKRVD VDKLTKEEVA SWKTGDVLLL NGKILTGRDA
351 AHKRLVNMLD KGEELPVDFE NRIYYVGPV DPGDEVVGP AGPTTATRMD
401 KFTROMLKQT GLLGMIGKSE RGAATCEAIA DNKAVYLMVA GGAAYLVAKA
451 IKSSKVLAFP ELGMEAVYEF EVKDMPVTVA VDSKGESIHA TAPRKWQAKI
501 GIIPVES*

```

g050-1/p14407

```

sp|P14407|FUMB_ECOLI FUMARATE HYDRATASE CLASS I, ANAEROBIC (FUMARASE)
>gi|280063|pir||B44511 fumarate hydratase (EC 4.2.1.2) fumB, iron-dependent - Escherichia coli
>gi|146048 (M27058) anaerobic class I fumarase (EC 4.2.1.2) [Escherichia coli] Length = 548
Score = 172 bits (432), Expect = 4e-42
Identities = 138/488 (28%), Positives = 216/488 (43%), Gaps = 22/488 (4%)

```

```

Query: 11 QSIDAFQFISYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAENNRPICQDTG 70
      Q+ DA + H K L+ E + K Q L NS + A+ P CQDTG
Sbjct: 53 QAFHDASFMLRPAHQKQVAAIILHDEPEASEND---KYVALQFLRNSEIAAKGVLPCTCQDTG 109

```

```

Query: 71 IATVFLKVMQDVQWDADMSVEKMVNEGVRRAYTWEENTLRASVLADPAGKRQNTKDNTPA 130
      A + K G V W E+ +++GV Y E N + A K NT N PA
Sbjct: 110 TAIIVGKKGQVRV-WTGGGD-EETLSKGVNTYI-EDNLRYSQNAALDMYKEVNTGTNLPA 166

```

```

Query: 131 VIHMSIVPGGKVEVTCAAKGGGSENKSKL-----AMLNPSDNIVDWVLKTIPTMGAGWCP 185
      I + V G + + C AKGGGS NK+ L A+L P + +++++ + T+G CP
Sbjct: 167 QIDLYAVDGDYKFLCVAKGGGSANKTYLYQETKALLTPG-KLKNFLVEKMRTLGTAAACP 225

```

```

Query: 186 PXXXXXXXXXTPEKAVLMAKESLSHIDIQELQEKAAASGAELSTTEALRLELFEKVNXXX 245
      P T + L + +H EL + + L EL E+
Sbjct: 226 PYHIAFVIGGTSATNLKTVKLASAHY-YDELPTGEGNEHQAFRDVQLEQELLEEAQKLG 284

```

```

Query: 246 XXXXXXXXXXXTVLDVKILDYPTTHAASKPIAMIPNCAATRHVEFELDGSG----PVELTPP 301
      D++++ P H AS P+ M +C+A R+++ +++ G +E P
Sbjct: 285 LGAQFGGKYFAH-DIRVIRLPRHGASCPVGMGVSADRNIAKINREGIWIEKLEHNPG 343

```

```

Query: 302 RVEDXPDLTYSPDNCKRVDVDKLTKE---EVASWKTGDVLLNGKILTGRDAAHKRLVNM 358
      + +VD+++ KE +++ + L L G I+ GRD AH +L +
Sbjct: 344 QYIPQELRQAGEGEAVKVDLNRPMKEILAQLSQYPVSTRLSLTGTIIVGRDIAHAKLKL 403

```

```

Query: 359 LDKGEELPVDFE NRIYYXXXXXXXXXXXXXXXXXXXXTTATRMDKFTROMLKQTGLLGMIGK 418
      +D G+ELP + IYY TTA RMD + + G + M+ K
Sbjct: 404 IDAGKELPQYIKDHPYIYAGPAKTPAGYPSGSLGPTTAGRMDSYVDLLQSHGGSMIMLAK 463

```

```

Query: 419 SERGAATCEAIADNKAVYLMVAVGG-AAYLVAKAIKSSKVLAFPPELGMEAVYEFVVDMPV 477
      R +A + YL ++GG AA L ++IK + +A+PELGMEA+++ EV+D P
Sbjct: 464 GNRSQQVTDACHKHGGFYLGSI GGPAVLAQOSIKHLECVAYPELGMEAIWKIEVEDFPA 523

```

```

Query: 478 TVAVDSKG 485
      + VD KG
Sbjct: 524 FILVDDKG 531

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 219>:

m050-1.seq

```

1  ATGACCGTCA TCAAACAGGA AGACTTTATC CAAAGCATTT GCGATGCCTT
51  CCAATTCATC AGCTACTATC ATCCCAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGGTGGCA GAAGGAAGAA AATCCTGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGTAT GTGTGCGGAA AACAACCGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCCTCAA AGTCGGTATG AACGTCCAAT
251 GGGATGCGGA CATGAGCGTG GAAGAGATGG TTAACGAAGG CGTACGCCGC

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301 GCCTACACTT GGAAGGCAA TACGCTGCGC GCTTCCGTCC TCGCCGATCC
351 GGCCGGGCAA CGCCAAAACA CCAAAGACAA CACCCCGGCC GTCATCCATA
401 TGAGCATCGT GCCGGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GGCGGCTCTG AAAACAAATC CAAACTCGCC ATGCTCAATC CTTCGGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATCCC GACCATGGGC GCGGGCTGGT
551 GTCCCTCCGG CATCTTGGGT ATCGGCATCG GCGGCACGCC CGAAAAAGCC
601 GTGCTGATGG CAAAGAGTC CCTGATGAGC CACATCGACA TTCAAGAATT
651 GCAGGAAAAG GCCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTTGAAAA GTCAACGCGC TGGGCATCG CGCACAAGGC
751 TTGGGCGGAC TGACCACCGT GTTGACGTG AAAATCCTCG ATTATCCGAC
801 CCACGCCGCC TCCAAACCGA TTGCCATGAT TCCGAAGTGC GCCGCCACCC
851 GCCACGTGCA ATTTGAATTG GACGGCTCAG GCCCTGTCGA ACTCAGCCCG
901 CCGCGCGTCG AAGACTGGCC CGATTTGACT TACAGCCCGC ACAACGGCAA
951 ACGCGTCGAT GTCGACAAGC TGACCAAAGA AGAAGTGGCA AGCTGAAAAA
1001 CCGGCGACGT ATTGCTGTTG AACGGCAAAA TCCTCACCAG CCGCGATGCC
1051 GCACACAAAC GCCTCGTCGA TATGCTCAAC AAAGGCGAAG AATTGCCCGT
1101 CGATTTCAAC AACCGCCTGA TTTACTACGT CGGCCCCGTC GATCCGGTCG
1151 GCGATGAAGT CGTCGGTCCG GCAGGTCCGA CCACAGCCAC CCGCATGGAC
1201 AAATTCACCC GCCAAATGCT CGAACAACCC GACCTCTTGG GCATGATCGG
1251 CAAATCCGAG CGCGGCGTGG CCACCTGCGA AGCCATCGCC GACAACAAAG
1301 CCGTGTACCT CATGGCAGTC GCGGCGCGCG CGTATCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GCGGTTCCCC GAATTGGGCA TGGGAAGCCAT
1401 TTACGAATTT GAAGTCAAAG ACATGCCCGT AACCGTCGCC GTAGATAGCA
1451 AAGGCGAATC CATCCACGCC ACCGCCCCGC GCAAATGGCA GCGGAAAATC
1501 GGCATCATCC CCGTCGAATC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 220; ORF 050-1>:

m050-1.pep

```

1  MTVIKQEDFI QSIDAFQFI SYHHPKDYID ALYKAWQKEE NPAAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVM NVQWDADMSV EEMVNEGVRR
101 AYTWEANTLR ASVLADPAGK RQNTKDNTPA VIHMSIVPGG KVEVTCAAKG
151 GGSENKSKLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMAKESLMS HIDIQELQEK AASGAELSTT EALRLELF EK VNALGIGAQG
251 LGGLTTVLDV KILDYPTHA SKPIAMIPNC AATRHVEFEL DGSGPVELTP
301 PRVEDWPDLT YSPDNGKRVD VDKLTKEEVA SWKTGDVLLL NGKILTRDA
351 AHKRLVDMLN KGEELPVDFE NRIIYVGPV DPGVDEVVGP AGPTTATRMD
401 KFTRQMLEQT DLLGMIGKSE RGVATCEAIA DNKAVYLMV GGAAYLVAKA
451 IKSSKVLAFP ELGMEAIYEF EVKDMPTVTA VDSKGESIHA TAPRKWQAKI
501 GIIPVES*

```

m050-1/g050-1 98.2% identity in 507 aa overlap

	10	20	30	40	50	60
m050-1.pep	MTVIKQEDFIQSIDAFQFISYHHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
g050-1	MTVIKQEDFIQSIDAFQFISYHHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m050-1.pep	NNRPICQDTGIATVFLKVMNVQWDADMSVEEMVNEGVRRAYTWEGNTLRASVLADPAGK					
g050-1	NNRPICQDTGIATVFLKVMNVQWDADMSVEEMVNEGVRRAYTWEGNTLRASVLADPAGK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m050-1.pep	RQNTKDNTPAVIHMSIVPGGKVEVTCAAKGGSENKSKLAMLNPSDNIVDWVLKTIPTMG					
g050-1	RQNTKDNTPAVIHMSIVPGGKVEVTCAAKGGSENKSKLAMLNPSDNIVDWVLKTIPTMG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m050-1.pep	AGWCPPGILGIGIGGTPEKAVLMAKESLSHIDIQELQEKAAASGAELSTTEALRLELF EK					
g050-1	AGWCPPGILGIGIGGTPEKAVLMAKESLSHIDIQELQEKAAASGAELSTTEALRLELF EK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m050-1.pep	VNALGIGAQGLGGLTTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPVELTP					
g050-1	VNALGIGAQGLGGLTTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPVELTP					
	250	260	270	280	290	300

256

	310	320	330	340	350	360
m050-1.pep	PRVEDWPDLT	YSPDNGKRVD	VDKLTKEEVASWKT	GDVLLNGKILT	GRDAAHKRL	VDMLN
g050-1	PRVEDXPDLT	YSPDNGKRVD	VDKLTKEEVASWKT	GDVLLNGKILT	GRDAAHKRL	VNMLD
	310	320	330	340	350	360
	370	380	390	400	410	420
m050-1.pep	KGEELPVDF	TNRLIYYVGP	VPVGVGDEV	VPAGPTTAT	RMDFTRQMLE	QTDLLGMIGKSE
g050-1	KGEELPVDF	TNRLIYYVGP	VPVGVGDEV	VPAGPTTAT	RMDFTRQMLE	KQTGLGMIGKSE
	370	380	390	400	410	420
	430	440	450	460	470	480
m050-1.pep	RGVATCEA	IADNKAVYLM	AVGGAAAYL	VAKAIKSSK	VLAFPELGME	AIYEFVVKDMPVTVA
g050-1	RGAATCEA	IADNKAVYLM	AVGGAAAYL	VAKAIKSSK	VLAFPELGME	AVYEFVVKDMPVTVA
	430	440	450	460	470	480
	490	500				
m050-1.pep	VDSKGESI	HATAPRKWQ	AKIGIIPVESX			
g050-1	VDSKGESI	HATAPRKWQ	AKIGIIPVESX			
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 221>:

a050-1.seq

1	ATGACCGTCA	TCAAACAGGA	AGACTTTATC	CAAAGCATTT	GCGATGCCTT
51	CCAATTTCATC	AGCTACTACC	ATCCCAAAGA	CTACATCGAC	GCGCTTTATA
101	AGGCGTGGCA	GAAGGAAGAA	AACCCCGCCG	CCAAAGACGC	GATGACGCAG
151	ATTTTGGTCA	ACAGCCGCAT	GTGTGCCGAA	AACAACCGCC	CCATCTGCCA
201	AGATACCGGT	ATCGCGACCG	TGTTTTTGAA	AGTCGGTATG	GATGTGCAAT
251	GGGATGCAGA	CATGAGCGTC	GAAGAGATGG	TTAACGAAGG	CGTGCGCCGC
301	GCCTACACTT	GGGAAGGCAA	TACGCTGCGC	GCTTCCGTTT	TCGCCGACCC
351	CGCCGGCAAA	CGCCAAAATA	CCAAAGACAA	CACGCCGCC	GTCATCCATA
401	TGAGCATCGT	GCCGGGCGAC	AAAGTCGAAG	TAACCTGCGC	GGCAAAAGGC
451	GGCGGTTCTG	AAAACAAATC	CAAACCTGCC	ATGCTCAACC	CTTCCGACAA
501	CATCGTTCAT	TGGGTATTGA	AAACCATTC	GACCATGGGC	GCGGGCTGGT
551	TCCTCCCGG	CATCTTGGGC	ATCGGCATCG	GCGGTACGCC	CGAAAAAGCC
601	GTGTTGATGG	CGAAAGAAATC	CCTGATGAGC	CACATCGACA	TCCAAGAATT
651	GCAGGAAAAA	GCCGCGTCCG	GCGCGGAATT	GTCCACCACC	GAAGCCCTGC
701	GCCTCGAACT	CTTTGAAAAA	GTCAACGCGC	TAGGCATCGG	CGCGCAAGGC
751	TTGGGCGGTC	TGACCACCGT	GTGGACGTG	AAAATCCTCG	ATTACCCGAC
801	CCACGCGGCC	TCCAAACCGA	TTGCCATGAT	TCCGAACTGC	GCCGCCACCC
851	GCCACGTCTG	ATTGAATTG	GACGGCTCAG	GCCCTGTCTG	ACTCACGCCG
901	CCGCGCGTCG	AAGACTGGCC	CGATTTGACT	TACAGCCCCG	ACAACGGCAA
951	ACGCGTCGAT	GTCGACAAGC	TGACCAAGA	AGAAGTGGCA	AGCTGGAAAA
1001	CCGCGGACGT	ATTGCTGTTG	AACGGCAAAA	TCCTACCCGG	CCGCGATGCC
1051	GCACACAAAC	GCCTCGTCGA	TATGCTCGAC	AAAGGCGAAG	AATTGCCCGT
1101	CGATTTCACC	AACCGCCTGA	TTACTACGT	CGGCCCCGTC	GATCCGGTCG
1151	GCGACGAAAT	CGTCGGCCCA	GCAGGTCGGA	CCACCGCCAC	CCGCATGGAC
1201	AAATTACCCC	GCCAAATGCT	CGAACAACCC	GACCTCTTGG	GCATGATCGG
1251	CAATCCGAG	CGCGGCGCGG	CCACCTGCGA	AGCCATCGCC	GACAACAAAG
1301	CCGTGTACCT	CATGGCAGTC	GGCGGCGCGG	CGTATCTCGT	GGCAAAAGCC
1351	ATCAAATCTT	CCAAAGTCTT	GGCGTTCCCC	GAATTGGGCA	TGGAAGCCAT
1401	TTACGAATTT	GAAGTCAAAG	ACATGCCCGT	AACCGTCGCC	GTAGACAGCA
1451	AAGGCGAATC	CATCCACGCC	ACCGCCCCGC	CCCAATGGCA	GGCGAAAATC
1501	GGCATCATCC	CCGTCAAATC	TTGA		

This corresponds to the amino acid sequence <SEQ ID 222; ORF 050-1.a>:

a050-1.pep

1	MTVIKQEDFI	QSICDAFQFI	SYHHPKDYID	ALYKAWQKEE	NPAAKDAMTQ
51	ILVNSRMCAE	NNRPICQDTG	IATVFLKVGM	DVQWDADMSV	EEMVNEGVR
101	AYTWEGNTLR	ASVLADPAGK	RQNTKDNTFA	VIHMSIVPGD	KVEVTCAAKG
151	GSSENKSKLA	MLNPSDNIVD	WVLKTIPTMG	AGWCPPGILG	IGIGGTPEKA
201	VLMAKESLMS	HIDIQELQEK	AASGAELSTT	EALRLELFKE	VNALGIGAOG
251	LGLLTTLVDV	KILDYPHTAA	SKPIAMIPNC	AATRHVEFEL	DGSGPVELTP
301	PRVEDWPDLT	YSPDNGKRVD	VDKLTKEEVA	SWKTGDVLLL	NGKILTGRDA
351	AKRLVDMLD	KGEELPVDF	TNRLIYYVGP	VPVGVGDEV	VPAGPTTAT
401	KFTRQMLEQT	DLGMIGKSE	RGAATCEAIA	DNKAVYLM	AVGGAAAYL
451	IKSSKVLAF	PELGMEAIYEF	EVKDMPTVA	VDSKGESIHA	TAPPQWQAKI
501	GIIPVKS*				

a050-1/m050-1 98.4% identity in 507 aa overlap

	10	20	30	40	50	60
a050-1.pep	MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAKDAMTQILVNSRMCAE					
m050-1	MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAKDAMTQILVNSRMCAE					
	10	20	30	40	50	60
a050-1.pep	70	80	90	100	110	120
m050-1	NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAYTWEGNLRASVLADPAGK					
	70	80	90	100	110	120
a050-1.pep	130	140	150	160	170	180
m050-1	RQNTKDNTPAVIHMSIVPGDKVEVTC AAKGGGSENKSKLAMLNPSDNIVDWVLKTIPTMG					
	130	140	150	160	170	180
a050-1.pep	190	200	210	220	230	240
m050-1	AGWCPPGILGIGIGGTPEKAVLMAKESLSHIDIQELQEKAASGAELSTTEALRLELFEK					
	190	200	210	220	230	240
a050-1.pep	250	260	270	280	290	300
m050-1	VNALGIGAQGLGGLTTVLDVKILDYPHTAASKPIAMIPNCAATRHVEFELDGS GPVELTP					
	250	260	270	280	290	300
a050-1.pep	310	320	330	340	350	360
m050-1	PRVEDWPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLD					
	310	320	330	340	350	360
a050-1.pep	370	380	390	400	410	420
m050-1	KGEELPVDFTNRLIYYVGPVDPVGDEIVGPAGPTTATRMDKFTRQMLEQTDLLGMIGKSE					
	370	380	390	400	410	420
a050-1.pep	430	440	450	460	470	480
m050-1	RGAATCEAIADNKAVYLMVGGAAAYLVAKAIKSSKVLAFPELGMEAIYEFV KDMPTVA					
	430	440	450	460	470	480
a050-1.pep	490	500				
m050-1	VDSKGESIHATAPPQWQAKIGIIPVKSX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 223>:

```

g052.seq
1  ATGGCTTTGG TGGCGGAGGA AACGAAATA TCCGCGCCGT GTTTCAAAGG
51  CTGCGAGCCG ACGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
151 AAGGGGTTGG ACGGCGTTTC CAAAAACAGC AGTTGGTGT TGGCTTTGAC
201 GGCGGCTTTC CATTCAATTA TATCAGTCGG CGACACGGG CTA CTCCGA
251 TGCCGAATTT GGTAAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA
351 CGCCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 224; ORF 052.ng>:

g052.pep

258

1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP
 51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN
 101 RLRLETTWSP ACRKVKNAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 225>:

m052.seq
 1 ATGGCTTTGG TGGCGGAGGA AACGGAATA TCCGCGCCGT GTTTCAAAGG
 51 CTGCGAGCCG ACGGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
 101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
 151 AAGGGGTTGG ACGGCGTTTC CAAAACAGC AGTTTGGTGT TGGCTTTGAC
 201 GGCGGCTTTC CATTCAATTA TATCAGTCGG CGACACGGG CTA CTCCGA
 251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
 301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA
 351 CGCCGCCTGA

This corresponds to the amino acid sequence <SEQ ID 226; ORF 052>:

m052.pep
 1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP
 51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN
 101 RLRLETTWSP ACRKVKNAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 227>:

a052.seq
 1 ATGGCTTTGG TCGCGGAGGA AACGGAATA TCCGCGCCGT GTTTCAAAGG
 51 CTGAGAGCCG ACAGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
 101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCTCCC
 151 AAGGGATTGG ACGGCGTTTC CAAAACAGC AGTTTGGTGT TGGCTTTGAC
 201 GGCGGCTTTC CATTGTTTA TATCAGTCGG CGACACGTGA CTA CTTCGA
 251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
 301 AGGCTGCGGC TGGAAATCAC ATGGTCGCCC GCCTGCAAAA AGGTGAAAAA
 351 CGCCGCCTGA

This corresponds to the amino acid sequence <SEQ ID 228; ORF 052.a>:

a052.pep
 1 MALVAEETEI SAPCFKG*EP TGDSRLLSTT KSAPMPCANS AKASKSATSP
 51 KGLDGVSKNS SLVLALTAAF HSFISVGD* LTSMPLVTM LLIKPTVVPN
 101 RLRLEITWSP ACKKVKNAA*

m052/a052 95.8% identity over a 119 aa overlap

	10	20	30	40	50	60
m052.pep	MALVAEETEISAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
a052	MALVAEETEISAPCFKGXEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m052.pep	SLVLALTA AFHSFISVGDTRLTPMPNLVTMLLIKPTVVPNRLRLETTWSPACRKVKNAAX					
a052	SLVLALTA AFHSFISVGDXTLTPMPNLVTMLLIKPTVVPNRLRLEITWSPACKKVKNAX					
	70	80	90	100	110	120

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 052 shows 95.8% identity over a 119 aa overlap with a predicted ORF (ORF 052.ng) from *N. gonorrhoeae*:

m052/g052

	10	20	30	40	50	60
m052.pep	MALVAEETEISAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					

259

```

g052      MALVAEETEISAPCFKGCEPTGDSRLLSTTKSAPMPCANSASAKASKSATSPKGLDGVSKNS
           10      20      30      40      50      60

           70      80      90      100     110     120
m052.pep  SLVLALTAAFHSFISVGDTWLTSMPLATMLLIKPTVVPNRLRLEITWSPACKVKVNAAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g052      SLVLALTAAFHSFISVGDTRLTPMPLVTMLLIKPTVVPNRLRLETTWSPACRKVKNAAX
           70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 229>:

```

g073.seq
1  ATGTGTATGC CATACGCAAT AAGGGTTTCA GACGGCATCT GCCGCATTTT
51  TCCGCCGATG CCGTCTGAAA CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101 AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151 AGTCCGGGGC GGatacCGGC GCGAGTTTTT TCTTCGGGCT GCATCCTGCC
201 GTGCGTGGTT GTCCACGGAT TGGTGATGGT CGAGCGCACG TCGCCGAGGT
251 TGGCGGTACG GGAAAAGAGT TCCACGACTT TCCACGCGGC TGCTTGGTCG
301 GCGACTTCAA AACCGATGAC GATGCCGCCG CCGTTTTGCT GTTTGCGGAT
351 AAGCTCCGCC TCGCGATGGT CGGGCAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 230; ORF 073.ng>:

```

g073.pep
1  MCMPYAIRVS DGICRIFPPM PSETRNQRAS ACFKSSIKSP TYSKPTDRRT
51  SPGRIPAASF SSGCILPCVV VHGLVMVERT SPRLAVREKS STTFHAAWS
101 ATSKPMTMPP PFCCLRISSA CGWSGNPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 231>:

```

m073.seq
1  ATGTGTATGC CATATAAGAT AAGGGTTTCA GACGGCATCT GCTGTCCAAT
51  GCCGTCTGAA ACACGCAATC AGCGTGCGAG TGCCTGTTTC AAATCGTCAA
101 TCAAATCGCC AACATATTCC AAACCGACCG ACAGGCGCAC CAATCCGGGG
151 CGGATGTTGG CCGCGAGTTT TTCTTCGGGC TGCATCCTGC CGTGCGTGGT
201 TGTCCACGGG TGGGTAATGG TCGAGCGCAC GTCACCGAGG TTGGCGGTGC
251 GGGAAAAGAG TTCCACGCCG TCCACAATT TCCACGCCGC TTCTTGATCG
301 GCAACTTCAA AGCCGATGAC GATGCCGCCG CCGTTTTGCT GTTTGCGGAT
351 AAGCGCCGCC TGAGGATGGT CGGACAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 232; ORF 073>:

```

m073.pep
1  MCMPYKIRVS DGICCPMPSE TRNQRASACF KSSIKSPTYS KPTDRRTNPG
51  RMLAASFSSG CILPCVVVHG WVMVERTSPR LAVREKSSTP STTFHAASXS
101 ATSKPMTMPP PFCCLRISAA XGWSNPNV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 233>:

```

a073.seq
1  ACGTGTATGT CATATAAGAT AAGGGTTTCA GACGGCATTT GCGGTGTTTT
51  TCCGCCGATG CCGTCTGAA. CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101 AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151 AATCCGGGGC GGATGTTGGC GCGAGTTTTT TCTTCGGGCT GCATCCTGCC
201 GTGCGTGGTT GTCCACGGAT GGGTAATGGT CGAGCGCACG TCGCCGAGGT
251 TGGCGGTACG GGAGAAAAGT TCGACGCCGT CCACGACTTT CCACGCGGCT
301 GCTTGGTCGG CCACTTCAA GCGGATGACG ATGCCGCCGC CGTTTTGCTG
351 TTTGCGGATA AGTCCGCCT GAGGATGGTC GGGTAATCCG GTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 234; ORF 073.a>:

```

a073.pep
1  TCMSYKIRVS DGICGVFPPM PSEXRNQRAS ACFKSSIKSP TYSKPTDRRT
51  NPGRMLAASF SSGCILPCVV VHGWVVERT SPRLAVREKS STPSTTFHAA
101 AWSATSKPMT MPPPFCLRI SSA*GWSGNP V*

```

m073/a073 92.3% identity over a 130 aa overlap

260

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICC---PMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
a073	TCMSYKIRVSDGICGVFPMPSEXRNQRASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVVHGWVVERTSPRLAVREKSSTPSTTFHAASXSATSKPMTMPPPFCLRI				
a073	SSGCILPCVVVHGWVVERTSPRLAVREKSSTPSTTFHAAAWSATSKPMTMPPPFCLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSNDPVX				
a073	SSAXGWSGNPVX				
		130			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 073 shows 87.0% identity over a 131 aa overlap with a predicted ORF (ORF 073.ng) from *N. gonorrhoeae*:

m073/g073

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICC---PMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
g073	MCMPIAIRVSDGICRIFPMPSETRNQRASACFKSSIKSPTYSKPTDRRTSPGRIPAAAF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVVHGWVVERTSPRLAVREKSSTPSTTFHAASXSATSKPMTMPPPFCLRI				
g073	SSGCILPCVVVHGLVMVERTSPRLAVREKSST---TFHAAAWSATSKPMTMPPPFCLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSNDPVX				
g073	SSACGWSGNPVX				
		120			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 235>:

g075.seq

```

1  ATGCCGCCTT ACTTCATCAC CCTCTTAACG ATGGAATA CAAAAAGCGC
51  GCGCAAAACG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CCGCTTCCAA AGCGTTTTTT GCCGTTTCGG GCAACGCTGC GTTTGCCTGT
151 GCCGCCAAAG CCAGCGGGGC GGCTGTTACA ACAGCCAGTT TTGCGCCGTA
201 TTTACGGCAG GTGTTAATAA ATTCATGAT ATTTTCCTTT ACGAAATTTT
251 TAAAAAATG TGTTCGCGG CTTTGTGAAG GTTTAGAGA CCGCTGCGG
301 GGCCTCTTAA ACTTAATCTT CTTTTCGTA GAATCCGAA ATTACAAATT
351 CCCCCTAT CTCTCCAAT GCCGAGCTAA AAGCGTCTT ATAGCTGTCA
401 TATTACCGG CTGA

```

This corresponds to the amino acid sequence <SEQ ID 236; ORF 075.ng>:

g075.pep

```

1  MPPYFITLLT MENTKSAKT PTTIQPASIP SAFAASKAFF AVSGNAAFAC
51  AAKASGAAVT TASFAPYLRQ VLINFMIFSF TKFLKKVCVG LCEGFRDLRP
101 GLLNLIFFFV ESENYKFPAY LFQCRKSVF IAVIFTG*

```


The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 237>:

```
m075.seq
  1 ATGCCGTCTT ACTTCATCAC TCTCTTAACG ATGGAAAATA CAAAAAGCGC
 51 GGCGAAAATG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CGGCTTCCAA AGCGTTTTTT GCCGTATCGG GCAACGTTGC ATTTGCATGT
151 GCGGCCAAAG CCAGGGGAGC AGCTGTTACA ACAGCCAGTT TTGCGCCGTA
201 TTTACGGCAG GTGTTAATAA ATTTTCATGAT ATTTTCCTTC AAAAAGTGTT
251 TGGCGGTAAT GGATGGAGCG TTTTTCAGAC GACCGCCGAA CATCCGAAAA
301 TCAGTCTTTC AAAAATCCGA ATACGACAAA TTCGTATTGG TTGCCGATTT
351 CTTCCAAACC TGCCTTAATC GCTTCTTCGA AGTCGTAGAA ATAATCGGCA
401 TTGGTGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 238; ORF 075>:

```
m075.pep
  1 MPSYFITLLT MENTKSAAKM PTTIQPASIP SAFAASKAFF AVSGNVAFAC
 51 AAKARGAAVT TASFAPYLRQ VLINFMIFSF KKCLAVMDGA FFRRPPNIRK
101 SVFQKSEYDK FVLVADFFQT CVNRFFEVEE IIGIGD*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 075 shows 65.7% identity over a 137 aa overlap with a predicted ORF (ORF 075.ng) from *N. gonorrhoeae*:

```
m075/g075

      10      20      30      40      50      60
m075.pep  MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT
          ||||||||||||||||| ||||||||||||||||| : ||||||| |||||
g075      MPPYFITLLTMENTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNAAFACAAKASGAAVT
          10      20      30      40      50      60

      70      80      90      100     110
m075.pep  TASFAPYLRQVLINFMIFSF----KKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVAD
          ||||||||||||||||| |||: : :| | : : :| | : : :|
g075      TASFAPYLRQVLINFMIFSFTKFLKKVCGLCEGFRDRLPGLNLNLIFFVESENYKFPAY
          70      80      90      100     110     120

      120     130
m075.pep  FFQTCVNRFFEVEEIIIGIGDX
          :|| :| :| :|
g075      LFQCRAKSVFIAVIFTGX
          130
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 239>:

```
a075.seq
  1 ATGCCGTCTT ACTTCATCAC TCTCTTAACG ATGGAAAAGA CAAAAAGCGC
 51 GGCGAAAACG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CGGCTTCCAA AGCGTTTTTT GCTGTATCGG GCAACGTTGC ATTTGCATGT
151 GCGGCCAAAG CCAGGGGAGC AGCTGTTACA ACAGCCAGTT TTGCGCCGTA
201 TTTACGGCAG GTGTTAATAA ATTTTCATGAT ATTTTCCTTC AAAAAGTGTT
251 TGGCGGTAAT GGATGGAGCG TTTTTCAGAC GACCGCCGAA CATCCGAAAA
301 TCAGTCTTTC AAAAATCCGA ATACGACAAA TTCGTATTGG TTGCCGATTT
351 CTTCCAAACC TGCCTTAATC GCTTCTTCGA AGTCGTAGAA ATAATCGGCA
401 TTGGTGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 240; ORF 075.a>:

```
a075.pep
  1 MPSYFITLLT MEKTKSAAKT PTTIQPASIP SAFAASKAFF AVSGNVAFAC
 51 AAKARGAAVT TASFAPYLRQ VLINFMIFSF KKCLAVMDGA FFRRPPNIRK
101 SVFQKSEYDK FVLVADFFQT CVNRFFEVEE IIGIGD*
```

m075/a075 98.5% identity over a 136 aa overlap

	10	20	30	40	50	60
m075.pep	MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT					
a075	MPSYFITLLTMEKTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m075.pep	TASFAPYLRQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
a075	TASFAPYLRQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
	70	80	90	100	110	120
	130					
m075.pep	CVNRFFEVEIIGIGDX					
a075	CVNRFFEVEIIGIGDX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 241>:

```

g080.seq
1   ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
51  CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
101 CGAATCATCT GCCCGTCAAG CAGGTGTCGC TGAAGGGCAA CCTGGTTTAT
151 TCCGATAAGA AGGCATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA
201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAAGCCTAC CGCCGGTATC
251 CGTGGATTGC GTCGGTCATG GTGCGCCGCC GTTTTCCCGA TACGGTTGAG
301 GTCGTCCTGA CCGAGCGCAA GCCGGTTGCA CGTTGGGGCG ACCATGCCTT
351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGCTTGGAC AGACCCGGAA
401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
451 TATGACGAAT TTTCGACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA
501 GATGACCTAT ACGGCACGTT CGGCGTGGAA TGTCGTTTTG GACAACGGCA
551 GATCCGTCAG GCTCGGACGG GAAAACgaGA TGAAACGCCT CCgGCTTTTT
601 ACcgAAGCGT GGCAGCATCT gttgcGTAAG AATAAAAATC GGTATATCTA
651 TGTGGATATG Aggtataagg acggatttTC agtcccccat gctCCGACG
701 GTTTACCCGA AAAAGAATcc gAAGAAAtt gggAACaggt ttgggacata
751 ttacggcctg gcgtcggaaa cggttcgacg caaatttcaa tcagttatAA
801 GGGCAGacga acaatggaac AGcagtaa
  
```

This corresponds to the amino acid sequence <SEQ ID 242; ORF 080.ng>:

```

g080.pep
1   MWDNAEAMER LTRWLLVMMA MLLAASGLVW FYNSNHLPVK QVSLKGNLVY
51  SDKKALGSLA KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDVE
101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RPGMPVFRGA EGTSAEMLRR
151 YDEFSTVLAK QGLGIKEMTY TARSAWNVVL DNGITVRLGR ENEMKRLRLF
201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVPH APDGLPEKES EEWYEQVWDI
251 LRPGVGNST QISISYKGRR TMEQQ*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 243>:

```

m080.seq
1   ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
51  CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
101 CGAATCATCT GCCCGTCAAG CAGGTGTCGC TGAAGGGCAA CCTGGTTTAT
151 TCCGATAAGA AGACATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA
201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAGGCCTAC CGCCGGTATC
251 CGTGGATTGC GTCGGTCATG GTGCGCCGCC GTTTTCCCGA CACGGTTGAG
301 GTCGTCCTGA CCGAGCGCAA GCCGGTCGCG CGTTGGGGCG ACCATGCCTT
351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGCTTGGAC AGACCCGGAA
401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
451 TATGACGAAT TTTCGACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA
501 GATGACCTAT ACGGCACGTT CGGCGTGGAT TGTCGTTTTG GACAACGGCA
551 TCACCGTCAG GCTCGGACGG GAAAACGAGA TGAAACGCCT CCGGCTTTTT
  
```

601 ACCGAAGCGT GGCAGCATCT GTTGCCTAAA AATAAAATC GGTTATCCTA
 651 TGTGGATATG AGGTATAAGG ACGGATTTTC AGTCCGCTAT GCTTCCGACG
 701 GTTTACCCGA AAAAGAATCC GAAGAATAG

This corresponds to the amino acid sequence <SEQ ID 2441; ORF 080>:

m080.pep
 1 MWDNAEAMER LTRWLLVMMA MLLAASGLVW FYNSNHLPVK QVSLKGNLVY
 51 SDKKTLGSLA KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDTVE
 101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RPGMPVFRGA EGTSAEMLRR
 151 YDEFSTVLAK QGLGIKEMTY TARSAWIVVL DNGITVRLGR ENEMKRLRLF
 201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVRY ASDGLPEKES EE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 080 shows 97.9% identity over a 242 aa overlap with a predicted ORF (ORF 080.ng) from *N. gonorrhoeae*:

m080/g080

m080.pep	10	20	30	40	50	60
	MWDNAEAMERL LTRWLLVMMA MLLAASGLVW FYNSNHLPVK QVSLKGNLVY SDKKTLGSLA					
080	MWDNAEAMERL LTRWLLVMMA MLLAASGLVW FYNSNHLPVK QVSLKGNLVY SDKKALGSLA					
	10	20	30	40	50	60
m080.pep	70	80	90	100	110	120
	KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDTVE VVLTERKPVARWGDHALVDG					
080	KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDTVE VVLTERKPVARWGDHALVDG					
	70	80	90	100	110	120
m080.pep	130	140	150	160	170	180
	EGNVFEARLD RPGMPVFRGA EGTSAEMLRRYDEFSTVLAK QGLGIKEMTY TARSAWIVVL					
080	EGNVFEARLD RPGMPVFRGA EGTSAEMLRRYDEFSTVLAK QGLGIKEMTY TARSANVVL					
	130	140	150	160	170	180
m080.pep	190	200	210	220	230	240
	DNGITVRLGRE NEMKRLRLF TEAWQHLLRK NKNRLSYVDMRYKDGFSVRY ASDGLPEKES					
080	DNGITVRLGRE NEMKRLRLF TEAWQHLLRK NKNRLSYVDMRYKDGFSVPHAPDGLPEKES					
	190	200	210	220	230	240
m080.pep	EEX					
080	EEYWEQVWDILRPGVGNSTQISISYKGRRTMEQQX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 245>:

a080.seq
 1 ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
 51 CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
 101 CGAATCATCT GCCCGTCAAG CAGGTGTGCG TGAAGGGCAA CCTAGTTTAT
 151 TCCGATAAGA AAGCATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA
 201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAGGCCTAC CGCCGTATC
 251 CGTGGATTGC GTCGGTCATG GTGCGCCGCC GTTTCCCGA CACGGTTGAG
 301 GTCGTCCTGA CCGAGCGCAA GCCGTCGCG CGTTGGGGCG ACCATGCCTT
 351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGTTTGGAC AGACCCGGAA
 401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
 451 TATGACGAAT TTTCGACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA
 501 GATGACCTAT ACGGCACGTT CGGCGTGGAT TGTCGTTTTG GACAACGGCA

264

551 TCACCGTCAG GCTCGGACGG GAAAACGAGA TGAAACGCCT CCGGCTTTTT
 601 ACCGAAGCGT GGCAACATCT GTTGCGTAAA AATAAAATC GGTTATCCTA
 651 TGTGGATATG AGGTATAAGG ACGGATTTTC AGTCCGCTAT GCTCCCGACG
 701 GTTTACCCGA AAAAGAATCC GAAGAATAG

This corresponds to the amino acid sequence <SEQ ID 246; ORF 080.a>:

a080.pep

1 MWDNAEAMER LTRWLLVMM MLLAASGLVW FYN SNHLPVK QVSLKGNLVY
 51 SDKKALGSLA KEYIHGNILR TDINGAQEAY RRY PWIASVM VRRRFPDVE
 101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RGPMPVFRGA EG TSAEMLRR
 151 YDEFSTVLAK QGLGIKEMTY TARS AWIVVL DNGITVRLGR ENEMKRLRLF
 201 TEAWQHLLRK KNRLSYVDM RYKDGFSVRY APDGLPEKES EE*

m080/a080 99.2% identity over a 242 aa overlap

m080.pep	10	20	30	40	50	60
	MWDNAEAMERL LTRWLLVMMAMLLAASGLVWFYNSNHLFPVKQVSLKGNLVYSDKKTGSLA					
a080	MWDNAEAMERL LTRWLLVMMAMLLAASGLVWFYNSNHLFPVKQVSLKGNLVYSDKKALGSLA					
	10	20	30	40	50	60
m080.pep	70	80	90	100	110	120
	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDVEVVLTERKPVARWGDHALVDG					
a080	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDVEVVLTERKPVARWGDHALVDG					
	70	80	90	100	110	120
m080.pep	130	140	150	160	170	180
	EGNVFEARLDRPGMPVFRGAEG TSAEMLRRYDEFSTVLAKQGLGIKEMTYTARS AWIVVL					
a080	EGNVFEARLDRPGMPVFRGAEG TSAEMLRRYDEFSTVLAKQGLGIKEMTYTARS AWIVVL					
	130	140	150	160	170	180
m080.pep	190	200	210	220	230	240
	DNGITVRLGRENMKRLRLFTEAWQHLLRKNKNRLSYVDMRYKDGFSVRYASDGLPEKES					
a080	DNGITVRLGRENMKRLRLFTEAWQHLLRKNKNRLSYVDMRYKDGFSVRYAPDGLPEKES					
	190	200	210	220	230	240
m080.pep	EEX					
a080	EEX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 247>:

g081.seq

1 ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
 51 GCCGTCTGAA AACAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGATA
 101 TTCGGGAAGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGACGCG
 151 CATGATTTTG TTGGAGGCGT ATTGTCTGCG GCGCGGGCGG CGGTTGTGGT
 201 TTCGCGCGAA GATTGCGCGG CTTTGGGCGG CGCGTTGAAA GTCGATGACA
 251 CGCTTGCCGC GTTGCAAACG TTGGCGAAGG CGTGGCGCGA TAATGTGAAC
 301 CCGTTTGTGT TCGGCATTAC CGGTTCCGGC GGCAAGACGA CGGTGAAGGA
 351 GATGCTGGCT GCGGTATTGC GCCGCCGTTT CGGCGATGAT GCCGTTTCGG
 401 CGACGGCAGG CAACTTCAAC AACCACAtcg gaTTGCCGCT GACTTTATTG
 451 AAATtaaAcg aAAAAACCG CTATGCCGTG ATTGAAATGG GCATGAACCA
 501 TTTTGGcgaa ctggcggTt taacgcaaaT CGCCAAACCC GATGCCGCTT
 551 TGGtcaACAA CGCCTGCGC GCCCATGTG GATGCGGTTt cgacggagtg
 601 GGCATATTG CCAAAGcgaa aagcGAGATT TatgcagGct tATGTTCAGA
 651 CGGCATGGCA CTGATTCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
 701 CGGCAACGTT TAATTGAAT ACGTGCACCT TCGGCGTCGA TAGCGGCGAT
 751 GTCCGCGCGG AAAATATCGT GCTGAAACCT TTGTCGTGCG AATTTGATT

265

```

801 GGTGTGCGGC GACGAGCGCA CTGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCCGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG CAAGGCTTCA GCAACATCAA
951 AGGCCGTCTG AACGTCAAAG CCGGCATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAATCCC GACAGTATGA AAGCCGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCCGCCG CATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAGGAc gaAGCCGCCG CCATGCACGC CGAagtcgGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGcggaAA AATTTGGCGC GGACGGTTTG TGGTTCGCCG CCAAAGACCC
1251 GTTGATTCAA GTGTTGAGCC ACGATTTGCC CGAACGCGCC ACCGTGTTGG
1301 TGAAAGGTTT GCGCTTTATG CAGATggAAG AAGTGGTCGA GGCATTGGAG
1351 GATAAGTga

```

This corresponds to the amino acid sequence <SEQ ID 248; ORF 081.ng>:

g081.pep

```

1 MKPLDLNFIC QALKLPMPSE NKPVSRIVTD SRDIREGDVF FALAGGRFDA
51 HDFVGGVLSA GAAAVVVSRE DCAALGGALK VDDTLAALQT LAKAWRDNVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDD AVSATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFE LAVLTQIAKP DAALVNNALR AHVGCDFDGV
201 GDIKAKSEI YAGLCSDGMA LIPOEDANMA VFKTATFNLN TCTFGVDSGD
251 VRAENIVLKP LSCEFVLVCG DERTAVVLPV PGRHNVHNAA AAAALALAAG
301 LSLNDVAEGL QGFSNIKGRL NVKAGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFV MGDMGELGED EAAAMHAEVG AYARDQGIEA AYFVGDNVSE
401 AAEKFGADGL WFAAKDPLIQ VLSHDLPERA TVLVKGSRFM QMEEVVEALE
451 DK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 249>:

m081.seq

```

1 ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51 GCCGCTTGAA AGCAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGAGCG GTTTGACGCG
151 CCGATTTTTG TTGAAGACGT ATTGGCTGCT GGTGCGCGCG CGGTTGTGGT
201 TTCGCGCGAA GATTGTGCTG CAATGGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTGCCGC ATTGCAAACG CTGGCAAAGG CGTGGCGTGA AAATGTGAAT
301 CCGTTTGTGT TCGGCATTAC CGGTCGGGC GGCAAGACGA CGGTGAAGGA
351 AATGCTGGCT GCGGTATTGC GCCgCCGTTT CGGCGATGAT GCCGTGTTGG
401 CAGCGGCAGG CAACTTCAAC AACCATATCG GATTGCCGCT GACTTTGTTG
451 AGATTAAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GCATGAACCA
501 TTTCGCGGAA CTGGCGGTTT TAACGCAmAT CGCCAAACCA AATGCCGCAT
551 TGGTCAACAA CGCCATGCGC GCCCATGTCG GCTGCGGTTT CGACGGAGTG
601 GGCGATATTG CCAAAGCGAA AAGCGAGATT TACCAAGGTT TATGTTCAGA
651 CGGCATTGCA CTGATTCTTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTTGAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTTCACGCGG AAAATATTGT GCTGAAACCG TTGTCGTGCG AATTTGATTT
801 GGTGTGCGGC GATGAGCGCG CCGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCCGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCCT GACAGCATGA AAGCTGCGAT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAACTG GCGGAGGACG AAGCCGCCGC TATGCACGCC GAAGTCGGCG
1151 CGTATGCCCG CGACCAAGGC ATCGAAGCGG CTTATTTTGT CGGCGACAAC
1201 AGCGTCGAAG CGGCGGAAAA ATTTGGCGCG GACGGTTTGT GGTTCGCCCG
1251 CAAAGACCCG TTGATTCAAG TGTTGCGCCA CGATTTGCCC GAACGCGCCA
1301 CCGTGTGGT GAAAGGTTTC CGCTTTATGC AGATGGAAGA AGTGGTCGAG
1351 GCATTGGAGG ATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 250; ORF 081>:

m081.pep

```

1 MKPLDLNFIC QALKLPMPSE SKPVSRIVTD SRDIRAGDVF FALAGERFDA
51 HDFVEDVLAA GAAAVVVSRE DCAAMDGALK VDDTLAALQT LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDD AVLATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFE LAVLTXIAKP NAALVNNAMR AHVGCDFDGV

```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 081 shows 94.1% identity over a 455 aa overlap with a predicted ORF (ORF 081.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m081.pep	MKPLDLNFTICQALKLPMPS	ESKPVSRIVTDSRDIRAGDV	VFALAGERFDAHDFVEDVLA			
g081	MKPLDLNFTICQALKLPMSEN	KPVSRIVTDSRDI	REGDVVFALAGGRFDAHDFV	GGVLSA		
	10	20	30	40	50	60
m081.pep	70	80	90	100	110	120
m081.pep	GAAAVVVSREDCAAMDGALKV	DDTLAALQTLAKAWRENVNPF	VFGITGSGGKTTVKEMLA			
g081	GAAAVVVSREDCAALGGALKV	DDTLAALQTLAKAWRDNVNPF	VFGITGSGGKTTVKEMLA			
	70	80	90	100	110	120
m081.pep	130	140	150	160	170	180
m081.pep	AVLRRRFGDDAVLATAGNFNNH	IGLPLTLLKLN	KEHRYAVIEMGMNHFGELAVLTX	IAKP		
g081	AVLRRRFGDDAVSATAGNFNNH	IGLPLTLLKLN	KEHRYAVIEMGMNHFGELAVLTQ	IAKP		
	130	140	150	160	170	180
m081.pep	190	200	210	220	230	240
m081.pep	NAALVNNAMRAHVGC	GFDGVGDI	AKAKSEIYQGLCSDGIALIPQEDANMAVFKTATL	NLN		
g081	DAALVNNALRAHVGC	GFDGVGDI	AKAKSEIYAGLCSDGMALIPQEDANMAVFKTATF	NLN		
	190	200	210	220	230	240
m081.pep	250	260	270	280	290	300
m081.pep	TRTFGIDSGDVHAENIVLKPLSCE	FDLVCGDERAAVVL	PVPGRHNVHNAAAAAALALAAG			
g081	TCTFGVDSDGVRAENIVLKPLSCE	FDLVCGDERTAVVL	PVPGRHNVHNAAAAAALALAAG			
	250	260	270	280	290	300
m081.pep	310	320	330	340	350	360
m081.pep	LSLNDVAEGLKGF	SNIKGRLNVKSGIKGATLIDDTYNANPDSMKAAIDVLARMPAPRIFV				
g081	LSLNDVAEGLQGFS	NIKGRLNVKAGIKGATLIDDTYNANPDSMKAAVDVLARMPAPRIFV				
	310	320	330	340	350	360
m081.pep	370	380	390	400	410	420
m081.pep	MGDMGELGELGEDEAAAMHAEV	GAYARDQGIEAAYFVGDN	SVEAAEKFGADGLWFAAKDP			
g081	MGDMGELGE--DEAAAMHAEV	GAYARDQGIEAAYFVGDN	SVEAAEKFGADGLWFAAKDP			
	370	380	390	400	410	
m081.pep	430	440	450			
m081.pep	LIQVLRHDLPERATVLVKGS	RFMQMEEVVEALEDKX				
g081	LIQVLSHDLPERATVLVKGS	RFMQMEEVVEALEDKX				
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 251>:

a081.seq

```

1   ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51  GCCGTCTGAA AGCAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGATGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCG GGTGCGGCGG CGGTTGTGGT
201 TTCGCGCGAA GATTGCGTTG CAATGGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTACCGC GTTGCAAATG TTGGCGAAGG CGTGGCGCGA GAATGTGAAC
301 CCGTTTGTGT TCGGTATTAC CGGCTCGGGC GGCAAGACGA CGGTGAAGGA
351 AATGTTGGCT GCGGTATTGC GCCGCCGTTT CGGCGATAAT GCCGTTTGTG
401 CGACGGCAGG CAACTTCAAC AACCACATCG GATTGCCGTT GACTTTGTTG
451 AAATTAAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GTATGAACCA
501 TTTTGGCGAA CTGGCGGTTT TGACACAAAT CGCCAAACCC GATGCCGCAT
551 TGGTCAACAA CGCCATGCGC GCCCATGTGC GCTGCGGTTT CGACGGAGTG
601 GCGGATATTG CCAAAGCGAA AAGCGAGATT TATCAAGGCT TATGTTCAGA
651 CGGCATGGCG CTGATTCCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTTGAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTCCACGCGG AAAATATCGT GCTGAAACCG TTGTCGTGCG AATTGATTTT
801 GGTGTGCGGC AACGAGTGCG CAGCCGTGGT TCTGCCCGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCCGCCGCCG CGCTGTCTTT GGCTGCAGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCCCT GACAGCATGA AAGCTGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGTGAGGAC GAAGCCGCCG CCATGCACGC CGAAGTCGGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGCGGAAA AATTTGGCGC GGACGGTTTG TGGTTCGCCG CCAAAGACCC
1251 GTTGATTCAA GTGTTGCGCC ACGATTTGCC CGAACGCGCC ACCGTGTTGG
1301 TGAAAGGTTT GCGCTTTATG CAGATGGAAG AAGTGGTCGA GGCATTGGAG
1351 GATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 252; ORF 081.a>:

a081.pep

```

1   MKPLDLNFIC QALKLPMPSE SKPVSRIVD SRDIRAGDVF FALAGGRFDA
51  HDFVEDVLAA GAAAVVVSRE DCVAMDGALK VDDTLTALQM LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDN AVLATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFGE LAVLTQIAKP DAALVNNAMR AHVCGCFDGV
201 GDIAKAKSEI YQGLCSDGMA LIPQEDANMA VFKTATLNLN TRTFGIDSGD
251 VHAENIVLKP LSCEFDLVCG NECAAVVLPV PGRHNVHNAA AAAALSLAAG
301 LSLNDVAEGL KGFSNIKGR LNVKSGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFV MGDMGELGED EAAAMHAEVG AYARDQGIEA AYFVGDNVSE
401 AAEKFGADGL WFAAKDPLIQ VLRHDLPERA TVLVKGSRFM QMEEVVEALE
451 DK*

```

m081/a081 96.7% identity over a 455 aa overlap

	10	20	30	40	50	60
m081.pep	MKPLDLNFICQALKLPMPSESKPVSRIVTDSDRDIRAGDVFFALAGERFDAHDFVEDVLAA					
a081	MKPLDLNFICQALKLPMPSESKPVSRIVTDSDRDIRAGDVFFALAGGRFDAHDFVEDVLAA					
	10	20	30	40	50	60
m081.pep	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
a081	GAAAVVVSREDCAAMDGALKVDDTLALQMLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
	70	80	90	100	110	120
m081.pep	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
a081	GAAAVVVSREDCAAMDGALKVDDTLALQMLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
	70	80	90	100	110	120
m081.pep	AVLRRRFGDDAVLATAGNFNHIGLPLTLLKLNEKHRYAVIEMGMNHFGEAVLTQIAKP					
a081	AVLRRRFGDNAVLATAGNFNHIGLPLTLLKLNEKHRYAVIEMGMNHFGEAVLTQIAKP					
	130	140	150	160	170	180
m081.pep	AVLRRRFGDDAVLATAGNFNHIGLPLTLLKLNEKHRYAVIEMGMNHFGEAVLTQIAKP					
a081	AVLRRRFGDNAVLATAGNFNHIGLPLTLLKLNEKHRYAVIEMGMNHFGEAVLTQIAKP					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m081.pep	NAALVNNAMRAHVGC GFDGVGDI AKAKSEIYQGLCS DGIALIPQEDANMAVFKTATLNLN					
a081	DAALVNNAMRAHVGC GFDGVGDI AKAKSEIYQGLCS DGMALIPQEDANMAVFKTATLNLN					
	250	260	270	280	290	300
m081.pep	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGDERAAVVLVPVGRHNVHNA A A A A A L A A A G					
a081	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGNECAAVVLVPVGRHNVHNA A A A A A L S L A A G					
	310	320	330	340	350	360
m081.pep	LSLNDVAEGLKGF SNIKGR LNVKSGIKGATLIDDTYNANPDSMKAAIDVLARMPAPRIFV					
a081	LSLNDVAEGLKGF SNIKGR LNVKSGIKGATLIDDTYNANPDSMKAAVDVLARMPAPRIFV					
	370	380	390	400	410	420
m081.pep	MGDMGELGELGEDEAAAMHAEV GAYARDQGIEAAYFVG DNSVEAAEKFGADGLWFAAKDP					
a081	MGDMGELGE---DEAAAMHAEV GAYARDQGIEAAYFVG DNSVEAAEKFGADGLWFAAKDP					
	430	440	450			
m081.pep	LIQVLRHDLPERATVLVKGSRFMQMEEVVEALEDKX					
a081	LIQVLRHDLPERATVLVKGSRFMQMEEVVEALEDKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 253>:

```

g082.seq
1   aTGTTGGTTGT TGAAGTTGCC TGCCGTCGCC GAAACGGCAT CATCGCCGAA
51  ACGGCGGCGC AATACCGCAG CCAGCATCTC CTTACCGTC GTCTTGCCGC
101 CCGAACCGGT AATGCCGAAC ACAAACGGGT TCACATTATC GCGCCACGCC
151 TCGCCAACG TTTGCAACGC GGCAAGCGTG TCATCGACTT TCAACGCGCC
201 GCCCAAAGCC GCGCAATCTT CGCGCGAAAC CACAACCGCC GCCGCGCCCG
251 CAGACAATAC GCCTCCAACA AAATCATGCG CGTCAAACCG CCCGCCCGCC
301 AATGCGAAAA ACACATCGCC TTCCCGAATA TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGT TTGTTT CAGACGCGAT CGGAAGCTTG AGGGCTTGGC
401 AGATGAAATT TAGGTCCAGT GGT TTCATAT TTGCTTTCGT TAATATTCCG
451 GCGCGGACAC CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTAAAACAC AGATTATTTT CCCATTCTCA TTCGGCATT TTTCTGTACG
551 TATCATTTTT TAGACGTATT TTAGCCGAT TTGCCTTTTC CCGCATACCA
601 CGGCGCGGGG TCGTCGGACT GTCTGTCGAT AAAGGCAAGG TTATTGCCTT
651 CGCCCGGCAC ATCGGGGACA TTCCCCCAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTCGATACC CGTCCAACG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 254; ORF 082.ng>:

```

g082.pep
1   MWLLKLPAVA ETASSPKRRR NTAASISFTV VLPPEPVMPN TNGFTLSRHA
51  FANVCNAASV SSTFNAPPKA AQSSRETTA AAPADNTPPT KSCASNRPPA
101 NAKNTSPSRI SRLSVTMRDT GLFSDGIGSL RAWQMKFRSS GFIFAFVNI
151 AADTSVAADF FIACFAVVKH RLFSHSHSAF FLYVSFFRRI FSRFAFSRIP
201 RRGVVGLSVD KGKVIAFARH IGDIPPKIIA VIGQLVGFD T RPTAESA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 255>:

```

m082.seq
1   ATGnnGTTGT TGAAGTTGCC TGCCGTCGCC AACACGGCAT CATCGCCGAA
51  ACGGcGGCGC AATACCGCAG CCAGCATTTC CTTACCGTC GTCTTGCCGC
101 CCGAACCGGT AATGCCGAAC ACAAACGGAT TCACATTTTC ACGCCACGCC
151 TTTGCCAGCG TTGCAATGC GGCAAGCGTG TCATCGACTT TCAACGCGCC

```



```

201 ATCCATTGCA GCACAATCTT CGCGCGAAAC CACAACCGCC GCCGCACCAG
251 CAGCCAATAC GTCTTCAACA AAATCATGCG CGTCAAACCG CTCGCCCGCC
301 AATGCGAAAA ACACATCGCC CGCGCGGATG TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTTTGCTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGCC
401 AGATGAAATT TAGGTCCAGT GGTTTCATAT TTACTTTCGT TAATATTCGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTAAAACAC AGATTATTTT CCCATTCTCA TTCGGsATT TTTCTGTACG
551 TATCATTTTT TAGACGTATT TTTAGTCGAT TTGCCTTTTC CCGCATACCA
601 CGGCGCGGGG TCGTCGGGCA GTCCGTCGAT AAAGGCAAGG TTATTGCCTT
651 CGCCCTGCAC ATCGGGAACA TTCCCCCAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTTCGATACC CGTCCAACG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 256; ORF 082>:

```

m082.pep
1 MXLLKLPAVA NTASSPKRRR NTAASISFTV VLPPEPVMPN TNGFTFSRHA
51 FASVCNAASV SSTFNAPSIA AQSSRETTA AAPAANTSST KSCASNRSPA
101 NAKNTSPARM SRLSVTMRDT GLLSDGIGSL RAWQMKFRSS GFIFTFVNIR
151 AADTSVAADF FIACFAVVKH RLFSHSHSXF FLYVSFFRRI FSRFAFSRIP
201 RRGVVGQSDV KGKVIAFALH IGNIPPKIIA VIGQLVGFD T RPTAESAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 082 shows 92.7% identity over a 247 aa overlap with a predicted ORF (ORF 082.ng) from *N. gonorrhoeae*:

```

m082/g082

          10          20          30          40          50          60
m082.pep MXLLKLPVAVANTASSPKRRRNTAASISFTVVLPPPEPVMPNTNGFTFSRHAFASVCNAASV
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082      MWLLKLPVAETAASSPKRRRNTAASISFTVVLPPPEPVMPNTNGFTLSRHAFANVCNAASV
          10          20          30          40          50          60

          70          80          90          100         110         120
m082.pep SSTFNAPSIAAQSSRETTTAAAPAANTSSTKSCASNRSPANAKNTSPARMSRLSVTMRDT
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082      SSTFNAPPKAAQSSRETTTAAAPADNTPPTKSCASNRPPANAKNTSPSRISRLSVTMRDT
          70          80          90          100         110         120

          130         140         150         160         170         180
m082.pep GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSXF
          | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082      GLFSDGIGSLRAWQMKFRSSGFIFAFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSAF
          130         140         150         160         170         180

          190         200         210         220         230         240
m082.pep FLYVSFFRRIFSRFAFSRIPRRGVVGQSDVKGKVIAFALHIGNIPPKIIAVIGQLVGFD T
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082      FLYVSFFRRIFSRFAFSRIPRRGVVGLSVDKGKVIAFARHIGDIPPKIIAVIGQLVGFD T
          190         200         210         220         230         240

m082.pep RPTAESAX
          | | | | | | |
g082      RPTAESAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 257>:

```

a082.seq
1 ATGTGGTTGT TGAAGTTGCC TGCCGTCGCC AAAACGGCAT TATCGCCGAA
51 ACGGCGGCGC AATACCGCAG CCAACATTC CTTCACCGTC GTCTTGCCGC

```

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```

101 CCGAGCCGGT AATACCGAAC ACAAACGGGT TCACATTCTC GCGCCACGCC
151 TTCGCCAACA TTTGCAACGC GGTAAGCGTG TCATCGACTT TCAACGCGCC
201 ATCCATTGCA ACGCAATCTT CGCGCGAAAC CACAACCGCC GCCGCACCCG
251 CAGCCAATAC GTCTTCAACA AAATCATGCG CATCAAACCG CCCGCCCGCC
301 AATGCGAAAA ACACATCGCC CGCGCGGATG TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTGTGCTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGGC
401 AGATGAAATT TAGGTCCAGT GGTTTCATAT TTACTTTCGT TAATATTCGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTAAAACAC AGATTATTTT CCCATTCTCA TTCGGCATT TTTCTGTACG
551 TATCATTTTT TAGACGTATT TTTAGTCGAT TTGCCTTTTC CCGCATACCA
601 CGGCGCGGGG TCGTCGGGCA GTCCGTCGAT AAAGGCAAGG TTATTGCCTT
651 CGCCCTGCAC ATCGGGAACA TTCCCCCAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTGATACC CGTCCAACG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 258; ORF 082.a>:

a082.pep

```

1 MWLLKLPVA KTALSPKRRR NTAANISFTV VLPPEPVIPN TNGFTFSRHA
51 FANICNAVSV SSTFNAPSIA TQSSRETTTA AAPAANTSST KSCASNRPFA
101 NAKNTSPARM SRLSVTMRDT GLLSDGIGSL RAWQMKFRSS GFIFTFVNIR
151 AADTSVAADF FIACFAVVKH RLFSSHSAF FLYVSFFRRI FSRFAFSRIP
201 RRGVVGQSDV KGVIAFALH IGNIPPKIIA VIGQLVGFD T RPTAESAX

```

m082/a082 95.5% identity over a 247 aa overlap

	10	20	30	40	50	60
m082.pep	MXLLKLPVANTASSPKRRRNTAASISFTVVLPPEVMPNTNGFTFSRHAFASVCNAASV					
a082	:	:	:	:	:	:
	10	20	30	40	50	60
	MWLLKLPVAKTALSPKRRRNTAANISFTVVLPPEVIPNTNGFTFSRHAFANICNAVSV					
	70	80	90	100	110	120
m082.pep	SSTFNAPSIAAQSSRETTTAAAPAANTSSTKSCASNRS PANAKNTSPARMSRLSVTMRDT					
a082	:	:	:	:	:	:
	70	80	90	100	110	120
	SSTFNAPSIAAQSSRETTTAAAPAANTSSTKSCASNRPANAKNTSPARMSRLSVTMRDT					
	130	140	150	160	170	180
m082.pep	GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSSHSHXF					
a082	:	:	:	:	:	:
	130	140	150	160	170	180
	GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSSHSAF					
	190	200	210	220	230	240
m082.pep	FLYVSFFRRIFSRFAFSRIPRRGVVGQSDVKGVIAFALHIGNIPPKIIAVIGQLVGFD					
a082	:	:	:	:	:	:
	190	200	210	220	230	240
	FLYVSFFRRIFSRFAFSRIPRRGVVGQSDVKGVIAFALHIGNIPPKIIAVIGQLVGFD					
m082.pep	RPTAESAX					
a082						
	RPTAESAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 259>:

g084.seq

```

1 ATGAAacaAT CCGcccgaat aAAAAATATG GATCAGACAT TAAAAAATAC
51 attgggcatt tGCGCGcttt tagcctTTTG TTTTggcgcG gccatCGCAT
101 CAGGTTATCA CTTGGAATAT GAATACGGCT ACCGTTATTC TGCCGTGGGC
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GCTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCCG CTGGCTGTAT GGTGCGCCTT CTTATCAGAT AGTCGGTTCG
301 ATATTGGAAA GCAATCCTGC CGAGGCGCGT GAATTTGTCT GCAATCTTCC
351 CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTT GGCTTGACAG

```

271

```

401 TTTGGAATA TTGTGTATCT GTGGGGGTAT TTGCTGACGT AAAAACTAT
451 AAACGTCGCA GCAAAATATG GCTGACCATA TTATTGACTT TGATTTTGTC
501 CTGCGCGGTG ATGGAGAAAA TCGccggcga taaAGATTGG CGAGaacctg
551 atgccggcct gttgttgaat ATTTTcgacc tgtattaCga cttggctttc
601 cgcgccggca cAATATGCCG CCAAGCGCGC CCACattttg gaagCagcaa
651 aaaaagcgtC AACATGGCAt atccgccaac ttgcgcccaa gTataa

```

This corresponds to the amino acid sequence <SEQ ID 260; ORF 084.ng>:

g084.pep

```

1 MKQSARIKMN DQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVG
51 ALASVVFLLL LARGFPRVSS VLLIYVGTT ALYLPVGWLY GAPSYYQIVGS
101 ILESNPPEAR EFVGNLPGSL YFVQALFFIF GLTVWKYCVS VGVFADVKNY
151 KRRSKIWLTI LLTLILSCAV MEKIAGDKDW REPDAGLLLN IFDLYYDLAF
201 RAGTICRQAR PHFGSSKKS SV NMAYPPTCAQ V*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 261>:

m084.seq

```

1 ATGAAACAAT CCGCCcGAAT AAAa.ATATG AATCAGACAT TACTTTTATAC
51 ATTGGGCATT TCGCGCCTTT TAACCTTTnn nnnnnnnnnnn nnnnnnnnnnn
101 nnnnnTATCA CCChGAATAT GAATACGGCT ACCGTTATTG TCCCGTGGT
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GTTTCGCCG
201 CGTTTCTTCA GTTGTTTTAC TGATTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCCG CTGGCTGTAT GGTGCGCCGT CTTATCAGAT AGTCGGTTCG
301 ATATTGAAA GCAATCCTGC CGAGGCGCGT GAATTGTCTG GCAATCTTCC
351 CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTT GGCTTGACAG
401 TTTGGAATA TTGTGTATCG GGGGGGTAT TTGCTGACGT AAAAACTAT
451 AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTC
501 CTGCGCGGTG ATGGATAAAA TCGCCAGCGA TAAAGATTG CGAGAACCTG
551 ATGCCGGCCT GTTGTGAAT ATTTTCGACC TGTATTACGA TTTGGCT.TC
601 CGCGCCGGCA CAATATGCCG CCAAGCGCGC CCACATTTTG GAAGCAGCAA
651 AAAAAGCGTC AACATGGCAT ATCCGTCATG TTGCGCCCAA GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 262; ORF 084>:

m084.pep

```

1 MKQSARIKXM NQTLTYTLGI CALLTFXXXX XXXXXYHPEY EYGYRYSAVG
51 ALASVVFLLL LARGFPRVSS VLLIYVGTT ALYLPVGWLY GAPSYYQIVGS
101 ILESNPPEAR EFVGNLPGSL YFVQALFFIF GLTVWKYCVS GGVFADVKNY
151 KRRSKIWLTI LLTLILSCAV MDKIASDKDL REPDAGLLLN IFDLYYDLAX
201 RAGTICRQAR PHFGSSKKS SV NMAYPSCAQ V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 084 shows 90.5% identity over a 231 aa overlap with a predicted ORF (ORF 084.ng) from *N. gonorrhoeae*:

m084/g084

```

              10      20      30      40      50
m084.pep      MKQSARIKXMNQTLTYTLGICALLTF-----YHPEYGYRYSAVGALASVVFLLL
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g084           MKQSARIKXMDQTLKNTLGI CALLAFCFGA AIASGYHLEYEYGYRYSAVGALASVVFLLL
              10      20      30      40      50      60

              60      70      80      90      100     110
m084.pep      LARGFPRVSSVLLIYVGTTALYLPVGWLYGAPSYYQIVGSILESNPPEARFVGNLPGSL
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g084           LARGFPRVSSVLLIYVGTTALYLPVGWLYGAPSYYQIVGSILESNPPEARFVGNLPGSL
              70      80      90      100     110     120

              120     130     140     150     160     170
m084.pep      YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g084           YFVQALFFIFGLTVWKYCVSVGVFADVKNYKRRSKIWLTI LLTLILSCAVMEKIAGDKDW
              130     140     150     160     170     180

```

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	180	190	200	210	220
m084 . pep	REPDAGLLLNIFDLYYDLAXRAGTICRQARPHFGSSKKSVMAYPSCCAQVX				
g084	REPDAGLLLNIFDLYYDLAFRAGTICRQARPHFGSSKKSVMAYPPTCAQVX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 263>:

a084 . seq

```

1  ATGAAACAAT CCGCCCGAAT AAAAAATATG GATCAGACAT TAAAAAATAC
51  ATTGGGCATT TGC GCGCTTT TAGCCTTTT TTTTGGCGCG GCCATCGCAT
101 CAGGTTATCA CTTGGAATAT GAATACGGCT ACCGTTATTC TGCCGTGGGT
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCGG CTGGCTGTAT GGTGCGCCGT CTTATCAGAT AGTCGGTTCG
301 ATATTGGAAT GCAATCCTGC CGAGGCGCGT GAATTTGTCG GCAATCTTCC
351 CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTT GGCTTGACAG
401 TTTGGAGATA TTGTGTATCG GGGGGGGTAT TTGCTGACGT AAAAAACTAT
451 AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTG
501 CTGCGCGGTG ATGGATAAAA TCGCCAGCGA TAAAGATTTC CGAGAACCTG
551 ATGCCGGCCT GTTGTGTAAT ATTTTCGACC TGTATTACGA TTTGGCTTCC
601 .GCGCCGGCA CAATATGCCG CCAAGCGCGC CCACATTTTG GAAGCAGCAA
651 AAAAAGCGTC AACATGGCAT ATCCGTCATG TTGCGCCCAA GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 264; ORF 084.a>:

a084 . pep

```

1  MKQSARIKMN DQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSVAVG
51  ALASVVFLLL LARGFPRVSS VLLIYVGT ALYLPVGWLY GAPSYQIVGS
101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTVWRYCVS GGVFADVKNY
151 KRRSKIWLTI LLTLILSCAV MDKIASDKDL REPDAGLLLN IFDLYYDLAS
201 XAGTICRQAR PHFGSSKKSVMAYPSCCAQ V*

```

m084/a084 92.2% identity over a 231 aa overlap

	10	20	30	40	50	60
m084 . pep	MKQSARIKXMNQTLTYLIGICALLTFXXXXXXHYHPEYGYRYSVAVGALASVVFLLL					
	: :					
a084	MKQSARIKMDQTLKNTLGI CALLAFCFGAAIASGYHLEYEYGYRYSVAVGALASVVFLLL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m084 . pep	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGSILES NPAEAR EFVGNLPGSL					
a084	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGSILES NPAEAR EFVGNLPGSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m084 . pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL					
	:					
a084	YFVQALFFIFGLTVWRYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL					
	130	140	150	160	170	180
	190	200	210	220	230	
m084 . pep	REPDAGLLLNIFDLYYDLAXRAGTICRQARPHFGSSKKSVMAYPSCCAQVX					
a084	REPDAGLLLNIFDLYYDLASXAGTICRQARPHFGSSKKSVMAYPSCCAQVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 265>:

g085 . seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCTG CGCGACGCGT TGAAAGATAA

```

```

51  GGCAAAAGGC GTGTTCTGA TCGGCGTCGA TCGCGCGCAA ATCCGCCGCG
101 ATTTGGACGG CTGCGGCTTG AACCTGACCG ACTGCGTCAC TTTGGAAGAG
151 GCGGTTTCTAGA CCGCATACGC CCAAGCCGAA GCGGGCGATA TTGTCTTGCT
201 CAGCCCCGCC TCGCGGAGTT TCGATATGTT TAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTT tatCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 266; ORF 085.ng>:

g085.pep

```

1  MGKGQDFTPL RDALKDKAKG VFLIGVDAPO IRRDLGCGCL NLTDCVTLEE
51  AVQTAYAQAE AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 267>:

m085.seq

```

1  ATGGGTAAAG GGCAGGACTT CACGCCCCTG CGCGATGCAC TGGTAGGCAA
51  GGCAAAAGGC GTGTTCTTGA TTGGTGTCTGA TCGCGCGCAA ATCCGCCGCG
101 ATTTGGACGG CTGCGGCTTG AATATGACCG ACTGCGCCAC TTTGGGAGAA
151 GCCGTTTCTAGA CCGCATATGC CCAAGCCGAA GCAGGCGATA TTGTGTTGCT
201 CAGCCCCGCC TCGCGGAGCT TTGATATGTT CAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTT TATCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 268; ORF 085>:

m085.pep

```

1  MGKGQDFTPL RDALVGKAKG VFLIGVDAPO IRRDLGCGCL NMTDCATLGE
51  AVQTAYAQAE AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 085 shows 94.7% identity over a 94 aa overlap with a predicted ORF (ORF 085.ng) from *N. gonorrhoeae*:

m085/g085

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGCLNMTDCATLGEAVQTAYAQAE					
g085	MGKGQDFTPLRDALKDKAKGVFLIGVDAPOIRRDLGCGCLNLTDCVTLEEAVQTAYAQAE					
	10	20	30	40	50	60
	70	80	90			
m085.pep	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
g085	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 269>:

a085.seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCCTG CGCGACGCGC TTGCCGGCAA
51  GGCAAAAGGC GTGTTCTGA TCGGTGTCTGA TCGCGCGCAA ATCCGCCGCG
101 ATTTGGACGG CTGCGATCTG AATATGACCG ACTGCGCCAC TTTGGAAGAA
151 GCGGTTTCTAGA AGGCATATGC CCAAGCCGAA GCGGGCGATA TCGTGCTGCT
201 CAGCCCCGCC TCGCGGAGTT TCGATATGTT TAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTT TATCGGGGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 270; ORF 085.a>:

a085.pep

```

1  MGKGQDFTPL RDALAGKAKG VFLIGVDAPO IRRDLGCDL NMTDCATLEE
51  AVQKAYAQAE AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

m085/a085 94.7% identity over a 94 aa overlap

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGCLNMTDCATLGEAVQTAYAQAE					

g086.seq

This corresponds to the amino acid sequence <SEQ ID 272; ORF 086.ng>:

g086 . pep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 273>:

m086.seq

1	ATGGTGGTGC	TGATGACGGC	GTTCAAGCTG	CTGATGATTT	ATTCGGCTTC
51	TGTGTATTTC	GCATCAAAAG	AAGGCGGCGA	TCAGTTTTTC	TATTTGACCA
101	GACAGGCGGG	GTTCGTCGTT	GCCGGCTTGA	TAGCGAGCGG	TTTGTTATGG
151	TTTCTTTTCA	GGATGAGGAC	ATGGCGGCGG	CTTGTCGGT	GGATTTTTGC
201	CCTATCCGGC	CTGTTGCTGG	TAGTCGTATT	GATTGCCGGG	CGCGAAATCA
251	ATGGCGCGAC	CCGTTGGATA	CCTTGGGTC	CGTTGAATTT	CCAGCCGACC
301	GAGCTGTTT	AGCtGGCGGT	CATCCTTTAT	TTGGCAAGCC	TGTTACGCG
351	CCGTGAAGAA	GTGTTGcGCA	GCATGGAAG	TTTGGGTTG	CAGTCGATTT
401	GCGGGGGGAC	GGCCAATCTG	ATCATCTCCG	CCACCAATCC	GCAGrCACGT
451	CGTGAAACAT	TAGAAATGTA	CGGCCGTwTC	CGGCGATCA	TCCTGCCGAT
501	TATGCTGGTG	GCGTTCGGTT	TGGTGCTGAT	AATGGTACAG	CCGGATTTTCG

```

551 GTTCGTTTGT CGTCATTACC GTCATTGCCG TTGGAATGCT GTTTTGGCA
601 GGATTGCCGT GGAAATATTT TTTCTCCTG GTAGGCAGCG TCTTGGGCGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CGGGTAGTGG
701 CATTTTGGGA CCCGTGGAAA GACCCGCAGG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGGTTCGGTA TGGGTTTGGG
801 TGCGAGTTTG AGCAAACGCG GCTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGGCCAT CATCGCCGAA GAATTCGGTT TCTTCGGTAT GTGCGTGCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGGG GCGTTTCCA TCGGCAAGCA
951 GTCGCGCGAT TTGGGTTTGA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTTGGAT CGGkrTCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA mCAAAGyCT GACGCGCCG Tg.AtGTCCw ATGGCGGTTC
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTkG CGTATAGATT
1151 ATGAAAACCG CCGGAAAATG CGCGGTTATC GGGTGGAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 274; ORF 086>:

```

m086.pep
1  MVVLMTAFSL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW
51  FLCRMRTWRR LVPWIFALSG LLLVVVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTRREE VLRSMESLGW QSIWRGTANL IMSATNPQXR
151 RETLEMYGRX RAILPIMLV AFGLVLIMVQ PDFGSFVVIT VIAVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFLDPWK DPQGAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIEA EFGFFGMCVL
301 IFCYGWLVR AFSIGKQSRD LGLTFNAYIA SGIGIWIGXQ SFFNIGVNIG
351 ALPKKGLTXP XMSXGSSVF FMLISMMLLX RIDYENRRKM RGYRVE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 086 shows 96.7% identity over a 396 aa overlap with a predicted ORF (ORF 086.ng) from *N. gonorrhoeae*:

m086/g086

	10	20	30	40	50	60
m086.pep	MVVLMTAFSL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW FLCRMRTWRR					
	: :					
g086	MVVLMTAFGL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGFLW FLCRMRTWRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m086.pep	LVPWIFALSGL LLLVVVLIAG REINGATRWI PLGPLNFQPT ELFKLAVILY LASLFTRREE					
	:					
g086	LVPWIFALSGL LLLVAVLIAG REINGATRWI PLGPLNFQPT ELFKLAVILY LASLFTRREE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m086.pep	VLRSMESLGW QSIWRGTANL IMSATNPQXR RETLEMYGRX RAILPIMLV AFGLVLIMVQ					
g086	VLRSMESLGW QSIWRGTANL IMSATNPQAR RETLEMYGRF RAILPIMLV AFGLVLIMVQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m086.pep	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
	:					
g086	PDFGSFVVITVITVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m086.pep	DPQGAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIEAEFGFFGMCVL					
g086	DPQGAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIEAEFGFFGMCVL					
	250	260	270	280	290	300
	310	320	330	340	350	360

```
m086.pep      IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGXQSFFNIGVNIGALPXKGLTXP
|||||
g086          IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGIQSFFNIGVNIGALPTKGLTLP
              310       320       330       340       350       360

              370       380       390
m086.pep      XMSXGGSSVFFMLISMMLLXRIDYENRRKMGRGYRVEX
|||
g086          LMSYGGSSVFFMLISMMLLLRIDYENRQKMRGYRVEX
              370       380       390
```

a086.seq

This corresponds to the amino acid sequence <SEQ ID 276; ORF 086.a>:

a086.pcp

1	MVVLMTAFSL	LMIYSASVYL	ASKEGGDQFF	YLTRQAGFVV	<u>AGLIASGLLW</u>
51	<u>FLCRMRTWR</u>	<u>LVPWIFALSL</u>	<u>LLLVVVLIG</u>	REINGATRWI	PLGPLNFQPT
101	ELFKLAVILY	LASLFTTRSE	VLRSMSLWAG	QSIWRGTANL	IMSATNPQAR
151	RETLEMYGRF	RAIILPIMLV	AFGLVLIMVQ	PDFGSFVVIT	VIAVGMLFLA
201	<u>GLPWKYFFVL</u>	<u>VGSVLGGMVL</u>	<u>MITAAPYRVQ</u>	<u>RVVAFDPWK</u>	<u>DPQGAGYQLT</u>
251	<u>HSLMAGIRGE</u>	<u>WFGMGLGASL</u>	<u>SKRGFLPEAH</u>	<u>TDFIFAIIEG</u>	<u>EFGFGMCMVL</u>
301	<u>IFCYGWLVR</u>	<u>AFSIMGQSRD</u>	<u>LGLTFNAYIA</u>	<u>SGIDIENIGI</u>	<u>SFFNIGVNIG</u>
351	<u>ALPTKGLTLP</u>	<u>LMSYGGSSVF</u>	<u>FGLISMMLLL</u>	<u>RGDIWNRKRM</u>	<u>RGYRVE*</u>

m086/a086 98.0% identity over a 396 aa overlap

	10	20	30	40	50	60
m086.pep	MVVLMTAFSLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
a086	MVVLMTAFSLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
	10	20	30	40	50	60
m086.pep	LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLTKLAVILYLASLFTTRREE					
a086	LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLTKLAVILYLASLFTTRREE					
	70	80	90	100	110	120

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	70	80	90	100	110	120
	130	140	150	160	170	180
m086.pep	VLRSMESL	GWQSIWRGTANLIMSATNPQXRRETLEMYGRXRAILPIMLVAFGLVLIMVQ				
a086	VLRSMESL	GWQSIWRGTANLIMSATNPQARRETLEMYGRFRAILPIMLVAFGLVLIMVQ				
	190	200	210	220	230	240
m086.pep	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
a086	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
	250	260	270	280	290	300
m086.pep	DPQGAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIAEEFGFFGMCVL					
a086	DPQGAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIAEEFGFFGMCVL					
	310	320	330	340	350	360
m086.pep	IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGXQSFNIGVNIAGLPXKGLTXP					
a086	IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGIQSFNIGVNIAGLPTKGLTLP					
	370	380	390			
m086.pep	XMSXGGSSVFFMLISMMLLXRIDYENRRKMRGYRVEX					
a086	LMSYGGSSVFFMLISMMLLLRIDYENRRKMRGYRVEX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 277>:

g087.seq

```

1   ATGGGCGGTA AAACCTTTAT GCTGATGGCG GCGGGAACGG GCGGACACAT
51  TTTCCCAGCT CTGGCTGTGG CGGATTCATT GCGCGTGCGC GGTCATCATG
101 TAATTTGGCT GGGCAGCAAG GATTTCGATG AAGAGCGCAT CGTGCCGCAA
151 TACGCATAC  GCTTGGAAC  GCTGGCGATT AAAGGAATAC GCGGCAACGG
201 CATCAAACGC AAGCTGATGC TTCCGTTTAC TCTGTACAAA ACCGTCCGCG
251 AAGCGCAGCG GATTATCCGC AAACACCGTG TCGAGTGCGT CATCGGCTTC
301 GCGGTTTTG  TTACCTTTC  CGGCGTCTG  GCGGCGAAAC TCTTGGGCGT
351 GCCGATTGTG ATTCACGAGC AAAACGCCGT GGCAGGCTTG TCCAACCGCC
401 AccTGTCGCG ctGGGCGAAA CGGGTGTGTG ACGCTTTTCC GAAAGCGTTC
451 AGCCACGAAG GCGGTTTGGT CGGCAACCCC GTCCGCGCCG ATATTAGCAA
501 CCTGCCCGTG CCTGCCGAAC GCTTCCAAGG GCGCGAAGGC CGTCTGAAAA
551 TTTTGGTGGT CGGCGGCAGT TTGGGTGCGG ACGTTTTGAA CAAAACCGTA
601 CCGCAGGCGT TGGCACTGCT GCCTGAAGAG GTGCGCCCGC AGATGTACCA
651 CCAGTCGGGG CGTAACAAGC TGGGCAATCT TCAGGCGGAT TATGACGCGT
701 TGGGCGTGAA AGCGGAATGC GTGGAATTTA TTACCGACAT GGTGTCCGCC
751 TACCGTGATG CCGATTGGT  GATTTGCCGT GCCGGCGCGC TGACGATTGC
801 CGAGTTGACG GCGGCGGGGC TGGGCGCGTT GTTAGTGCCG TATCCTCACG
851 CCGTTGATGA CCATCAAACC GCCAACGCGC GTTTCATGGT GCAGGCAGAA
901 GCGGGGCTGC TGTGCCGCA  AACCAGTTG  ACGGCGGAAA AACTCGCCGA
951 AATCCTCGGC AGCCTCAACC GCGAAAAATG CCTCAAATGG GCGGAAACG
1001 CCCGTACGTT GGCATTGCCG CACAGCGCGG ATGACGTTGC CGAAGCCGCG
1051 ATTGCGTGTG CGGCGTAAA

```

This corresponds to the amino acid sequence <SEQ ID 278; ORF 087.ng>:

g087.pep

```

1   MGGKTFMLMA GGTGGHIFPA LAVADSLRVR GHVIVLWLSK DSMEERIVPQ
51  YGIRLETIAI KGIRNGIKR KLMLPFTLYK TVREAQRIIR KHRVECVIGF
101 GGFVTFPGGL AAKLLGVPIV IHEQNAVAGL SNRHLSRWAK RVLVYAFPKAF
151 SHEGGLVGNP VRADISNLPV PAERFQREG  RLKILVVGGS LGADVLNKTV

```

201 PQALALLPEE VRPQMYHQSG RNKLGNLQAD YDALGVKAEC VEFITDMVSA
 251 YRDADLVICR AGALTIAELT AAGLGALLVP YPHAVDDHQT ANARFMVQAE
 301 AGLLLPQTQL TAEKLAELG SLNREKCLKW AENARTLALP HSADDVAEAA
 351 IACAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 279>:

m087.seq
 1 ATGGGCGGTA AAACCTTTAT GCTGAwkkCG GCGGGAACGG GCGGACATAT
 51 TTCCCCGCG CTGGCGGTGG CGGATTCATT GCGCGCGCGC GGCCATCATG
 101 TGATTGGCT GGGCAGCAAG GATTTCGATGG AAGAGCGTAT CGTGCCGCAA
 151 TACGGCATACT GCTTGGAAAC GCTGGCGATT AAAGGCGTGC GCGGCAACGG
 201 CATCAAACGC AAATGATGC TGCCGGTTAC TTTGTATCAA ACCGTCCGCG
 251 AAGCGCAGCG GATTATCCGC AAACACCGTG TCGAGTGCCT CATCGGCTTC
 301 GCGGCTTCG TTACCTTCCC CGGCGGTTTG GCGGCGAAGC TATTArGCGT
 351 GCGGATTGTG ATTCACGAGC AAAACGCCGT GCGAGGTTTG TCCAACCGCC
 401 ACCTGTGCGC CTGGGCGAAG CGGGTGTGTG ACGCTTTTCC GAAAGCGTTC
 451 AGCCACGAAG GCGGCTTGGT CGGCAACCCC GTCCGCGCCG ATATTAGCAA
 501 CTGCCCCGTG CCTGCCGAAC GCTTCCAAGG GCGTGAAGGC CGTCTGAAAA
 551 TTTTGGTGGT CGGCGGCAGT TTGGGCGCGG ACGTTTTGAA CAAAACCGTA
 601 CCGCATGCAT TGGCTTTGCT GCGCGACAAT GCGCGTCCGC ATATGTACCA
 651 CCAATCGGGA CGGGGCAAGC TGGGCATCTT GCAGGCGnnn nnnnnnnnnn
 701 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 751 nnnGCGGGAT TGGGTGCGTT GTTAGTGCCG TATCCTCACG CGGTTGACGA
 801 TCACCAAACC GCCAACGCGC GTTTTATGGT GCAGGCGGAG GCGGGATTGC
 851 TGTGCGGCA AACCAGTTG ACGGCGGAAA AACTCGCCGA GATTCTCGGC
 901 GGCTTAAACC GCGAAAAATG CCTCAAATGG GCAGAAAACG CCCGTACGTT
 951 GGCACTGCCG CACAGTGGC ACGACGTGGC GGAAGCCGCG ATTGCGTGTG
 1001 CGGCGTAA

This corresponds to the amino acid sequence <SEQ ID 280; ORF 087>:

m087.pep
 1 MGGKTFMLXX GGTGGHIFPA LAVADSLRAR GHVHVLGSK DSMEERIVPQ
 51 YGIRLETLAI KGVGRNGIKR KLMLPVTLYQ TVREAQRIIR KHRVECVIGF
 101 GGFVTFPGLL AAKLLXVPIV IHEQNAVAGL SNRHLSRWAK RVLVAFPKAF
 151 SHEGGLVGNP VRADISNLPV PAERFQREG RLKILVVGGS LGADVLNKT
 201 PHALALLPDN ARPHMYHQSG RGKLGILQAX XXXXXXXXXXXX XXXXXXXXXXXX
 251 XAGLGALLVP YPHAVDDHQT ANARFMVQAE AGLLLPQTQL TAEKLAELG
 301 GLNREKCLKW AENARTLALP HSADDVAEAA IACAA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 087 shows 83.9% identity over a 355 aa overlap with a predicted ORF (ORF 087.ng) from *N. gonorrhoeae*:

m087/g087

m087.pep	10	20	30	40	50	60
	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVHVLGSKDSMEERIVPQYGIRLETLAI					
g087	MGGKTFMLMAGGTGGHIFPALAVADSLRVRGHHVHVLGSKDSMEERIVPQYGIRLETLAI					
	10	20	30	40	50	60
m087.pep	70	80	90	100	110	120
	KGVGRNGIKRKLMLPVTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGLAALKLLXVPIV					
g087	KGIRGNGIKRKLMLPFTLYKTVEQAQRIIRKHRVECVIGFGGFVTFPGLAALKLLGVPIV					
	70	80	90	100	110	120
m087.pep	130	140	150	160	170	180
	IHEQNAVAGLSNRHLSRWAKRVLVAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
g087	IHEQNAVAGLSNRHLSRWAKRVLVAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
	130	140	150	160	170	180

279

	190	200	210	220	229
m087.pep	RLKILVVGGSLGADV	LNKTVPHALALLPDN	ARPHMYHQSGR	KGILQA-----	
g087	RLKILVVGGSLGADV	LNKTVQALALLPEE	VRPQMYHQSGRN	KLGNLQADYDAL	GVKAEC
	190	200	210	220	230
m087.pep	-----			AGLGALLVPYPH	AVDDHQTANARFM
g087	VEFITDMVSAYRDA	DLVICRAGALTIAE	LTAAAGLGALLVP	YPHAVDDHQTAN	ARFMVQAE
	250	260	270	280	290
m087.pep	AGLLLPQTQLTAE	KLAEILGGLNREK	CLKWAENARTLAL	PHSADDVAEAAI	ACAAX
g087	AGLLLPQTQLTAE	KLAEILGSLNREK	CLKWAENARTLAL	PHSADDVAEAAI	ACAAX
	310	320	330	340	350

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 281>:

a087.seq

1	ATGGGCGGTA	AAACCTTTAT	GCTGATGGCG	GGCGGAACGG	GCGGACATAT
51	TTTCCCCGCG	CTGGCGGTGG	CGGATTCATT	GCGCGCGCGC	GGCCATCATG
101	TAATTTGGCT	GGGCAGCAAG	GATTCGATGG	AAGAGCGCAT	CGTGCCGCAA
151	TACGACATCC	TGCTCGAAAC	GCTGGCGATT	AAAGGCGTGC	GCGGCAACGG
201	CATCAAACGC	AAGCTGATGC	TGCCGTTTAC	TTTGTATCAA	ACTGTCCGCG
251	AAGCGCAGCA	GATTATCCGC	AAACACCGTG	TCGAGTGCCT	CATCGGCTTC
301	GGCGGCTTCG	TTACCTTTCC	CGGCGGTTTG	GCGGCGAAGT	TATTAGGCGT
351	GCCGATTGTG	ATTACAGAGC	AAAACGCCGT	GGCAGGTTTG	TCCAACCGCC
401	ACCTGTCGCG	CTGGGCGAAG	CGGGTGTTGT	ACGCTTTTCC	GAAAGCGTTC
451	AGCCACGAAG	GCGGCTTGGT	CGGCAACCCC	GTCCGCGCCG	ATATTAGCAA
501	CCTGCCCGTG	CCTGCCGAAC	GCTTCCAAGG	GCGTGAAGGC	CGTCTGA AAA
551	TTTTGGTGGT	CGGCGGCAGT	TTGGGCGCGG	ACGTTTTGAA	CAAAACCGTA
601	CCGAGGCAT	TGGCTTTGCT	GCCCCACAAT	GCGCGTCCGC	AGATGTACCA
651	CCAATCGGGA	CGGGGCAAGC	TGGGCAGCTT	GCAGGCGGAT	TACGACGCGC
701	TGGGCGTGCA	AGCGGAATGC	GTGGAATTTA	TTACCGATAT	GGTGTCCGCC
751	TACCGCGATG	CCGATTGGT	GATTTGCCGT	GCCGCGCGCG	TGACGATTGC
801	CGAGTTGACG	GCGGCGGGAT	TGGGTGCGTT	GTTAGTGCCG	TATCCTCACG
851	CCGTTGATGA	CCATCAAACC	GCCAACGCGC	GTTTTATGGT	GCAGGCGGAG
901	GCGGGATTGC	TGTTGCCGCA	AACCCAGTTG	ACGGCGGAAA	AACTCGCCGA
951	GATTCTCGGC	GGCTTAAACC	GCGAAAAATG	CCTCAAATGG	GCAGAAAACG
1001	CCCGTACGTT	GGCACTGCCG	CACAGTGCGG	ACGACGTTGC	CGAAGCCGCG
1051	ATTGCGTG TG	CGGCGTAA			

This corresponds to the amino acid sequence <SEQ ID 282; ORF 087.a>:

a087.pep

1	MGGKTFMLMA	GGTGGHIFPA	LAVADSLRAR	GHHVIWLGSK	DSMEERIVPQ
51	YDILLET LAI	KGVRGNGIKR	KLMLPFTLYQ	TVREAQQIIR	KHRVECVIGF
101	GGFVTFPGGL	AAKLLGVPIV	IHEQNAVAGL	SNRHLSRWAK	RVLYAFPKAF
151	SHEGGLVGNP	VRADISNLPV	PAERFQREG	RLKILVVGGS	LGADV LNKT V
201	PQALALLPDN	ARPQMYHQSG	RGKLGSLQAD	YDALGVQAE	VEFITDMVSA
251	YRDADLVICR	AGALTIAELT	AAGLGALLVP	YPHAVDDHQT	ANARFMVQAE
301	AGLLLPQTQL	TAEKLAEILG	GLNREKCLKW	AENARTLALP	HSADDVAEAA
351	IACAA*				

m087/a087 85.4% identity over a 355 aa overlap

	10	20	30	40	50	60
m087.pep	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVIWLGSKDSMEERIVPQYGIRLET LAI					
a087	MGGKTFMLMAGGTGGHIFPALAVADSLRARGHHVIWLGSKDSMEERIVPQYDILLET LAI					
	10	20	30	40	50	60

280

	70	80	90	100	110	120
m087.pep	KGVGRNGIKRKLMPLVTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLXVPIV					
a087	KGVGRNGIKRKLMPLFTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLGVPIV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m087.pep	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQGREG					
a087	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQGREG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m087.pep	RLKILVVGGSLGADVLNKTVPHALALLPDNARPHMYHQSGRGKLGILQAXXXXXXXXXXX					
a087	RLKILVVGGSLGADVLNKTVPQALALLPDNARPMYHQSGRGKLSLQADYDALGVQAEC					
	190	200	210	220	230	240
	250	260	270	280		
m087.pep	XX-----XXXXXXXXXAGLGALLVPYPHAVDDHQTANARFMVQAE					
a087	VEFITDMVSAYRDADLVICRAGALTIAELTAAGLGALLVPYPHAVDDHQTANARFMVQAE					
	250	260	270	280	290	300
	290	300	310	320	330	
m087.pep	AGLLLPQTQLTAEKLAELGGLNREKCLKWAENARTLALPHSADDDVAEAAIACAAX					
a087	AGLLLPQTQLTAEKLAELGGLNREKCLKWAENARTLALPHSADDDVAEAAIACAAX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 283>:

g088.seq

```

1  ATGTTTTTAT  GGCTCGCACA  TTTCAGCAAC  TGGTTAACCG  GTCTGAATAT
51  TTTTCAATAC  ACCACATTCC  GCGCCGTTAT  GGCGCGTTG  ACCGCCTTGG
101 CGTTTTCCCT  GATGTTCCGC  CCGTGGACGA  TACGCAGGCT  GACCGCGCTC
151 AAATGCGGGC  AGGCAGTGCG  TACCGACGGC  CCGCAAACCC  ACCTCGTCAA
201 AAACGGCACG  CCGACGATGG  GCGGTTTCGCT  GATTCTGACC  GCCATTACCG
251 TGTCCACCCT  GTTGTGGGGC  AACTGGGCGA  ACCCGTATAT  CTGGATTCTC
301 TTGGGCGTAC  TGCTTGCCAC  CGGTGCGCTC  GGTTTTTACG  ACGACTGGCG
351 CAAAGTCGTT  TATAAAGACC  CCAACGGCGT  GTCCGCCAAA  TTCAAAATGG
401 TGTGGCAGTC  AAGCGTTGCC  GTTatcgCG  GTttggcaTT  GTTTTACcTT
451 gCcgCAATT  CCGCCAACAA  TATTTTGATT  GTCCCGtttT  TCAACAAAT
501 CGCCCTGCCG  CTGGGCGTGG  TCGGCTTttt  gGtgttgTCT  TACCTGACCA
551 TCGTCGGCAC  ATCCAACGCC  GTCAACCTCA  CcgaCGGCTT  GGACGGCCCT
601 GCGCCTcttc  cgttcgctct  cgttgccgcC  GGGCTCGCCA  ttttcgccTA
651 CGTCAGCGGA  CACTACCAAT  TTTCCCAATA  CCTCCAGCTT  CCCTATGTCG
701 CCGGCGCGAA  CGAAGTCGCT  ATATTCTGCA  CCGCCATGTG  CGGCGCGTGC
751 CTCGGATTTT  TGTGGTTCAA  CGCCTATCCC  GCGCAAGTCT  TTATGGGCGA
801 TGTCGGCGCG  CTGGCATTGG  GTGCCGCGCT  CGGTaccGtt  gCCGTcaTcg
851 tCCGCCAAGA  ATTTGTcctc  gtcattaTGG  GCGGTCTGTT  cgtcgtagaa
901 gccgtgTCCG  TTATGCTTCa  tgtcggCTGG  TACAAGAAAA  Ccaaaaaacg
951 CATCTTcCTg  acgGcaccga  ttcacaccca  ttaCCAactt  cgatgCTGGa
1001 aagaaacgca  agtcgtcgct  CGTTtCTGGA  TTAtTaccat  cgtcgtgggt
1051 tTgatagggt  tGagtaccct  caAAattcgc  ggaaactatg  ccgTCCGAAC
1101 ACCTTTCAGA  CGGCATTGTA  ACGCGCAATA  A

```

This corresponds to the amino acid sequence <SEQ ID 284; ORF 088.ng>:

g088.pep

```

1  MFLWLAHFSN  WLTGLNIFQY  TTFRAVMAAL  TALAFSLMFG  PWTIRRLTAL
51  KCGQAVRTDG  PQTHLVKNGT  PTMGGSILIT  AITVSTLLWG  NWANPYIWL
101  LGVLLATGAL  GFYDDWRKVV  YKDPNGVSAK  FKMVWQSSVA  VIAGLALFYL
151  AANSANNILI  VPFQKIALP  LGVVGFVLVS  YLTIVGTSNA  VNLTDGLDGL

```

281

201 AAFPFVLVAA GLAIFAYVSG HYQFSQYLQL PYVAGANEVA IFCTAMCGAC
 251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGLFVVE
 301 AVSVMLHVGW YKKTKKRIFL TAPIHHHYQL RCWKETQVVV RFWIITIVVV
 351 LIGLSTLKIR GNYAVRTPFR RHLNAQ*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 285>:

m088.seq

1 ATGTTTTTAT GGCTCGCACA TTTCAGCAnC TGGTTAACCG GTCTGAATnn
 51 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 101 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 151 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 201 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 251 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 301 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 351 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 401 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 451 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
 501 nnnnnnnnnnnn nnnGGCGTGG TCGGCTTTTT GGTGTTGTCT TACCTGACCA
 551 TCGTCGGCAC ATCCAATGCC GTCAACCTCA CCGACGGCTT GGACGGCCTT
 601 GCGACCTTCC CCGTCGTCCT CGTTGCCGCC GGCCTCGCCA TCTTCGCCTA
 651 TGCCAGCGGC CACTCACAAAT TTGCCCAATA CCTGCAATTA CCTTACGTTG
 701 CCGGCGCAAA CGAAGTGGTG ATTTTCTGTA CCGCCATGTG CGGCGCGTGC
 751 CTCGGTTTCT TGTGGTTTAA CGCCTATCCC GCGCAAGTCT TTATGGGCGA
 801 TGTCGGTGCA TTGGCATTGG GTGCCGCGCT CGGTACCGTC GCCGTATCG
 851 TCCGCCAAGA GTTTGTCCTC GTCATTATGG GCGGATTATT TGTCGTAGAA
 901 GCCGTATCCG TTATGCTTCA GGTGCGCTGG TATAAGAAAA CCAAAAAACG
 951 CATCTTCCTG ATGGCGCCCA TCCATCACCA CTACGAACAA AAAGGCTGGA
 1001 AAGAAACCCA AGTCGTCGTC CGCTTTTGGG TTATTACCAT CGTCTTGGTG
 1051 TTGATCGGTT TGAGTACCCT CAAAATCCGC TGAACCTATG CCGTCTGAAC
 1101 ATCTTTCAGA CGGCATTGGA ACGCGCAATA A

1 MFLWLAHFSN WLTGLNIFOY TTFRAVMAAL TALAFSLMFG PWTIRRLTAL
 51 KCGQAVRTDG PQTHLVKNGT PTMGGSLILT AITVSTLLWG NWANPYIWIL
 101 LGVLLATGAL GFYDDWRKV YKDPNGVSAS FKMVWQSSVA VIAGLALFYL
 151 AANSANNILI VPFFKQIALP LGVVGFLVLS YLTIVGTSNA VNLTGDLGL
 201 AAFPFVLVAA GLAIFAYVSG HYQFSQYLQL PYVAGANEVA IFCTAMCGAC
 251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGLFVVE
 301 AVSVMLHVGW YKKTKKRIFL TAPIHHHYQL RCWKETQVVV RFWIITIVVV
 351 LIGLSTLKIR GNYAVRTPFR RHLNAQ*

This corresponds to the amino acid sequence <SEQ ID 286; ORF 088>:

m088.pep

1 MFLWLAHFSX WLTGLNXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
 51 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
 101 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
 151 XXXXXXXXXXX XXXXXXXXXXX XGVVGFLVLS YLTIVGTSNA VNLTGDLGL
 201 ATFPVVLVAA GLAIFAYASG HSQFAQYLQL PYVAGANEVV IFCTAMCGAC
 251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGLFVVE
 301 AVSVMLQVGW YKKTKKRIFL MAPIHHHYEQ KGWKETQVVV RFWIITIVLV
 351 LIGLSTLKIR XTYAVXTSFR RHLNAQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 088 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 088.ng) from *N. gonorrhoeae*:

m088/g088

m088.pep
 10 20 30
 GVVVGFLVLSYLTIVGTSNAVNLTGDLGLA
 |||||
 g088 IAGLALFYLAANSANNILIVPFFKQIALPLGVVGFLVLSYLTIVGTSNAVNLTGDLGLA
 150 160 170 180 190 200

	40	50	60	70	80	90
m088.pep	TFPVVLVAAGLAI FAYASGHSQFAQYLQLPYVAGANEVVI FCTAMCGACLGFLWFNAYPA					
	: : : :					
g088	AFPFLVAAGLAI FAYVSGHYQFSQYLQLPYVAGANEVAI FCTAMCGACLGFLWFNAYPA					
	210	220	230	240	250	260
	100	110	120	130	140	150
m088.pep	QVFMGDVGALALGAALGTVAIVIRQEFVLVIMGGLFVVEAVSVMLQVGWYKTKKRIFLM					
	:					
g088	QVFMGDVGALALGAALGTVAIVIRQEFVLVIMGGLFVVEAVSVMLHVGWYKTKKRIFLT					
	270	280	290	300	310	320
	160	170	180	190	200	
m088.pep	APIHHHYEQKGWKETQVVVRFWIIITIVLVLIGLSTLKI RXTYAVXTSFRRLNAQX					
	:					
g088	APIHHHYQLRCWKETQVVVRFWIIITIVVLIGLSTLKI RGNAYVRTPFRRLNAQX					
	330	340	350	360	370	

a088.seq	1	ATGTTTTTAT	GGCTCGCACA	TTTCAGCAAC	TGGTTAACCG	GTCTGAATAT
51	TTTTCAATAC	ACCACATTCC	GCGCCGTCAT	GGCGGCGTGT	ACCGCCTTGG	
101	CGTTTTCCCT	GATGTTCCGG	CCGTGGACGA	TACGCAAGCT	GACCGCGCTC	
151	AAATGCCGGC	AGGCAGTGCG	TACCGACGGT	CCGCAAACCC	ACCTCGTCAA	
201	AAACGGCACG	CCGACGATGG	GCGGTTGCT	GATTCTGACC	GCCATTACCG	
251	TGTCCACCTT	GTTGTGGGGC	AACTGGGCAA	ACCCGTATAT	CTGGATTCTC	
301	TTGGGCGTAT	TGCTCGCCAC	GGCGGCACCT	GGTTTTTACG	ACGACTGGCG	
351	CAAAGTCGT	TATAAAGACC	CCAACGGCGT	GTCCGCCAAA	TTCAAAATGG	
401	TGTGGCAGTC	AAGCGTTGCC	ATTATCGCCG	GTTTGGCATT	GTTTTACCTT	
451	GCCGCCAATT	CCGCCAACAA	TATTTTGATT	GTCCCGTTCT	TCAAACAAAT	
501	CGCCCTGCCG	CTGGGCGTGG	TCGGCTTTTT	GGTGTTGTCT	TACCTGACCA	
551	TCGTCGGCAC	ATCCAAATGCC	GTCAACCTCA	CCGACGGCTT	GGACGGCCTT	
601	GCGACCTTCC	CCGTCGTCTT	CGTTGCCGCC	GGCCTCGCCA	TCTTCGCCTA	
651	TGCCAGCGGC	CACCTACAAT	TTGCCCAATA	CCTGCAATTA	CCTTACGTTG	
701	CCGGCGCAAA	CGAAGTGGTG	ATTTTCTGTA	CCGCCATGTG	CGGCGCGTGC	
751	CTCGGTTTCT	TGTGGTTTTAG	CGCCTATCCC	GCGCAAGTCT	TTATGGGCAT	
801	TGTCGGTGCA	TTGCCATTGG	GTGCCGCGCT	CGGTACCGTC	GCCGTCATCG	
851	TTCCGCCAAG	TTTGTCTCTC	GTCATTATGG	CGGGATTATT	TGTCGTAGAA	
901	GCCGTATCCG	TTATGCTTCA	GGTCGGCTGG	TATAAGAAAA	CCAAAAAACG	
951	CATCTTCTTG	ATGGCGCCCA	TCCATCACCA	CTACGAACAA	AAAGGCTGGA	
1001	AAGAAACCCA	AGTCGTCTCT	CGCTTTTGGA	TTATTACCAT	CGTCTTGGTG	
1051	TTGATCGGTT	TGAGTAGCCCT	CAAAATCCGC	TGAACCTATG	CCGTCTGAAC	
1101	ACCTTTTGAGA	CGGCATTTGA	ACGCGCAATA	A		

a088.pep

1	MFLWLAHFSN	WLTGLNIFOY	<u>TTFR</u> AVMAAL	TALAFSLMFG	PWTIRRLTAL
51	KCGQAVRTDG	PQTHLVKNGT	PTMGGSILIT	AITVSTLLWG	NWANPYIWL
101	<u>LGVL</u> LATGAL	GFYDDLKRVV	YKDPNGVSAK	FKMVQSSWA	IIAGLALFYL
151	AANSANNILI	VPFFKQIALP	LGVVGFVLVS	YLTIVGTSNA	VNLTDLGLDGL
201	<u>ATFP</u> VVLVAA	GLAIFAYASG	HSQFAQYLQL	PYVAGANEVY	IFCTAMCGAC
251	<u>LGFL</u> WFNAYP	AQVFMGDVGA	LALGAALGTV	AVIVRQEFVL	VIMGGLFVVE
301	<u>AVSVM</u> LQVGW	YKTKTKKRIFL	MAPIHHHYEQ	KGWKETQVVV	REWIITIVLV
351	LIGLSTLKIR	*TYAV*TPFR	RHLNAQ*		

m088.pep XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXGVVGFLVLSYLTIVGTSNAVNLT DGLDGLA
|||||
a088 IAGLALFYLAANSANNILIVPFFKQIALPLGVVGFLVLSYLTIVGTSNAVNLT DGLDGLA

283

	150	160	170	180	190	200
	210	220	230	240	250	260
m088.pep	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVIFCTAMCGACLGLWFNAYPA					
a088	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVIFCTAMCGACLGLWFNAYPA					
	210	220	230	240	250	260
	270	280	290	300	310	320
m088.pep	QVFMGDVGALALGAALGTVAIVRQEFVLVIMGGFLVVEAVSVMLQVGWYKTKKRIFLM					
a088	QVFMGDVGALALGAALGTVAIVRQEFVLVIMGGFLVVEAVSVMLQVGWYKTKKRIFLM					
	270	280	290	300	310	320
	330	340	350	360	370	
m088.pep	APIHHHYEQKGWKETQVVVRFWIITIVLVLIGLSTLKIRXTYAVXTSFRRLNAQX					
a088	APIHHHYEQKGWKETQVVVRFWIITIVLVLIGLSTLKIRXTYAVXTSFRRLNAQX					
	330	340	350	360	370	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 289>:

```

g089.seq
1  ATGCCGCCCA AAATCACGAA GAGCGGGTTT TGCAAACCGG CAATCGCGGC
51  GGCAGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATG AATACCACGC
101 CGTTTTTCTC GCCGATTTT TCCACACGGT GCGGCAAGCC TTGGAAGGTT
151 TTGACGTGTT CCAGCAATGC TTCGCGCGGC AAACCGACGG CCTCGCACAA
201 AGCCACGGCA GCCATAACGT TGGCGGCGTT GTGCAAACCT TGCAGCGGGA
251 TGTCTTGCGT AGAAATCAAA TCTTCATTGC CTTGTTTAA ACAGCCCCTC
301 CCGCGTTCCA ACCAAAAATC GGCTTCGTGT TCCAAGGAAA ACCGTTTCAC
351 TTCACGCCCT GCCCGTTTCA TGGCGCGGCA GAACACGTCG TCCGCATTCA
401 AAACCTGCAC TCCATCGCCA CGGAAAATCT CGGCTTTGGT ATGCGCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 290; ORF 089.ng>:

```

g089.pep
1  MPPKITKSGF CKPAIAAAVA PTFVPLLSSM NTPFFSPIF STRCGKPWKV
51  LTCSSNASRG KPTASHKATA AITLAALCKP CSGMSCVEIK SSLPCFKQPV
101 PRSNQKSASC SKENRFTSRP ARFMARQNTS SAFKTCTPSP RKISALVCA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 291>:

```

m089.seq
1  ATGCCGCCCA AAATCACKAw GAGCGGATTT TGCAAACCGG CAATCGCGGC
51  GGCAGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATA AACACCACGC
101 CGTTTTTCTC GCCGATTTT TCCACGCGGT GCGGCAGGCC TTGGAAGGTT
151 TTGACGTGTT CGAGCAATGC TTCGCGCGAC AAACCGATGG CCTCACACAA
201 AGCCACKGCA GCCATGACGT TAGCGGCGTT GTGCAKACCT TGCAACGGwA
251 TGTCTTGCGT GACAATCAAA TCTTCATTGC CTTGTTTCAG GCGGCCTGTC
301 TCGCGTTCCA ACCAGAAATC AGCTTCGTGT TCCAACGAAA ACCATTTTAC
351 CTCGCGCCCG GCACGCTTCA TCGCGCGGCA GAACGCATCG TCCGCATTCA
401 AAACCTGCAC GCCGTCGCCA CGGAAAATCT TGGCTTTGGT ATGCGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 292; ORF 089>:

```

m089.pep
1  MPPKITXSGF CKPAIAAAVA PTFVPLLSSI NTPFFSPIF STRCGRPWKV
51  LTCSSNASRD KPMASHKATA AMTLAALCXP CNGMSCVTIK SSLPCFRPV
101 SRSNQKSASC SNENHFTSRP ARFIARQNAS SAFKTCTPSP RKILALVCA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 089 shows 88.6% identity over a 149 aa overlap with a predicted ORF (ORF 089.ng) from *N. gonorrhoeae*:

m089/g089

284

	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPT FVPLLSSINTTPFFSPIFSTRCGRPWKVLTCSSNASRD					
	: : : : :					
g089	MPPKITKSGFCKPAIAAAVAPT FVPLLSSMNTTPFFSPIFSTRCGRPWKVLTCSSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPCNGMSCVTIKSSLPCFRRPVSRNQKSASCSNENHFTSRP					
	: : : : : :					
g089	KPTASHKATAAITLAALCKPCSGMSCVEIKSSLPCFKQPVPRSNQKSASCSKENRFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	: : : : :					
g089	ARFMARQNTSSAFKTCTPSPRKISALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 293>:

a089.seq

1	ATGCCGCCTA	AAATCACGAA	GAGCGGATTT	TGCAAACCGG	CAATCGCGGC
51	GGCGGTGCGA	CCGACGTTCG	TGCCTTTGCT	GTCGTCGATG	AACACCACGC
101	CATTTTCTC	GCCGATTTT	TCCACGCGGT	GCGGCAGGCC	TTGAAAGGTT
151	TTGACGTGTT	CGAGCAATGC	TTCGCGCGGC	AAACCGACGG	CTTCGCACAA
201	GGCAACGGCA	GCCATCACGT	TAGTGGCGTT	GTGCAAGCCT	TGCAGCGGAA
251	TATCTTGCGT	GGCAATCAAA	TCTTCATTGC	CTTGTTTCAG	GCGACCTGTC
301	TCACGTTCCA	ACCAAAAATC	GGCTTCGTAT	TCCAACGAAA	ACCATTTCAC
351	CTCGCGCCCG	GCGCGCTTCA	TCGCACGACA	GAACGCATCG	TCCGCATTCA
401	AAACCTGCAC	ACCGTCGCCA	CGGAAAATCT	TGGCTTTGGT	ATGCGCGTAG

This corresponds to the amino acid sequence <SEQ ID 294; ORF 089.a>:

a089.pep

1	MPPKITKSGF	CKPAIAAAVA	PTFVPLLSSM	NTTPFFSPIF	STRCGRP*KV
51	LTCSSNASRG	KPTASHKATA	AITLVALCKP	CSGISCVAIK	SSLPCFRRPV
101	SRSNQKSASY	SNENHFTSRP	ARFIARQNAS	SAFKTCTPSP	RKILALVCA*

m089/a089 91.9% identity over a 149 aa overlap

	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPT FVPLLSSINTTPFFSPIFSTRCGRPWKVLTCSSNASRD					
	: : : : :					
a089	MPPKITKSGFCKPAIAAAVAPT FVPLLSSMNTTPFFSPIFSTRCGRPXKVLTCSSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPCNGMSCVTIKSSLPCFRRPVSRNQKSASCSNENHFTSRP					
	: : : : : :					
a089	KPTASHKATAAITLVALCKPCSGISCVAIKSSLPCFRRPVSRNQKSASYSNENHFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	: : : : :					
a089	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 295>:

g090.seq

1	ATGCGCGTAG	TCGAGCAAAT	CGTCGTAGCG	GTCGAGATGG	TCTTCGGAAA
---	------------	------------	------------	------------	------------

g090 . pep

m090.seq

m090 . pep

m090/g090

a090.seq

This corresponds to the amino acid sequence <SEQ ID 300; ORF 090.a>:

286

a090.pep

```

1 MRVVEQVVVA VEMVFGNVQH CRRSRAQAFG VFQLETGKLQ HPHVRLFAFA
51 LQFRLQNRRA DIARDNGIQP TLDAEIADQA RYRGFAVAAG NRNHLVAAAV
101 HNVRRQQFDVA QHAXRRFA*

```

m09/a090 91.5% identity over a 117 aa overlap

	10	20	30	40	50	60
m090.pep	MRIVEQVVVA	VEMVFGNVQH	RRRSRTQAF	GVFQLEAGKLQ	HPHVRLFAFA	LPFRLQNRRA
a090	MRVVEQVVVA	VEMVFGNVQH	CRRSRAQAF	GVFQLETGKLQ	HPHVRLFAFA	LQFRLQNRRA
	10	20	30	40	50	60

	70	80	90	100	110	119
m090.pep	DIARDNGIQP	ALDTEIADQ	ARYRGFAVA	AGNRNLYV	PAVHNVRR	QQFDVAQHAXRRFAX
a090	DIARDNGIQP	TLDAEIADQ	ARYRGFAVA	AGNRNHLV	AAAVHNVRR	QQFDVAQHAXRRFAX
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae*

g090-1.seq This sequence contains multiple stop codons (not shown)

This corresponds to the amino acid sequence < ORF 090-1.ng>:

g090-1.pep (not shown)

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2>:**m090-1.seq**

```

1 ATGACGGCGT TTGCATTTCA GACGGCATCA CAAAGCCTTA AACGCTTCGA
51 TAAACACTTC CGAACGGTGC GCGTAGCCTT TGAACATATC AAAGCTCGCG
101 CAGGCGGGGC TGAGCAACAC AATATCGCCT GCTTCGGCTT GGCATATGCG
151 CGTCTGAACG GCTTCTCCCA AAGTGGCGCA GTCGGTCATA TTCAAGCCGC
201 AGCCGTCCAA ATCGCGGCGG ATTTGCGGCG CATCGACACC AATCAAGAAC
251 ACGCCTTTTG CTTGCTTAC CAGTGCATCG CGCAGGGGCG TGAAGTCCTG
301 CCCTTTACCC ATGCGGCCCA AAATCACGAA GAGCGGATT TGCAAACCGG
351 CAATCGCGGC GGCAGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATA
401 AACACCACGC CGTTTTCTC GCCGATTTT TCCACGCGGT GCGGCAGGCC
451 TTGGAAGGTT TTGACGTGTT CGAGCAATGC TTCGCGCGAC AAACCGATGG
501 CCTCACACAA AGCCACGGCA GCCATGACGT TAGCGGCGTT GTGCAGACCT
551 TGCAACGGAA TGTCTTGCGT GACAATCAAA TCTTCATTGC CTGTTTCAG
601 GCGGCCTGTC TCGCGTTCCA ACCAGAAATC AGCTTCGTGT TCCAACGAAA
651 ACCATTTTAC CTCGCGCCCG GCACGCTTCA TCGCGCGGCA GAACGCATCG
701 TCCGCATTCA AAACCTGCAC GCCGTCGCCA CGGAAAATCT TGCTTTGGT
751 ATCGCGCATG TCGAGCAAGT CGTCGTAGCG GTCGAGATGG TCTTCGGA
801 TGTTCAGCAC CGTCGCCGCA GTCGGACGCA GGCTTTCGTT GTTTCCAGT
851 TGGAAGCTGG AAAGCTCCAA CACCCACACG TCCGCCTTTT TGCCTTCGCG
901 CTGCCATTCC GCCTCCAAA CCGGCGTGCC GATATTGCC GCGATAACGG
951 TATCCAGCCC GCACTTGATA CAGAGATAGC CGACCAGGCT CGTTACCGTG
1001 GTTTTGCCGT TGCTGCCGGT AATCGCAATT ACCTGTGCT CCCGCGGTT
1051 CACAATGTCC GCCAGCAATT CGATGTCGCC CAACACGCGT CCGCCGTTT
1101 GCTTGAACGC CTCAATATCC GGCTGCCGCT CGCTGATGCC GGGACTGAGA
1151 GCCAGAATAT CGAAACCGTT GTCCAGCGCA TCTTTCAGAC GGCCCGTGTA
1201 AAACACCAAC CCGTCAAACA TCTTACCGAT TTGCGACACG CGTTCCGGCT
1251 TCAGCTCCGC ATCATACGCA GCAACCTCCG CGCCGTTTTT GCGCAGGTAG
1301 GCAATCATGG AAATACCCGT ACCGCCGAGT CCGCGCACGA GGATTTTTTT
1351 GTTTTGAAAA GTCATTTTGG TTTGTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 3; ORF 090-1>:

m090-1.pep

```

1 MTAFAFQTAS QSLKRFDKHF RTVRVAFEDI KARAGGAEQH NIACFGLGIC
51 RLNGFSQSGA VGHQAQAAVQ IAADLRRIDT NQEHAFCLAY QCIAQGREVL
101 PFTHAAQNH ERLQTDGNRG GSRADIRAF VVDKHHAVEL ADFFHAVRQA
151 LEGFDVFQEC FARQTDGLTQ SHGSHDVSGV VQTLQRNVLR DNQIFIALFO
201 AACLAFOPEI SFVFORKPFY LAPGTLHRAA ERIVRIQNLH AVATENLGFG
251 MRIVEQVVVA VEMVFGNVQH RRRSRTQAFG VFQLEAGKLQ HPHVRLFAFA
301 LPFRLQNRRA DIARDNGIQP ALDTEIADQA RYRGFAVAAG NRNLYVPAV
351 HNVRRQQFDVA QHASAVLLER LNIRLPLADA GTESQNIETV VQRIFQTAHV
401 KHQPVKHLTD LRHAFRLQLR IIRSNLRAVE AQVGNHGNTR TAESGDEDF
451 VLKSHFGLS*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 303>:

g091.seq

```

1  ATGGAATAC CCGTGCCGCC AAGTCCGGCG ACGAGGATTT TTTGTTTGA
51  AAGTCATTTT GGTTTTGTCC TAAAACAAAT CATATTGGGC AGGAGACGTC
101 CGCCCTTGCC CAAGCCGCTT TCAGACGGCA TCGCGAGCCG ATTAATAACC
151 CGCCTTCAGG CGTTGGTCAT TGTCGCAGCT GTTTGGTCT CCGTTTGTAC
201 AAGCCTTGCC AAGCCATTGT TGAGCGAGCG CAAGGTCTTG GCGCACGCCG
251 CGTCCATCGT AATACATCAA GCCCAAATTG TATTGGGCTT GGGCATCCCC
301 TTGTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 304; ORF 091.ng>:

g091.pep

```

1  MEIPVPPSPA TRIFLFESHF GFVLKQIILG RRRPPLPKPL SDGIASRLIT
51  RLQALVIVAA VLVSVLTSLA KPILLSERKVL AHAASIVIHQ AQIVLGLGIP
101  LF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 305>:

m091.seq

```

1  ATGGAATAC CCGTACCGCC GAGTCCGGCG ACGAGGATTT TTTGTTTGA
51  AAAGTCATTT TGGTTTGTCC TAAAACAAAT CATATTGAGC AGGAGATGTC
101 CGCCCTTGCC CAAGCCGCTT TCAGACGGCA TCGCGAGCTG TTCAATAACC
151 CGCCTTCAGG CGTTGGTCAT TGTCGCAGCC GTCTTGGTCT CCGTTTGTAC
201 AAGCCTTGCC AAACCATCTT TGTGCAAGGG CGCGGTCTTG GCGCACGCCG
251 CGTCTTTCGG CATACATCAC GCCCAAATTG TTTTGGGCTT GGGCTACCCC
301 CTGCGC...

```

This corresponds to the amino acid sequence <SEQ ID 306; ORF 091>:

m091.pep

```

1  MEIPVPPSPA TRIFLFEKSF WFLVKQIILS RRCPPPLPKPL SDGIASCSIT
51  RLQALVIVAA VLVSVLTSLA KPFLCKGAVL AHAASFGIHH AQIVLGLGYPLR
101  LR.

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 091 shows 84.2% identity over a 101 aa overlap with a predicted ORF (ORF 091.ng) from *N. gonorrhoeae*:

m091/g091

	10	20	30	40	50	60
m091.pep	MEIPVPPSPATRIFLFEKSFVFLVKQIILSRRCPPPLPKPLSDGIASCSITRLQALVIVAA					
	: :					
g091	MEIPVPPSPATRIFLFESHFGFVLVKQIILGRRPPPLPKPLSDGIASRLITRLQALVIVAA					
	10	20	30	40	50	60
	70	80	90	100		
m091.pep	VLVSVLTSLAKPFLCKGAVLAHAASFGIHHQAQIVLGLGYPLR					
	: : : :					
g091	VLVSVLTSLAKPILLSERKVLHAASIVIHQAQIVLGLGIPLEX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 307>:

a091.seq

```

1  ATGGAATAC CCGTGCCGCC AAGTCCGGCG ACGAGGATTT TTTGTTTGA
51  GAAATCATTT TGGTTTGTCC TAAAACAAAT CATATTGAGC AGGGGATGTC
101 TGATCCTGCT CAAGCCGCTT TCAGACGGCA TCGCGAGCTG TTCAATAACC
151 CGCTTTCAGG CGTTGGTCAT TGTCGCAGCT GTCTTGGTAT CCGTTTGTAC
201 AAGCCTTGCC AAGCCATTCT TGTGCAAGGG CGCGGTCTTG GCGCACGCCG
251 CGTCTTTCGG CATACATCAC GCCCAAATTG TTTTGGGC

```

This corresponds to the amino acid sequence <SEQ ID 308; ORF 091.a>:

a091.pep

```

1  MEIPVPPSPA TRIFLFWKSF WFLVKQIILS RGCLILLKPL SDGIASCSIT
51 RFQALVIVAA VLVSVLTSLA KPFLCKGAVL AHAASFGIHH AQIVLG

```

m091/a091 93.8% identity over a 96 aa overlap

	10	20	30	40	50	60
m091.pep	MEIPVPPSPATRI	FLFEKSFVFLVKQIILS	RRCPLPKPLSDGIASCSIT	RLQALVIVAA		
a091	MEIPVPPSPATRI	FLFEKSFVFLVKQIILS	RGCLILLKPLSDGIASCSIT	RFQALVIVAA		
	10	20	30	40	50	60
	70	80	90	100		
m091.pep	VLVSVLTSLAKPFLCKGAVL	AHAASFGIHH	AQIVLGLGYPLR			
a091	VLVSVLTSLAKPFLCKGAVL	AHAASFGIHH	AQIVLG			
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 309>:

g092.seq

```

1  ATGTTTTTTTA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGTGCGC
51  AAACGGTCAG ACCTTTAAAA TAACGCCTTT ACGCACTAAA AACCAACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTAA GCAACATCCA TTTTGTCGGT
151 ATCGGCGGCG TCGGCATGAG CGGTATCGCC GAAGTCTTGC ACAATTTGGG
201 CTTTAAAGTT TCCGGTTCCG ATCAGGCGCG AAATGCCGCT ACCGAGCATT
251 TGAGCAGCCT GGCATTCAA GTTATCCCG GCCATACCGC AGAACACGTT
301 AACGGTgcgg ATGTCGTCGT TGCTCTACC GCCGTCAAGA AAGAAaatcC
351 CGAAGTtgtc gcTGCgTTGG AGCGGCAAAT TCCCGTTATT CCGCGCGCCT
401 TGATGCTGGC AGAGCTGATG CGCTTCCGTG ACGGcatcgc cattgccggT
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTC GACCCCACTT TCGTTATCGG CGGCAAACTC AACGCCGCAG
551 GCACCAACGC CCGCTTGGGC AAAGCGGAAT ACATCGTTGC CGAAGCCGAC
601 GAATCCGATG CCTCTTTCCT ACATCTGACC CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGC GTCGAAAAAC
701 TGCATCAGGC GTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTTGT GTGTTGACAG CGAACACGTC CGCGCGATTT TGCCCAAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCAAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGc gtggcGCTgg
1001 aagtcGgCGC ATcggttgAA GCGAtcCAAA AaggCTTGCT CGGCTTTGAA
1051 GGCGTCGGCC GCGCTTCCA AAAATAcggc gacatCAagt tgccaaacgg
1101 cggGaccgCT TTgctGGTGG ACGATTAcgg ACACCACCCC GTCGAAATGG
1151 CGGcaaccct tgccgcTGCA CGCGGCGCGT ATCCGAAAAA acgtTTGGTG
1201 CtcgCCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTACTCAATA CCGTTGatgC GCTGGTACTG ACCGAAGTTT
1301 AtgccgcccG CGAAGAGCCG GTTGCCGCCG CCGactcCCG CGCCTTGGCG
1351 CGTGCTATCC GCGTATTGGG CAACTTGAG CCGATTACT GCGAAAtgt
1401 cgccgACCTG CCGCAATGC TGATGAATGT TTTACAGGAT Ggcgatgttg
1451 tgttgAATAT GggTgcggga agcatcaacc gcgttccttc cgcgctgttg
1501 gaattgtcga AACAGAtttg A

```

This corresponds to the amino acid sequence <SEQ ID 310; ORF 092.ng>:

g092.pep

```

1  MFFISIRYIF VRKLWCANGQ TFKITPLRTK NQPERNIMMK NRVSNIHFVG
51  IGGVGMMSGIA EVLHNLGFKV SGSDQARNAA TEHLSSLGIQ VYPGHATAEHV
101 NGADV VVAST AVKKENPEVV AALERQIPVI PRALMLAELM RFRDGI A IAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK

```

```

251 AFLCVDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEV GASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP VAAADSRALA
451 RAIRVLGKLE PIYCENVADL PQMLMNVLQD GDVVLNMGAG SINRVPSALL
501 ELSKQI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 311>:

```

m092.seq
1 ATGTTTTTTT TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGCGCGC
51 AACCGGTCAG CCCTTTAAAA TAACGCCTTT ACGCATCGAA AATCCACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTTA CCAACATCCA TTTTGTCTGGT
151 ATCGGCGGCG TCGGCATGAG CGGCATCGCC GAAGTCTTGC ACAATTTGGG
201 CTTTAAAGTT TCCGGTTCGG ATCAGGCGCG AAATGCCGCT ACCGAGCATT
251 TGGGCAGCCT GGGCATTCAA GTTTATCCCG GCCATACCGC CGAACACGTT
301 AACGGTGCGG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCGTG ACGGCATCGC CATTGCCGGC
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAATC AACGCCGCAG
551 GACTAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGC GTCGAAAAAC
701 TGATCAGGC GTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTTGT GTATTGACAG CGAACACGTC CGCGCGATT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGG CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCAAAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATGCGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GCGCTCGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 CGGGACCGCG CTCTTGGTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CGGCGACCTT TGCCGCCGCA CGCGCGCGT ATCTGGAAAA ACGTTTGGTA
1201 CTCGCCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTCCTCAATA CCGTTGACGC GCTGGTGCTG ACCGAAGTTT
1301 ATGCCGCCGG TGAAGAGCCG ATTGCCGCCG CCGATTCCCG CGCTCTTGCC
1351 CGCGCCATCC GCGTGTGGG CAAACTCGAG CCGATTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTGAAACGT TTTGCAGGAC GCGACATCG
1451 TGTTGAATAT GGGCGCGGGA AGCATCAACC GCGTCCCCGC CGCGCTGCTG
1501 GCATTGTCGA AACAGATTTG A

```

This corresponds to the amino acid sequence <SEQ ID 312; ORF 092>:

```

m092.pep
1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVTNIHFGV
51 IGGVGMGSGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKENPEVV AALEQQIPVI PRALMLAELM RFRDGLAIAIAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEV GASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYLEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP IAAADSRALA
451 RAIRVLGKLE PIYCENVADL PEMLLNVLQD GDIVLNMAG SINRVPAALL
501 ALSKQI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 092 shows 96.6% identity over a 506 aa overlap with a predicted ORF (ORF 092.ng) from *N. gonorrhoeae*:

```

m092/g092
10 20 30 40 50 60
m092.pep MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFGVIGGVGMGSGIA

```

a092.seq

1	ATGTTTTTTTA	TTTCAATCCG	CTATATATTT	GTCAGAAAAC	TATGGCGCGC
51	AAACGGTCAG	CCCTTTAAAA	TAACGCCTTT	ACGCATCGAA	AATCCACCGG
101	AACGCAACAT	TATGATGAAA	AATCGAGTGA	CCAACATCCA	TTTGTCGGT
151	ATCGGCGGGC	TCGGCATGAG	CGGTATCCGC	GAAGTCTTGC	ACAATTTGGG
201	TTTTAAAGTT	TCGGTTCCGG	ATCAGGCGCG	AAATGCCGTG	ACCGAGCATT
251	TGGGCAGCCT	GGGCATTCAA	GTTTATCCCG	GCCATACCGC	AGAACACGTT

```

301 AACGGTGCGG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCGTG ACGGCATCGC CATTGCCGGC
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAACTC AACGCCGCAG
551 GCACCAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGT GTTGAGAAGC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTTGT GTATTGACAG CGAACACGTC CGCGCGATT TGGCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGG CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCGAAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GGTGTCGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 TGAACCGCG CTCTTGGTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CGCGACCCCT TTCCGCCGCA CGCGGCGCGT ATCCGGAAAA ACGTTTGGTGTA
1201 CTCGCCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTCCTCAATA CCGTTGACGC GCTGGTGCTG ACCGAAGTTT
1301 ATGCCGCCGG TGAAGAGCCG ATTGCCGCCG CTGATTCCCG CGCTCTTGCC
1351 CGCGCCATCC GCGTGTTGGG CAAACTCGAG CCGATTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTTGAACGT TTTGCAGGAC GGCGACATCG
1451 TGTTGAATAT GGGTGCGGGA AGCATCAACC GCGTCCCGC CGCGCTGCTG
1501 GAATTGTCGA AACAGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 314; ORF 092.a>:

a092.pep

```

1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVTNIHFGV
51 IGGVGMMSGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKENPEVV AALEQQIPVI PRALMLAELM RFRDGIATAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEV GASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPLNGGTA LLVDDYGHHP VEMAATLSAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP IAAADSRALA
451 RAIRVLGKLE PIYCENVADL PEMLLNVLQD GDIVLNMGAG SINRVPAALL
501 ELSKQI*

```

m092/a092 99.4% identity over a 506 aa overlap

	10	20	30	40	50	60
m092.pep	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFGVIGGVGMMSGIA					
a092	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFGVIGGVGMMSGIA					
	10	20	30	40	50	60
m092.pep	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNAGADVVTSTAVKKENPEVV					
a092	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNAGADVVTSTAVKKENPEVV					
	70	80	90	100	110	120
m092.pep	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNAGADVVTSTAVKKENPEVV					
a092	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNAGADVVTSTAVKKENPEVV					
	130	140	150	160	170	180
m092.pep	AALEQQIPVIPRALMLAELMRFRDGIATAGTHGKTTTTSLTASILGAAGLDPTFVIGGKL					
a092	AALEQQIPVIPRALMLAELMRFRDGIATAGTHGKTTTTSLTASILGAAGLDPTFVIGGKL					
	190	200	210	220	230	240
m092.pep	NAAGTNARLGKGEYIVAEADESDASFLHLPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
a092	NAAGTNARLGKGEYIVAEADESDASFLHLPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					

292

	190	200	210	220	230	240
	250	260	270	280	290	300
m092.pep	FIHRMPFYGKAFLCIDSEHVRAILPKVSKPYATYGLDDTADIYATDIENVGAQMKFTVHV					
a092	FIHRMPFYGKAFLCIDSEHVRAILPKVSKPYATYGLDDTADIYATDIENVGAQMKFTVHV					
	310	320	330	340	350	360
m092.pep	QMKGHEQGSFEVVLNMPGRHNVNLAAIGVALEV GASVEAIQKGLLGFEVGRRFQKYG					
a092	QMKGHEQGSFEVVLNMPGRHNVNLAAIGVALEV GASVEAIQKGLLGFEVGRRFQKYG					
	370	380	390	400	410	420
m092.pep	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYLEKRLVLAQPHRYTRTRDLFEDFTK					
a092	DIKLPNGGTALLVDDYGHHPVEMAATLSAARGAYPEKRLVLAQPHRYTRTRDLFEDFTK					
	430	440	450	460	470	480
m092.pep	VLNTVDALVLTEVYAAGEEPIAAADSRALARAIRVLGKLEPIYCENVADLPEMLLNVLQD					
a092	VLNTVDALVLTEVYAAGEEPIAAADSRALARAIRVLGKLEPIYCENVADLPEMLLNVLQD					
	490	500				
m092.pep	GDIVLNMGAGSINRVPAALLALSQIX					
a092	GDIVLNMGAGSINRVPAALLELSQIX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 315>:

```

g093.seq
1  aTGCAGAAAtt ttgGCAAAGT ggccgtATTG ATGGGtggtT TTTCCAGCGA
51  ACGAGAAatc tcgcTGGACA GCgGTACCGC CATTTTGAAC GCCTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGACC CTAAGGAAAC GCCGTTATCC
151 GAACTGAAGG AGCGGGGCTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGCGGAA GACGGGGCTG TTCAGGGTGC ATTGGAAGTGTG TGGGGCATTC
251 CCTATACCGG CAGCGGTGTC GCCGCCTCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTTGGCA GGCATTGGGA TTACCCGTTT CCGAGTTCGC
351 CGTACTGTAC GATGATACCG ATTTTCGATGC CGTCGAAGAA AAATTGGGTC
401 TGCCGATGTT TGTGAAGCCG GCGGCCGAAG GCAGCAGCgt cggcgtggtta
451 aAAGTCAAAG AAAaaggccg TCTGAAAAGC GTTtacgaag aatTGAAaCA
501 CCTTcagggg cgaAAtcatt gccgAacgTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACGG CAAAGGGCTG CCCGGCATA ACATCATCCC
601 CGCAACCGAG TTTTACGAct acgaagccaa GtacaaCCGA GACGAcacca
651 tttatCAATG TCCTTCGGAA GATTTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTCGCGG CGCACAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 316; ORF 093.ng>:

```

g093.pep
1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKERGFQTA FNILHGTYGE DGAVQGALEL LGIPYTGSCV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLY DDTDFDAVEE KLGLPMFVKP AAEGSSVGVV
151 KVKEKGR LKS VYEELKHLQG RNHCRTFYRR RRIFLPRPER QRAARHTHHP
201 RNRVLR LRSQ VQPRRHLSM SFGRFDRSRR KPDARTGGS RTGNRCGR LR
251 ARFPQRYRR QTLVGNQHP ARYDRP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 317>:

m093.seq


```

1  ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CTAAAGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCrAA GACGGGGCGG TTCAGGTGC ATTGGAAGT TTGGGCATTTC
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGCGCA GGCATTGGGA TTGCCCCTTC CCGAGTTCGC
351 CGTCCTGCAC GACGACACTG ATTTTCGATC CGTCGAAGAA AAATTGGGCC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGCTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTTACGAAG AATTGAAACA
501 CCTTCAGG. CGAAATCATT GCCGAACGTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACGG CAAAGGGCTG CCCGGCATAC ACATCATTCC
601 CGCAACCGAG TTTTACGACT ACGAAGCCAA GTACAACCGC GACGACACCA
651 TTTATCAATG TCCTTCGGAA GATTTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAAGTGG CGGTTTCGCG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACGAGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 318; ORF 093>:

```

m093.pep
1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGX DGAVQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AAEGSSVGUV
151 KVKGKGR LKS VYEELKHLQX RNHCRTFYRR RRIFLPRPER QRAARHTHS
201 RNRVLR LRSQ VQPRRHLSM SFGRFDRSRR KPDARTGGSR RAGNRCGRLR
251 ARRFQRYRR QTLVGNQHP ARYDEP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 093 shows 96.7% identity over a 276 aa overlap with a predicted ORF (ORF 093.ng) from *N. gonorrhoeae*:

m093/g093

	10	20	30	40	50	60
m093.pep	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPL SELKAQGFQTA					
g093	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPL SELKERGFQTA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m093.pep	FNILHGTYGX DGAVQGALEL LGIPYTGSGV AASAIGMDKY RCKLIWQAL GLPVPEFAVLH					
g093	FNILHGTYGEDGAVQGALEL LGIPYTGSGV AASAIGMDKY RCKLIWQAL GLPVPEFAVLY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m093.pep	DDTDFDAVEE KLGLPMFVKP AAEGSSVGUV KVKGKGR LKSVYEELKHLQX RNHCRTFYRR					
g093	DDTDFDAVEE KLGLPMFVKP AAEGSSVGUV KVEKGR LKSVYEELKHLQGR RNHCRTFYRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m093.pep	RRIFLPRPER QRAARHTHS RNRVLR LRSQVQPRRHLSM SFGRFDRSRR KPDARTGGSR					
g093	RRIFLPRPER QRAARHTH PNRVLR LRSQVQPRRHLSM SFGRFDRSRR KPDARTGGSR					
	190	200	210	220	230	240
	250	260	270			
m093.pep	RAGNRCGRLR ARRFQRYRR QTLVGNQHP ARYDEPX					
	:					
g093	RTGNRCGRLR ARRFQRYRR QTLVGNQHP ARYDRPX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 319>:

a093.seq

```

1  ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CCAAGGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCGAA GACGGGGCTG TTCAGGGTGC ATTGGAACG TTGGGCATTG
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGGCA GGCATTGGGA TTGCCCGTTC CCGAGTTCGC
351 CGTCCTGCAC GACGACACTG ATTTTCGATG CGTCGAAGAA AAATTGGGCC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGGTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTTACGAAG AATTGAAACA
501 CTTTCAGGG. CGAAATCATT GCCGAACGGT TTATCGGCGG CCGCGAATAT
551 TCCTGCCCTG TGTTGAACGG CAAAGGCCTG CCCGGCATA ACATCATCCC
601 CGCGACCGAG TTTTATGACT ACGAAGCCAA GTACAACCGC AACGACACCA
651 TTTATCAATG TCCTTCGGAA GATCTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTGCGCG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCTCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 320; ORF 093.a>:

a093.pep

```

1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGE DGA VQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AEGSSVGVV
151 KVKGKGR LKS VYEELKHFQX RNHCRTVYRR RRIFLPCVER QPARHTHHP
201 RDRVL* LRSQ VQPQRHLSM SFGSRDSR SR KPDARTGGS RAGNRCGR LR
251 ARRFPPQRYRR QTL SVGNQHP ARYDRP*

```

m093/a093 95.7% identity over a 276 aa overlap

	10	20	30	40	50	60
m093.pep	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLSELKAQGFQTA					
a093	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLSELKAQGFQTA					
	10	20	30	40	50	60
m093.pep	FNILHGTYGDGAVQGALELLGIPYTGSGVAASAIGMDKYRCKLIWQALGLPVPEFAVLH					
a093	FNILHGTYGEDGAVQGALELLGIPYTGSGVAASAIGMDKYRCKLIWQALGLPVPEFAVLH					
	70	80	90	100	110	120
m093.pep	DDTDFDAVEEKLGLPMFVKPAAEGSSVGVV KVKGKGR LKS VYEELKHLQXRNHCRTFYRR					
a093	DDTDFDAVEEKLGLPMFVKPAAEGSSVGVV KVKGKGR LKS VYEELKHFQXRNHCRTVYRR					
	130	140	150	160	170	180
m093.pep	RRIFLPRPERQRAARHTHHSRNRVLR LRSQVQPRRHLSMSFGRFDRSR RKP DARTGGS R					
a093	RRIFLPCVERQPARHTHHPDRVLXLRSQVQPQRHLSMSFGRSDRSR RKP DARTGGS R					
	190	200	210	220	230	240
m093.pep	RAGNRCGR LRARRFPQRYRRQTL SVGNQHPARYDEPX					
a093	RAGNRCGR LRARRFPQRYRRQTL SVGNQHPARYDRPX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 321>:

```
g094.seq
  1  ATGTATTTCGC CTTTGCCCAA GCGGGCGTTG GTGCCTGCGG CGTTGAGTTT
 51  GCCGCCGATA ACGAAAGTGG GGTGAGTCC TGCCGCGCCG AGGATGGAGG
101  CGGTCAGGCT GGTGGTCGTG GTTTTGCCGT GCGTAccggc aatggcgatg
151  cCGTCACGGA AGCGCATCAG CTCTGCCAGC ATCAAGGCGC GCGGAATAAC
201  GGGAAATTTGC CGCTCCAACG CAgcgacaAC TTCGGgattT TCTTTCTTGA
251  CGGCGGTAGA GGCAACGACG ACATccgcAC CGTTAACGTG TTCTGCGGTA
301  TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 322; ORF 094.ng>:

```
g094.pep
  1  MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
 51  PSRKRISAS IKARGITGIC RSNAATTSGF SFLTAVEATT TSAPLTCSAV
101  WPG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 323>:

```
m094.seq
  1  ATGTATTTCGC CTTTGCCCAA GCGGGCGTTA GTGCCTGCGG CGTTGAGTTT
 51  GCCGCCGATA ACGAAAGTCG GGTCAAGTCC TGCCGCGCCG AGGATGGAGG
101  CGGTCAGGCT GGTGGTCGTG GTTTTGCCGT GCGTGCCGGC AATGGCGATG
151  CCGTCACGGA AGCGCATCAA CTCCGCCAAC ATCAGGGCGC GCGGAATAAC
201  GGGAAATTTGC TGCTCCAACG CAGCGACAAC TTCGGGATTT TCTTTTTTGA
251  CGGCGGTAGA GGTAACGACG ACATCCGCAC CGTTAACGTG TTCGGCGGTA
301  TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 324; ORF 094>:

```
m094.pep
  1  MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
 51  PSRKRINSAN IRARGITGIC CSNAATTSGF SFLTAVEVTT TSAPLTCSAV
101  WPG*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 094 shows 95.1% identity over a 103 aa overlap with a predicted ORF (ORF 094.ng) from *N. gonorrhoeae*:

```
m094/g094

      10      20      30      40      50      60
m094.pep  MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKRINSAN
          |||||||||||||||
g094      MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKRISAS
          10      20      30      40      50      60

      70      80      90     100
m094.pep  IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX
          |:|||||||
g094      IKARGITGICRSNAATTSGFSFLTAVEATTTSAPLTCSAVWPGX
          70      80      90     100
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 325>:

```
a094.seq
  1  ATGTATTTCGC CTTTGCCCAA GCGGGCGTTG GTGCCTGCGG CGTTGAGTTT
 51  GCCGCCGATA ACGAAAGTGG GGTCAAGTCC TGCCGCGCCG AGGATGGAGG
101  CGGTCAGGCT GGTGGTCGTG GTTTTGCCGT GCGTGCCGGC AATGGCGATG
151  CCGTCACGGA AGCGCATCAA CTCCGCCAAC ATCAGGGCGC GCGGAATAAC
201  GGGAAATTTGC TGCTCCAACG CAGCGACAAC TTCGGGATTT TCTTTTTTGA
251  CGGCGGTAGA GGTAACGACG ACATCCGCAC CGTTAACGTG TTCTGCGGTA
301  TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 326; ORF 094.a>:

a094.pep

```

1  MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
51  PSRKRINSAN IRARGITGIC CSNAATTSGF SFLTAVEVTT TSAPLTCSAV
101 WPG*

```

m094/a094 100.0% identity over a 103 aa overlap

```

              10      20      30      40      50      60
m094.pep      MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKRINSAN
              |||
a094           MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKRINSAN
              10      20      30      40      50      60

              70      80      90     100
m094.pep      IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX
              |||
a094           IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX
              70      80      90     100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 327>:

```

g095.seq
1  ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCAATTGC GCGCCGACGT
51  TTTGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
101 GCATAAGGTT TGCTCACTTT GGGCAAATC GCGCGGACGT GTTCGCTGTC
151 AACACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
201 TAAACGCCTG ATGCAGTTT TCGACGCTGT GCGCGTAGGT ATCCATATGG
251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGGGTCA GTGTAGGAAA
301 GAGGCATCGG ATCGTCGGCT TCGGCAACGA TGTATTCGCC TTTGCCCAAG
351 CGGGCGTTGG TGCCTGCGGC GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 328; ORF 095.ng>:

```

g095.pep
1  MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
51  NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRGQCRK
101 EASDRRLRQR CIRLCPSGRW CLRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 329>:

```

m095.seq
1  ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCAATTGC GCGCCGACGT
51  TTTGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
101 GCATAAGGTT TGCTCACTTT GGGCAAATC GCGCGGACGT GTTCGCTGTC
151 AATACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
201 TAAACGCCTG ATGCAGTTT TCGACGCTGT GCGCGTAGGT ATCCATATGG
251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGTGTCA GTGCAGAAAG
301 GATGCATCCG ACCGTCGGCT TCGGCAACGA TGTATTCGCC TTTGCCCAAG
351 CGGGCGTTAG TGCCTGCGGC GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 330; ORF 095>:

```

m095.pep
1  MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
51  NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRGQCRK
101 DASDRRLRQR CIRLCPSGRX CLRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 095 shows 97.6% identity over a 124 aa overlap with a predicted ORF (ORF 095.ng) from *N. gonorrhoeae*:

```

m095/g095
              10      20      30      40      50      60
m095.pep      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
              |||

```

297

```

g095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60
           70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
           |||||
g095      HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKEASDRRLRQRCIRLCPSGRW
           70      80      90      100     110     120

m095.pep  CLRRX
           ||||
g095      CLRRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 331>:

```

a095.seq
  1  ATGTCCTTTC  ATTTGAACAT  GGACGGTGAA  TTTCATTTGC  GCGCCGACGT
 51  TTTTCGATGTC  GGTGGCGTAG  ATGTCGGCGG  TATCGTCCAA  ACCGTAAGTA
101  GCATAAGGTT  TGCTCACTTT  GGGCAAAATC  GCGCGGACGT  GTTCGCTGTC
151  AATACACAAA  AAGGCTTTGC  CGTAGAAGGG  CATACGGTGG  ATGAAATCGA
201  TAAACGCCTG  ATGCAGCTTC  TCAACACTGT  GCCCGTAGGT  ATCCATATGG
251  TCTTCGTCGA  TATTGGTAAC  GACGGACATA  ATCGGTGTCA  GTGCAGAAAG
301  GATGCATCCG  ACCGTCGGCT  TCGGCAACGA  TGTATTGCGC  TTTGCCCAAG
351  CGGGCGTTGG  TGCCTGCGGC  GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 332; ORF 095.a>:

```

a095.pep
  1  MSFHLNMDGE  FHLRADVFDV  GGVDVGGIVQ  TVSSIRFAHF  GQNRADVFAV
 51  NTQKGFAVEG  HTVDEIDKRL  MQLLNTVPVG  IHMFVDIGN  DGHNRQCQRK
101  DASDRRLRQR  CIRLCPSGRW  CLRR*

m095/a095  96.0% identity in 124 aa overlap

           10      20      30      40      50      60
m095.pep  MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           |||||
a095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60
           70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
           |||||
a095      HTVDEIDKRLMQLLNTVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRW
           70      80      90      100     110     120

m095.pep  CLRRX
           ||||
a095      CLRRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 333>:

```

g096.seq
  1  ATGGCCGGTC  ATACCGGGCA  GGGTGTGAT  TTCCAACAGA  TAGAGTTTGC
 51  CGTCGGTATC  TTTGAGGAAA  TCGACGCGCA  CGCAGCCTTC  CGCACCATT
101  GCCTGTGCGC  CGCGAACCGC  CAGTTCGCGC  ATCAGGCTTT  CTTCGGCTTC
151  GGTCAAATCT  TCCGAAGGAC  ATTGAtaaat  ggtgTCGTCT  CGGttgtaCt

```

```

201  tggcttcgta  gTCGTAAAC  TCGGTTGCGG  GGATGATGTG  TATGCCGGGC
251  AGCCCTTTGC  CGTTCAGGAC  GGGGCAGGAA  TATTCGCCGC  CGCCGATAAA
301  AcgtTcggca  atgaTTtcgc  ccctgAAGGT  GttTCAattc  ttcgtaAACG
351  CTTTTCAGAc  ggccttTTTC  TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 334; ORF 096.ng>:

g096.pep

```

1  MAGHTGQGVDFQQIEFAVGI FEEIDAHA AFRTDCLCAANR QFAHQAFFGF
51  GQIFRRTLIN GVVSVVLGFV VVKLGCGDDV YAGQPFQVQD GAGIFAAADK
101 TFGNDFAXEG VSILRKRFSD GLFL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 335>:

m096.seq

```

1  ATGGCTCGTC ATACCGGGCA GGGTGTGAT TTCCAACAGA TAGAGTTTGC
51  CGTCGGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCATT
101 GCCTGCGCGC CGCGAACC GCAGTTCGCGC ATCAGGCTTT CTTCGGCTTC
151 GGTCAAATCT TCCGAAGGAC ATTGATAAAT GGTGTCGTCG CGGTTGTACT
201 TGGCTTCGTA GTCGTAAAAC TCGGTTGCGG GAATGATGTG TATGCCGGGC
251 AGCCCTTTGC CGTTCAGGAC GGGGCAGGAA TATTCGCCGC CGCCGATAAA
301 ACGTTCGGCA ATGATTTTCG CC.TGAAGGT GTTTC AATTC TTCGTAAACG
351 CTTTTCAGAC GGCCTTTTCC TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 336; ORF 096>:

m096.pep

```

1  MARHTGQGVDFQQIEFAVGI FEEIDAHA AFRTDCLRAANR QFAHQAFFGF
51  GQIFRRTLIN GVVAVVLGFV VVKLGCGNDV YAGQPFQVQD GAGIFAAADK
101 TFGNDFAXEG VSILRKRFSD GLFL*

```

m096/g096 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m096.pep	MARHTGQGVDFQQIEFAVGI FEEIDAHA AFRTDCLRAANR QFAHQAFFGF GQIFRRTLIN					
	:					
g096	MAGHTGQGVDFQQIEFAVGI FEEIDAHA AFRTDCLCAANR QFAHQAFFGF GQIFRRTLIN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m096.pep	GVVAVVLGFVVVKLGCGNDV YAGQPFQVQD GAGIFAAADK TFGNDFAXEG VSILRKRFSD					
	:					
g096	GVVSVVLGFVVVKLGCGDDV YAGQPFQVQD GAGIFAAADK TFGNDFAXEG VSILRKRFSD					
	70	80	90	100	110	120
m096.pep	GLFLX					
g096	GLFLX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 337>:

a096.seq

```

1  ATGGCCGGTC ATACCGGGCA GGGTGTGAT TTCCAACAGA TAGAGTTTGC
51  CGTCGGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCATT
101 GCCTGCGCGC CGCGAACC GCAGTTCGCGC ATCAGGCTTT CTTCGGCTTC
151 GGTCAGATCT TCCGAAGGAC ATTGATAAAT GGTGTCGTTG CGGTTGTACT
201 TGGCTTCGTA GTCATAAAAC TCGGTCGCGG GGATGATGTG TATGCCGGGC
251 AGCCCTTTGC CGTTC AACAC AGGGCAGGAA TATTCGCCGC CGCCGATAAA
301 CCGTTCGGCA ATGATTTTCG CCT.GAAAGT GTTTC AATTC TTCGTAAACG
351 CTTTTCAGAC GGCCTTTTCC TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 338; ORF 096.ng>:

a096.pep

```

1  MAGHTGQGVDFQQIEFAVGI FEEIDAHA AFRTDCLRAANR QFAHQAFFGF

```

299

51 GQIFRRTLIN GVVAVVLGFV VIKLGRGDDV YAGQAFVQH RAGIFAAADK
101 PFGNDFAXES VSILRKRFSD GLFL*

m096/a096 92.7% identity in 124 aa overlap

	10	20	30	40	50	60
m096.pep	MARHTGQGVDFQQIEFAVGIFEEIDAHA	AARTDCLRAANRQFAHQAFFGFGQIFRRTLIN				
a096	MAGHTGQGVDFQQIEFAVGIFEEIDAHA	AARTDCLRAANRQFAHQAFFGFGQIFRRTLIN				
	10	20	30	40	50	60
	70	80	90	100	110	120
m096.pep	GVVAVVLGFVVVKLGCGNDVYAGQPF	AVQDGAGIFAAADKTFGNDFAXEGVSILRKRFSD				
a096	GVVAVVLGFVVIKLRGDDVYAGQAFVQH	RAGIFAAADKPFGNDFAXESVSILRKRFSD				
	70	80	90	100	110	120
m096.pep	GLFLX					
a096	GLFLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 339>:

g097.seq

```

1  ATGGATATTT CAAAACAAAC ATTGCTGGAT AGGGTTTTTA ACCTGAAGGC
51  AACCGGTACG ACGGTACGTA CCGAGTTGAT GCGGGGTTTG ACGACCTTTT
101 TGACGATGTG CTACATCGTT ATCGTCAATC CCCTGATTTT GGGCGAGACC
151 GGAATGGATA TGGGGGCGGT ATTCGTCGCT ACCTGTATCG CATCCGCCAT
201 CCGCTGTTTT GTCATGGGTT TTATCGGCAA CTATCCGATT GCGCTTGCCC
251 CGGGGATGGG GCTGAATGCC TATTTCACCT TTGCCGTCGT TAAGGGTATG
301 GGCGTGCCCT GGCAGGTGGC GTTGGGTGCG GTGTTCATTT CCGGTCTGAT
351 TTTCATCCTG TTCAGCTTTT TTAAAGTCAG GGAAATGCTG GTCAACGCAC
401 TGCCATGCGG TTTGAAAATG TCGATTGCCG CCGGTATCGG TTTGTTTTTG
451 GCACTGATTT CCCTGAAAGG CGCAGGCATT ATCGTTGCCA ATCCGGCAAC
501 CTTGGTCGGC TTGGGCGATA TTCATCAGCC CAGCGCACTG TTGGCATTGT
551 TCGGTTTTGT CATGGTGGTC GTATTGGGGT ATTTCCGCGT TCAAGGCGCA
601 ATCATCATCA CCATTCTGAC GATTACCGTC ATTGCCAGCC TGATGGGTTT
651 GAACGAGTTT CACGGCGTGG TCGGCGAAGT ACCGGGCATT GCGCCGACCT
701 TTATGCAGAT GGATTTTAAA GGTCTGTTTA CCGTCAGCAT GGTCAAGCAG
751 ATTTTCGTCT TCTTCTTGGT CGATTTGTTC GACAGTACCG GAACGCTGGT
801 CGGCGTATCC CACCGTGCCG GACTGCTGGT GGACGGTAAG CTGCCCCGCC
851 TGAAACGCGC ACTGCTTGCA GACTCTACCG CCATTGTGGC AGGTGCGGCT
901 TTGGGTACTT CTTCAACCAC GCCTTATGTG GAAAGCGCGG CGGGCGTATC
951 GGCAGGCGGA CGGACCGGCC TGACGGCGGT TACCGTCGGC GTATTGATGC
1001 TGGCGTGTCT GATGTTCTCC CCATTGGCGA AAAGTGTTC GGTATTTGCC
1051 ACCGCGCCCG CACTGCTTTA TGTCGGCACG CAGATGCTCC GCAGTGCAG
1101 GGACATTGAT TGGGACGATA TGACTGAAGC CGCGCCCGCG TTCCTGACCA
1151 TTGTCTTCAT GCCGTTTACC TATTCGATTG CAGACGGCAT CGCCTTCGGC
1201 TTCATCAGCT ATGCCGTGGT CAAACTTTTG TGTCGCCGGA CTGGGGACGT
1251 GCCGCCTATG GTATGGGTG TTGCCGTATT GTGGGCATTG AAATTCTGGT
1301 ATTTGGGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 340; ORF 097.ng>:

g097.pep

```

1  MDISKQTLTD RVFNLKANGT TVRTELMAGL TFLTMCIYIV IVNPLILGET
51  GMDMGAVFVA TCIASAIGCF VMGFIGNYPI ALAPGMGLNA YFTFAVVKGM
101 GVPWQVALGA VFISGLIFIL FSFFKVREML VNALPMGLKM SIAAGIGLFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFVMV VLG YFRVQGA
201 IITILTITV IASLMGLNEF HGVVGEVPGI APTFMQMDFK GLFTVSMVSV
251 IFVFFLVDLF DSTGTLVGVS HRAGLLVDGK LPRLKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VLMLACLMFS PLAKSVPVFA
351 TAPALLYVGT QMLRSARDID WDDMTEAAPA FLTIVFMPFT YSIADGIAFG

```

m097.seq						
1	ATGGACACTT	CAAAACAAAC	ACTGTTGGAC	GGGATTTTTTA	AGCTGAAGGC	
51	AAACGGTACK	ACGGTGCCTA	CCGAGTTGAT	GGCGGGTTTG	ACAACCTTTT	
101	TGACGATGTG	CTACATCGTT	ATCGTCAACC	CTCyGATTTT	GGGCGAGACC	
151	GGCATGGATA	TGGGGGCGGT	ATTCGTGCGT	ACCTGTATCG	CGCTGTCATT	
201	CGGCTGTTTT	GTTATGGGTT	TTGTCGCGAA	CTATCCGATT	GCACTCGCAC	
251	CGGGGATGGG	GCTGAATGCC	TATTTACCT	TTGCCGTCGT	TAAGGGTATG	
301	GGCGTGCCTT	GGCAGGTTGC	GTTGGGTGCG	GTGTTTCATCT	CCGGTCTGAT	
351	TTTTATCCTG	TTCAGCTTTT	TTAAAGTCAG	GGAAATGCTG	GTCAACGCAC	
401	TGCTATGGG	TTTGA AAAATG	TCGATTGCTG	CCGGTATCGG	TTTGTTTTTTG	
451	GCACTGATTT	CCCTGAAAGG	CGCAGGCATT	ATCGTGTCCA	ATCCGGCAAC	
501	CTTGGTCGGT	TGGGCGGATA	TTTCATCAGC	GTCGCGCTTG	TTGGCATTGT	
551	TCGGTTTTGC	TATGTTGGTC	GATTGGGAC	ATTTCCGCGT	TCAAGGCGCA	
601	ATCATCATCA	CCATCTTGAC	CATTACCGTC	ATTGCCAGCC	TGATGGGTTT	
651	GAATGAATTT	CACGGCATCA	TCGGCGAAGT	ACCGAGCATT	GCGCCGACTT	
701	TTATGCAGAT	GGATTTTGAA	GGCCTGTTTA	CCGTCAGCAT	GGTCAGTGTG	
751	ATTTCGTCT	TCTTCTTGGT	CGATCTATTT	GACAGTACCG	GAACGCTGGT	
801	CGGCATATCC	CACCGTGCCG	GGCTGCTGGT	GGACGGTAAG	CTGCCCCGCC	
851	TGAAACGCGC	ACTGCTTGCA	GACTCTACCG	CCATTGTGGC	AGGTGCGGTT	
901	TTGGGTACTT	TCTCCACCAC	GCGTTATGTG	GAAAGCGCGG	CGGGCGTATC	
951	GGCAGGCGGA	CGGACCGGCC	TGACGGCGGT	TACCGTCGGC	GTATTGATGC	
1001	TCGCTGCCT	GATGTTTTCA	CCTTTGGCGA	AAAGTGTTCC	CGCTTTTGCC	
1051	ACCGCGCCCG	CCCTGCTTTA	TGTCGGCACG	CAGATGCTCC	GCAGTGCGAG	
1101	GGATATTGAT	TGGGACGATA	TGACGGAAGC	CGCACCTGCG	TTCCTGACCA	
1151	TTGTTTTCAT	GCCGTTTACT	TATTCGATTG	CAGACGGCAT	CGCTTTCGGC	
1201	TTCATCAGTT	ATGCCGTGGT	TAAACTTTTA	TGCCGCCGCA	CCAAAGACGT	
1251	TCCGCCTATG	GATATGGATTG	TTGCCGTATT	GTGGGCACTG	AAATTCTGGT	
1301	ATTTGGGCTG	A				

This corresponds to the amino acid sequence <SEQ ID 342; ORF 097>:

```
m097.pep
1  MDTSKQTLDD GIFKLKANGT TVRTELMAGL TTFITMCYIV IVNPXILGET
51  GMDMGAVFVA TCIASAIGCF VMGFVGNYP I ALAPGMGLNA YFTFAVVKGM
101 GVPWQVALGA VFISGLFIL FSFFKVREML VNALPMGLKM SIAAGIGLFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFAMVV VLGHFRVQGA
201 IIITILTITV IASLMGLNEF HGIIGEVP SI APTFMQMDFE GLFTVSMVSV
251 IFVFLLVDLF DSTGTLVGIS HRAGLLVDGK LPRLKRALLA DSTAIVGAAV
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VLMLACL MFS PLAKSVPAFA
351 TAPALLYVGT QMLRSARDID WDDMTEAAPA FLTIVFMPFT YSIADGIAFG
401 FISYAVVKLL CRRTKDVPPI VWIVAVLWAL KFWYLG*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 097 shows 96.3% identity over a 436 aa overlap with a predicted ORF (ORF 097.ng) from *N. gonorrhoeae*:

m097/g097

	10	20	30	40	50	60
m097.pep	MDTSKQTLLDGIFKCLKANGTTVRTELMAGLTTFLTMCIYIVIVNPXILGETGMDMGAVFVA					
	:					
g097	MDISKQTLDDRNVFNCLKANGTTVRTELMAGLTTFLTMCIYIVIVNPLILGETGMDMGAVFVA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m097.pep	TCIASAIGCFVMGFVGNYPIALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
	:					
g097	TCIASAIGCFVMGFIGNYPIALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
	70	80	90	100	110	120
	130	140	150	160	170	180

301

m097.pep	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL
g097	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL
	130 140 150 160 170 180
m097.pep	LALFGFAMVVVLGHFRVQGAIIITILTITVIASLMGLNEFHGIIGEVPSIAPTQMDFE
g097	LALFGFAMVVVLGHFRVQGAIIITILTITVIASLMGLNEFHGVVGEVPGIAPTQMDFK
	190 200 210 220 230 240
m097.pep	GLFTVSMVSVIFVFFLVDLFDSTGTLVGISHRAGLLVDGKLPRLKRALLADSTAIVAGAA
g097	GLFTVSMVSVIFVFFLVDLFDSTGTLVGVS HRAGLLVDGKLPRLKRALLADSTAIVAGAA
	250 260 270 280 290 300
m097.pep	LGTSSSTTPYVESAAAGVSAGGRTGLTAVTVGVMLACLMSPLAKSVPAFATAPALLYVGT
g097	LGTSSSTTPYVESAAAGVSAGGRTGLTAVTVGVMLACLMSPLAKSVPVFATAPALLYVGT
	310 320 330 340 350 360
m097.pep	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVPMM
g097	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTGDVPPM
	370 380 390 400 410 420
m097.pep	VWIVAVLWALKFWYLGX
g097	VWVVAVLWALKFWYLGX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 343>

a097.seq

```

1  ATGGACACTT CAAAACAAAC ACTGTTGGAC GGGATTTTTA AGCTGAAGGC
51  AAACGGTACG ACGGTGCGTA CCGAGTTGAT GCGGGGTTTG ACAACTTTTT
101 TGACGATGTG CTACATCGTT ATCGTCAACC CTCTGATTTT GGGCGAGACC
151 GGCATGGATA TGGGGCGGTT ATTCGTCGCT ACCTGTATCG CGTCTGCCAT
201 CGGCTGTTTT GTTATGGGTT TTGTCGGCAA CTATCCGATT GCACTCGCAC
251 CGGGGATGGG GCTGAATGCC TATTTACCTT TTGCCGTCGT TAAGGGTATG
301 GCGGTGCCTT GGCAGGTTGC GTTGGGTGCG GTGTTTCATCT CCGGTCTGAT
351 TTTTCATCTG TTCAGCTTTT TTAAAGTCAG GGAAATGCTG GTCAACGCAC
401 TGCCTATGGG TTTGAAAATG TCGATTGCTG CCGGTATCGG TTTGTTTTTG
451 GCACTGATTT CCCTGAAAGG CGCAGGCATT ATCGTTGCCA ATCCGGCAAC
501 CTTGGTTCGGC TTGGGCGATA TTCATCAGCC GTCCGCGTTG TTGGCACTGT
551 TCGGTTTTGC CATGGTGGTC GTATTGGGAC ATTTCCGCGT TCAAGGCGCA
601 ATCATCATCA CCATTTTGAC GATTACCGTC ATTGCCAGCC TGATGGGTTT
651 GAACGAATTT CACGCGATCA TCGGCGAAGT GCCGAGCATT GCGCGCACTT
701 TTATGCAGAT GGATTTTAAA GGGTTGTTTA CCGTCAGCAT GGTCAGCGTG
751 ATTTTCGTCT TTTTCTAGT CGATCTGTTT GACAGTACCG GAACACTGGT
801 CGGTGTATCG CATCGTGCCG GACTGCTGGT GGACGGTAAG CTGCCCCGCC
851 TGAAACGCGC ACTGCTTGCA GACTCTACCG CTATTGTGGC AGGTGCGGCT
901 TTGGGTACTT CTCAACCAC GCCTTATGTG GAAAGTGCGG CGGCGGTATC
951 GGCAGGCGGG CGGACAGGTC TGACGGCGGT TACCGTCGGC GTATTGATGC
1001 TCGCCTGCCT GATGTTTTCA CCTTGGCGCA AAAGTGTTCG CGCTTTTGCC
1051 ACCGCGCCCG CCTGCTTTTA TGTCGGCACG CAGATGCTCC GCAGTGCAGG
1101 GGACATCGAT TGGGACGATA TGACGGAAGC CGCACCAGCA TTCCTGACCA
1151 TTGTCTTCAT GCCGTTTACC TATTCGATTG CAGACGGCAT CGCTTTCGGC
1201 TTCATCAGTT ATGCCGTGGT TAAACTTTTA TGCCGCGGCA CCAAAGACGT
1251 TCCGCTATG GTATGGATTG TTGCCGTATT GTGGGCACTG AAATTCTGGT

```

302

1301 ATTTGGGCTG A

This corresponds to the amino acid sequence <SEQ ID 344; ORF 097.a>:

a097.pep

```

1  MDTSKQTLTD GIFKLKANGT TVRTELMAGL TTFLTMCYIV IVNPLILGET
51  GMDMGAVFVA TCIAAIGCF VMGFVGNYP I ALAPGMGLNA YFTFAVVKGM
101 GVPWQVALGA VFISGLIFIL FSFFKVREML VNALPMGLKM SIAAGIGLFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFAMVV VLGHFRVQGA
201 IIITILTITV IASLMGLNEF HGIIGEVPSI APTFMQMDFK GLFTVSMVSV
251 IFVFFLVDLF DSTGTLVGVS HRAGLLVDGK LPRLKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VLMLACLMFS PLAKSVPAFA
351 TAPALLYVGT QMLRSARDID WDDMTEAAPA FLTIVFMPFT YSIADGIAFG
401 FISYAVVKLL CRRTKDVP PM VWIVAVLWAL KFWYLG*

```

m097/a097 99.3% identity in 436 aa overlap

m097.pep	10	20	30	40	50	60
	MDTSKQTLTDGIFKLKANGTTVRTELMAGLTTFLTMCYIVIVNPNXILGETGMDMGAVFVA					
a097	MDTSKQTLTDGIFKLKANGTTVRTELMAGLTTFLTMCYIVIVNPLILGETGMDMGAVFVA					
	10	20	30	40	50	60
m097.pep	70	80	90	100	110	120
	TCIAAIGCFVMGFVGNYP IALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
a097	TCIAAIGCFVMGFVGNYP IALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
	70	80	90	100	110	120
m097.pep	130	140	150	160	170	180
	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL					
a097	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL					
	130	140	150	160	170	180
m097.pep	190	200	210	220	230	240
	LALFGFAMVVVLGHFRVQGAIITILTITVIASLMGLNEFHGIIGEVPSIAPTFMQMDFE					
a097	LALFGFAMVVVLGHFRVQGAIITILTITVIASLMGLNEFHGIIGEVPSIAPTFMQMDFK					
	190	200	210	220	230	240
m097.pep	250	260	270	280	290	300
	GLFTVSMVSVIFVFFLVDLFDSTGTLVGISHRAGLLVDGKLPRLKRALLADSTAIVAGAA					
a097	GLFTVSMVSVIFVFFLVDLFDSTGTLVGVS HRAGLLVDGKLPRLKRALLADSTAIVAGAA					
	250	260	270	280	290	300
m097.pep	310	320	330	340	350	360
	LGTSSTTPYVESAAGVSAGGRTGLTAVTVGVMLACLMFSPLAKSVPAFATAPALLYVGT					
a097	LGTSSTTPYVESAAGVSAGGRTGLTAVTVGVMLACLMFSPLAKSVPAFATAPALLYVGT					
	310	320	330	340	350	360
m097.pep	370	380	390	400	410	420
	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVP PM					
a097	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVP PM					
	370	380	390	400	410	420
m097.pep	430					
	VWIVAVLWALKFWYLGX					
a097	VWIVAVLWALKFWYLGX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 345>:

```
g098.seq
  1 ATGACCGCCG ACGGTCTCTT CGTCGCTTTC AACTTCAATA CGTTTGCCGT
 51 TGTGCGAATA TTGATACCAG TACAGCAGGA TGCTGCCAG GCTGGCGATC
101 AGTTTGTCGG CGATGTCGCG CGCTTCGCTG TCGGGATGGC TTTCGCGTTC
151 GGGATGAACG CAGCCGAGCA TGGACACGCC GGTACGCATC ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTTGAG CTTGGTTTTA TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAAGTG TGCGACTTCT TCAAACCTCGC
351 ATTTTGTGTC CAAATTAGAA TGTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 346; ORF 098.ng>:

```
g098.pep
  1 MTADGLFVAF NFNTFAVVRI LIPVQDAAQ AGDQFVGDDVA RFAVGMAFAF
 51 GMNAAEHGHA GTHVHRMG MCRQAFQNFNH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV GDFFKLAFLC QIRMS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 347>:

```
m098.seq
  1 ATGACCGCCG ATGGTCTCTT CGTCGCTTTC AACCTCAATG CGTTTGCCGT
 51 TGTGCGAATA TTGATACCAG TACAAGAGGA TGCTGCCAG GCTGGCGATC
101 AGTTTGTCGG CGATGTCGCG CGCTTCACTT TCCGGATGGC TTTCACGTTT
151 AGGATGAACG CAGCCCAGCA TGGATACGCC GGTACGCATT ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTTGAG CTTGGTTTTA TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAGGTG GGCGACTTCT TCAAACCTCGC
351 ATTTTGTGTC CAAATCAGAA TGTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 348; ORF 098>:

```
m098.pep
  1 MTADGLFVAF NLNAFAVVRI LIPVQEDAAE AGDQFVGDDVA RFTFRMAFTF
 51 RMNAAQHGYA GTHVHRMG MCRQAFQNFNH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV GDFFKLAFLC QIRMS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 098 shows 89.6% identity over a 125 aa overlap with a predicted ORF (ORF 098.ng) from *N. gonorrhoeae*:

```
m098/g098

      10      20      30      40      50      60
m098.pep  MTADGLFVAFNLNAFAVVRI LIPVQEDAAEAGDQFVGDDVARFTFRMAFTFRMNAAQHGYA
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g098      MTADGLFVAFNFNTFAVVRI LIPVQDAAQAGDQFVGDDVARFAVGMAFAFGMNAAEHGHA
          10      20      30      40      50      60

      70      80      90     100     110     120
m098.pep  GTHVHRMG MCRQAFQNFNH TDRQAAHGFE LGFISGQLEFVGQMAVNQQV GDFFKLAFLC
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g098      GTHHVHRMG MCRQAFQNFNH TDRQAAHGFE LGFISGQLEFVGQMAVNQQV CDFFKLAFLC
          70      80      90     100     110     120

m098.pep  QIRMSX
          |||||
g098      QIRMSX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 349>:

```
a098.seq
  1 ATGACCGCCG ATGGTCTCTT CGTCGCTTTC AACCTCAATG CGTTTGCCGT
 51 TGTGCGAATA TTGATACCAG TACAAGAGGA TGCTGCCAG GCTGGCGATC
```

304

```

101 AGTTTGTCCG CGATGTCGCG CGCTTCACTT TCCGGATGGC TTTCACGTTT
151 AGGATGAACG CAGCCCAGCA TGGATACGCC GGTACGCATT ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTGAG CTTGGTTTAA TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAGGTG GGCGACTTCT TCAAACCTCG
351 ATTTTGTGTC CAAATCAGAA TGTCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 350; ORF 098.a>:

a098.pep

```

1 MTADGLFVAF NLNAFAVVR I LIPVQEDAAE AGDQFVG DVA RFTFRMAFTF
51 RMNAAQHGYA GTHYVHRMG M CRQAFQNFNH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV GDFFKLAFLC QIRMS*

```

m098/a098 100.0% identity in 125 aa overlap

	10	20	30	40	50	60
m098.pep	MTADGLFVAFNLNAFAVVRILIPVQEDAAEAGDQFVG DVARFTFRMAFTFRMNAAQHGYA					
a098	MTADGLFVAFNLNAFAVVRILIPVQEDAAEAGDQFVG DVARFTFRMAFTFRMNAAQHGYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m098.pep	GTHYVHRMGMC RQAFQNFNHTDRQAAHGFELGFISGQLEFVGQMAVNQQV GDFFKLAFLC					
a098	GTHYVHRMGMC RQAFQNFNHTDRQAAHGFELGFISGQLEFVGQMAVNQQV GDFFKLAFLC					
	70	80	90	100	110	120
m098.pep	QIRMSX					
a098	QIRMSX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 351>:

g099.seq

```

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTGGA
51 GCTGACGGGC AAACGGCAGG CGGGCATTAC TGCCACAGAC ATCGTGTGG
101 CACTGACCGA ATTCTTGCCT AAAGAGCGCG TGGTCGGGGC GTTTGTGCGA
151 TTTTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGGAGT TCGGCGCGAC TGCCGCCATG TTCGCCATCG
251 ACGCGCAAAC TATTGATTAT TTGAAACTGA CCGACGTGA CGACGCGCAG
301 GTGAAATTGG TGGAAACCTA CGCCAAAACC GCAGGCTTAT GGGCAGGTGG
351 CTTGAAAACC GCCGTTTATC CGCGCGTTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCGAGCAACC CGCACGCGCG TTTTGCCACC
451 GCCGATTTGG CGGCGAAAGG GCTGGCGAAG CCTTACGAAG AGCCTTCAGA
501 CGGCCAAATG CCTGACGGTG CAGTGATTAT TGCCGCGATT ACTTCGTGTA
551 CCAATACTTC CAACCCGCGC AACGTTGTCT CCGCCGCACT GTTGGCACGC
601 AATGCCAACC GCCTCGGCTT GAAACGCAAA CCTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGGAATCTA TTTGAAAGAA GCAGGCTTGT
701 TGCCCCGAAAT GGAAAACTC GGCTTCGGTA TCGTCGCCTT CGCATGTACC
751 ACCTGTAACG GCATGAgcgG CGCGCTcgac CCGAAAATCC AACAAAGAAAT
801 CATCGACCGC GAttgtacg cCACCGCCGT ATTGTCAGGC AACC GCAACT
851 TCGACGGCCG TATCCATCCG TATGCGAAAC AGGCTTTCCT CGCTTCGCTT
901 CCTTTGGTCG TTGCCTACGC ATTGGCAGGT AGCATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGGCCG CGAAATCCGC CTGAAAAGATA
1001 TCTGGCCGAC AGACGAAGAA ATCGATGCCA TCGTTGCCGA ATATGTGAAA
1051 CCGCAACAAT TCCGCGACAT TTATATCCCG ATGTCCGACA CCGGCACAGC
1101 GCAAAAAGCA CCAAGCCCGC TGTACGACTG GCGACCGATG TCCACCTACA
1151 TCCGCCGTCC GCCCTATTGG GAAGGCGCAC TGGCAGGGGA ACGTACATTA
1201 AGAGGTATGC GTCCGCCGGC GATTTTGCCC GACAACATCA CCACCGACCA
1251 CATCTCgcca tCCAATGCGA TTTTGGCCGG cagTGCgca ggtgaATATT

```

```

1301 TGGCGAAAAT GGGTTTGCCT GAAGAagaCT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTtcgt
1451 tggcacgcgT tgaacCAGAA GGCCAAACCA TGC GCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTT ATCATCATTG CCGGTGCGGA
1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC GGCGAAGGGC GTGCGGCTGG
1601 CGGGTGTGGA AGCCATCGCC GCCGAAGGTT TCGAGCGCAT CCACCGCACC
1651 AACCTCATCG GCATGGGCGT CTTGCCGCTG CAATTCAAAC CCGGCACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTGCGCG
1751 AACGCACACC GCGCTGCGGC CTGACCCTCG TGATTCACCG TAAAAACGGA
1801 GAAACCGTCG AAGTTCCGGT TACCTGCCGC CCCGATACCG CAGAAGAAGC
1851 ATTGGTATAT GAAGCCGGCG GCGTATTGCA ACGGTTTGCA CAGGACTTTT
1901 TGGAAGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 352; ORF 099.ng>:

g099.pep

```

1 MLGRASMMRL PDIVGVELTG KROAGITATD IVLALTEFLR KERVVGAFVE
51 FFGEGARSLS IGDRATISNM TPEFGATAAM FAIDAQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWAGGLKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAAKGLAK PYEEPSDGQM PDGAVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLKRK PWVKSSFAPG SKVAGIYLKE AGLLPEMEKL GFGIVAFACF
251 TCNGMSGALD PKIQEIIDR DLYATAVLSG NRNFDGRIHP YAKQAFILAS
301 PLVVAYALAG SIRFDIENDV LGVADGREIR LKDIWPTDEE IDAIVAEYVK
351 PQQFRDIYIP MSDTGTAQKA PSPLYDWRPM STYIRRPYPW EGALAGERTL
401 RGMRPAILP DNITTDHISP SNAILAGSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMNKQPL IIIAGADYGO GSSRDWAAKG VRLAGVEAIA AEGFERIHRT
551 NLIGMGVLPL QFKPGTNRHT LQLDGTETYD VVGERTPRCG LTLVIHRKNG
601 ETVEVPVTCR PDTAEEALVY EAGGVLRFA QDFLEGNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 353>:

m099.seq

```

1 ATGTGCGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTTGA
51 GCTGAACGGC AAACGGCAGG CGGGCATTAC GGCGACGGAT ATTGTGTTGG
101 CACTGACCGA GTTCTGCGC AAAGAACGCG TGGTCGGGGC GTTGTGCGAA
151 TTCTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGGAGT TCGGCGCGAC TGCCGCGATG TTCGCTATTG
251 ATGAGCAAAC CATTGATTAT TTGAAACTGA CCGGACGCGA CGACGCGCAG
301 GTGAAATTGG TGGAAACCTA CGCCAAAACC GCAGGCTTGT GGGCAGTATG
351 CTTGAAAACC GCCGTTTATC CTCGCGTTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCAAGTAACC CGCATGCCCG TTTTGCAGAC
451 GCCGATTTGG CGGCGAAAGG GCTGGCGAAG CCTTACGAAG AGCCTTCGGA
501 CGGCCAAATG CCCGACGGCT CCGTCATCAT CGCCGCGATT ACCAGTTGCA
551 CCAACACTTC CAACCCGCGC AACGTTGTTG CCGCCGCGCT CTTGGCACGC
601 AATGCCAACC GTCTCGGCTT GAAACGCAA CCTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGAAATCTA TTTGAAAGAA GCGGGCCTGT
701 TGCCCCGAAAT GGAAAACTC GGCTTCGGTA TCGTCGCCTT CGCCTGCACC
751 ACCTGCAACG GCATGAGTGG CGCGCTGGAT CCGAAAATCC AGAAAGAAAT
801 CATCGACCGC GATTTGTACG CCACCGCCGT ATTATCAGGC AACCGCAACT
851 TCGACGGCCG TATCCACCCG TATGCGAAAC AGGCTTTTCT CGCTTCGCCT
901 CCGTTGGTCG TTGCCCTACG GCTGGCAGGC AGTATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGCGAA GGAAATCCGC CTGAAAGACA
1001 TTTGGCCTGC CGATGAAGAA ATCGATGCCG TCGTTGCCGA ATATGTGAAA
1051 CCGCAGCAGT TCCGCGATGT GTATGTACCG ATGTTGACA CCGGCACAGC
1101 GCAAAAAGCA CCCAGTCCGC TGTACGATTG GCGTCCGATG TCCACCTACA
1151 TCCGCCGTCC GCCTTACTGG GAAGGCGCGC TGGCAGGGGA ACGCACATTA
1201 AGAGGTATGC GTCCGCTGGC GATTTTGGCC GACAACATCA CCACCGACCA
1251 CCTCTCGCCG TCCAATGCGA TTTTGGCCGT CAGTGCCGCA GGCGAGTATT
1301 TGGCGAAAAT GGGTTTGCCT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGACC ACTTGACCGC CCAACGCGCT ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAAAA ACGAAGACGG CAGCGTGC GC CAAGGCTCGT
1451 TCGCCCGCGT CGAACCCGAA GGCGAAACCA TGC GCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGTGCGGA

```

```

1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAAGGC GTACGCCTCG
1601 CCGGCGTAGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACCTTATCG GCATGGGCGT GTTGCCGCTG CAGTTCAAAC CCGACACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTGGTCGGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTCG TGATTACCG TAAAAACGGC
1801 GAAACCGTTG AAGTTCCCGT TACCTGCTGC CTCGATACTG CAGAAGAAGT
1851 ATTGGTATAT GAAGCCGCGC GCGTGTGCA ACGGTTGCA CAGGATTTTT
1901 TGGAAGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 354; ORF 099>:

```

m099.pep
  1  MLGRASMMRL PDIVGVELNG KRQAGITATD IVLALTEFLR KERVVGAFVE
 51  FFGEGARSLS IGDRATISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
101  VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151  ADLAAKGLAK PYEEPSDGQM PDGSVIAAI TSCTNTSNPR NVVAAALLAR
201  NANRLGLKRR PWVKSSFAPG SKVAEIIYLKE AGLLPEMEKL GFGIVAFAC
251  TCNGMSGALD PKIQKEIIDR DLYATAVLSG NRNFDGRIHP YAKQAFASP
301  PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPADEE IDAVVAEYVK
351  PQQFRDVYVP MFDGTGAQKA PSPLYDWRPM STYIRRPYVW EGALAGERTL
401  RGMRLAILP DNITDHLSP SNAILAVSAA GEYLAKMGLP EEDFNSYATH
451  RGDHLTAQRA TFANPKLFNE MVKNEDGSVR QGSFARVEPE GETMRMWEAI
501  ETYMNRRKQPL IIIAGADYQG GSSRDWAAKG VRLAGVEAIV AEGFERIHRT
551  NLIGMGVLPL QFKPDTNRHT LQLDGTETYD VVGERTPRCD LTLVIHRKNG
601  ETVEVPVTCC LDTAEVLVY EAGGVLQRFA QDFLEGNA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 099 shows 96.2% identity over a 639 aa overlap with a predicted ORF (ORF 099.ng) from *N. gonorrhoeae*:

m099/g099

m099.pep	10	20	30	40	50	60
	MLGRASMMRLPDIVGVELNGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
g099	MLGRASMMRLPDIVGVELTGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
	10	20	30	40	50	60
m099.pep	70	80	90	100	110	120
	IGDRATISNMTPEFGATAAMFAIDEQTIDYKLKLTGRDDAQVKLVETYAKTAGLWADALKT					
g099	IGDRATISNMTPEFGATAAMFAIDAQTIDYKLKLTGRDDAQVKLVETYAKTAGLWAGGLKT					
	70	80	90	100	110	120
m099.pep	130	140	150	160	170	180
	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEEPSDGQMPDGSVIAAI					
g099	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEEPSDGQMPDGAIVIAAI					
	130	140	150	160	170	180
m099.pep	190	200	210	220	230	240
	TSCTNTSNPRNVVAAALLARNANRLGLKRPWKSSFAPGSKVAEIIYLKEAGLLPEMEKL					
g099	TSCTNTSNPRNVVAAALLARNANRLGLKRPWKSSFAPGSKVAGIYLKEAGLLPEMEKL					
	190	200	210	220	230	240
m099.pep	250	260	270	280	290	300
	GFGIVAFACCTTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFASP					
g099	GFGIVAFACCTTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFASP					
	250	260	270	280	290	300
	310	320	330	340	350	360

307

m099.pep	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIWPADEEIDAVVAEYVKPQQFRDVYVP
g099	PLVVAYALAGSIRFDIENDVLGVADGREIRLKDIWPTDEEIDAIVAEYVKPQQFRDIYIP
	310 320 330 340 350 360
m099.pep	MFDTGTAQKAPSPLYDWRPMSYIRRPYWEGALAGERTLRGMRPLAILPDNITTDHLS
g099	MSDTGTAQKAPSPLYDWRPMSYIRRPYWEGALAGERTLRGMRPPAILPDNITTDHISP
	370 380 390 400 410 420
m099.pep	SNAILAVSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVKNEDGSVR
g099	SNAILAGSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVRNEDGSVR
	430 440 450 460 470 480
m099.pep	QGSFARVEPEGETMRMWEAIETYMNKQPLIIAGADYQGSSRDWAAGVRLAGVEAIV
g099	QGSLARVEPEGQTRMWEAIETYMNKQPLIIAGADYQGSSRDWAAGVRLAGVEAIA
	490 500 510 520 530 540
m099.pep	AEGFERIHRTNLIGMVLPLQFKPDNRLTLQDGTETDYDVVGERTPRCDLTLVIHRKNG
g099	AEGFERIHRTNLIGMVLPLQFKPDNRLTLQDGTETDYDVVGERTPRCGLTLVIHRKNG
	550 560 570 580 590 600
m099.pep	ETVEVPVTCCLDTAEVVLVEAGGVLQRFQDFLEGNAAX
g099	ETVEVPVTCRPDTAEELVVEAGGVLQRFQDFLEGNAAX
	610 620 630 640

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 355>:

a099.seq

1	ATGCTGGGAC	GCGCGTCCAT	GATGCGCCTG	CCCGATATTG	TCGGCGTTGA
51	GCTGAACGGC	AAACGGAAGG	CGGGCATTAC	GGCGACGGAT	ATTGTGTTGG
101	CACTGACCGA	GTTTCTGCGC	AAAGAACGCG	TGGTCGGGGC	GTTTGTGCGAA
151	TTCTTCGGCG	AGGGCGCGAG	AAGCCTGTCT	ATCGGCGACC	GCGCGACCAT
201	TTCCAACATG	ACGCCGAGT	TCGGCGCGAC	TGCCGCGATG	TCGCTATTG
251	ATGAGCAAAC	CATTGATTAT	TTGAACTGA	CCGACGCGA	CGACGCGCAG
301	GTGAAATTGG	TGGAAACCTA	CGCCAAAACC	GCAGGCTTGT	GGCAGATGC
351	CTTGAAAACC	GCCGTTTATC	CGCGCGTTT	GAAATTGAT	TTGAGCAGCG
401	TAACGCGCAA	TATGGCAGGC	CCGAGCAACC	CGCACGCGCG	TTTTCGCACC
451	GCCGATTTGG	CCGGCAAAGG	CTTGGCTAAA	CCTTACGAAG	AGCCTTCAGA
501	CGGCCAAATG	CCTGACGGTG	CAGTGATTAT	TGCCGCGATT	ACTTCCTGTA
551	CCAATACTTC	CAATCCGCGC	AACGTTGTG	CCGCCGCGCT	GTTGGCACGC
601	AATGCCAACC	GCCTCGGCTT	GCAACGCAAA	CCTTGGGTGA	AATCTTCGTT
651	TGCCCCGGGT	TCAAAAGTAG	CCGAAATCTA	TTTGAAAGAA	GCAGATCTGC
701	TGCCCCGAAAT	GGAAAACTC	GGCTTCGGTA	TCGTTGCCTT	CGCATGTACC
751	ACCTGTAACG	GCATGAGCGG	CGCGCTGGAT	CCGAAAATCC	AGAAAGAAAT
801	CATCGACCGC	GATTGTACG	CCACCGCCGT	ATTGTCAGGC	AACCGCAACT
851	TTGACGGCCG	TATCCATCCG	TATGCGAAAC	AGGCTTTCCT	CGCTTCGCCT
901	CCGTTGGTCG	TTGCCACGC	GCTGGCAGGC	AGCATCCGTT	TCGATATTGA
951	AAACGACGTA	CTCGGCGTTG	CAGACGGCAA	AGAAATCCGC	CTGAAAGACA
1001	TTTGGCCTAC	CGATGAAGAA	ATCGATGCCA	TCGTTGCCGA	ATATGTGAAA
1051	CCGCAGCAAT	TTTCGCGACG	TTATATCCCG	ATGTTGCGACA	CCGGCAGCAGC
1101	GCAAAAAGCA	CCAAGCCCGC	TGTACGACTG	GCGTCCAATG	TCTACCTATA
1151	TCCGCCGCCC	ACCTTACTGG	GAAGGCGCAC	TGGCAGGGGA	ACGCACATTA
1201	AGCGGTATGC	GTCCGCTGGC	GATTTTGCCC	GACAACATCA	CCACCGACCA

```

1251 TCTCTCGCCA TCCAATGCGA TTTTGGCAAG CAGTGCCGCA GGCGAATATT
1301 TGGCAAAAAT GGGTTTGCCT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGTGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTTTCGC
1451 TGGCACGCGT TGAACCCGAA GGCCAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGCGCGGA
1551 CTACGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAAGGC GTACGCCTCG
1601 CCGGCGTGGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACTTGATCG GTATGGGCGT GTTGCCGCTG CAGTTCAAAC CGGGTACCAA
1701 CCGCCACACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTGCGCG
1751 AACGCACACC GCGTGCACG CTGACCCTTG TGATTACCG TAAAAACGGC
1801 GAGACCGTCG AAGTCCCCAT TACCTGCCGC CTCGATACCG CAGAAGAAGT
1851 GTTGGTATAT GAAGCCGGTG GCGTATTGCA ACGGTTTGCA CAGGATTTT
1901 TGGAAGGGAA CCGCGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 356; ORF 099.a>:

a099.pep

```

1 MLGRASMMRL PDIVGVELNG KRKAGITATD IVLALTEFLR KERVVGAFVE
51 FFGEGARSLs IGDRTISNM TPEFGATAAM FAIDEQIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAGKGLAK PYEEPSDGQM PDGAVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLQRK PWVKSSFAPG SKVAEIYLKE ADLLPEMEKL GFGIVAFAC
251 TCNGMSGALD PKIQKEIIDR DLYATAVLSG NRNFDGRIHP YAKQAFLASP
301 PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPDEE IDAIVAEYVK
351 PQQFRDVYIP MFDTGTAQKA PSPLYDWRPM STYIRPPYW EGALAGERTL
401 SGMRLAILP DNITDHLSP SNAIASSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMNKQPL IIIAGADYGQ GSSRDWAAKG VRLAGVEAIV AEGFERIHRT
551 NLIGMGVLPL QFKPGTNRHT LQLDGTETYD VVGERTPRCD LTLVIHRKNG
601 ETVEVPITCR LDTAEVLVY EAGGVLQRF A QDFLEGNA*

```

m099/a099 97.5% identity in 639 aa overlap

	10	20	30	40	50	60
m099.pep	MLGRASMMRLPDIVGVELNGKRQAGITATDIVLALTEFLRKERVVGAFVEFFFGEGARSLs					
a099	MLGRASMMRLPDIVGVELNGKRKAGITATDIVLALTEFLRKERVVGAFVEFFFGEGARSLs					
	10	20	30	40	50	60
m099.pep	70	80	90	100	110	120
	IGDRATISNMTPEFGATAAMFAIDEQIDY LKLTGRDDAQVKLVETYAKTAGLWADALKT					
a099	IGDRATISNMTPEFGATAAMFAIDEQIDY LKLTGRDDAQVKLVETYAKTAGLWADALKT					
	70	80	90	100	110	120
m099.pep	130	140	150	160	170	180
	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAGLAKPYEEPSDGQMPDGSVIIAAI					
a099	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAGKGLAKPYEEPSDGQMPDGAIIAAI					
	130	140	150	160	170	180
m099.pep	190	200	210	220	230	240
	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWVKSSFAPGSKVAEIYLKEAGLLPEMEKL					
a099	TSCTNTSNPRNVVAAALLARNANRLGLQRPWVKSSFAPGSKVAEIYLKEADLLPEMEKL					
	190	200	210	220	230	240
m099.pep	250	260	270	280	290	300
	GFGIVAFAC T TCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAF L ASP					
a099	GFGIVAFAC T TCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAF L ASP					
	250	260	270	280	290	300
m099.pep	310	320	330	340	350	360
	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIWPADEEIDAIVAEYVKPQQFRDVYVP					

g102.seq

This corresponds to the amino acid sequence <SEQ ID 358; ORF 102.ng>:

g102.pep

```

1  MSAKTPSLFG  GAMIAGKVI  GAGMFPNPTA  NLGDGLIGSL  IVLLYTWFPF
51  SSGALMILEV  NTHNPRGASF  DTMVKDLLGR  GWNIINGIAV  ALVLYGSTYA
101 YILVGGDLTA  KGIGSAVGGK  ISLTVGQLVF  FGILAFVCWA  SARLVDREFTG
151 VLIGGMVLTF  IWATGGLVAD  AKPSVLFDTQ  APVGTGYWIY  AATALPVCLA
201 SFGFHGNVSS  LLKYFKGDAP  KVAKSIWAGT  LVALVIYVLW  QTAIQSNLPR
251 NEFAPVIAAE  RQSVLNETL  SKFAQTGDM  KILSLFPYMA  IATSFLGVTL
301 GLFDNIADIF  KWNDMSMRG  TKTVLNLFLP  PLISWLLLP  GFFTAIGASG
351 LAATVWDQGI  IPAMLLYVSP  QKIGAGKTYK  VYGGWLWMLV  FLFGIANIAA
401 QVLSQMEVLP  VFKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 359>:

```

m102.seq
1  ATGCCCAACA  AAACCCCTTC  ACTGTTCCGC  GGC CGCATGA  TTATCGCCGG
51  CACGGTCATC  GGC CGAGGCA  TGCTCGCCAA  CCCGACCGCC  ACATCCGGCG
101 TATGGTTTAC  CGGCTCGCTG  GCCGTGTTGC  TGTACACCTG  GTTTTCTATG
151 CTTTCCAGCG  GCCTGATGAT  TTGGAAAGTC  AACACCCATT  ATCCGCACGG
201 CGCAAGTTTC  GACACGATGG  TCAAAGACCT  GCTCGGACGC  GGCTGGAACA
251 TCATCAACGG  CATCGCCGTC  GCCTTCGTTT  TATACCTGCT  TACTTACGCT
301 TATATCTTCG  TCGCGCGCGA  CCTGACCGCC  AAAGGCTTAG  GCAGCGCGGC
351 AGGCGGCGAC  GTTCACTCA  CCGTCGGACA  ACTCGTCTTC  TTCGGCATCC
401 TCGCCTTTTG  CGTATGGGCA  TCCGCACGCT  TGGTCGACCG  CTTCACCGGC
451 GTCCTTATCG  GCGGCATGGT  ATGACCTTT  ATTTGGGCGG  CCGGCGGGCT
501 GATTGCCGAT  GCCAAGCCGT  CCGTCCTCTT  CGATACCCAA  GCCCCGCGCG
551 GCACAAACTA  CTGGATTAC  GCCGCCACCG  CCCTGCCCGT  CTGCCTCGCT
601 TCCTTCGGCT  TCCACGGCAA  CGTCTCCAGC  CTGCTCAAAT  ACTTTAAAGG
651 CGACGCGCCC  AAAGTGGCTA  AATCCATCTG  GACGGGCACA  CTGATTGCGC
701 TGGTAATTTA  CGTCTCTGG  CAAACCGCCA  TCCAAGGCAA  CCTGCCGCGC
751 AACGAGTTCG  CCCCCGTCAT  CGCCGCCGAA  GGGCAAGTCT  CCGTCTCAT
801 CGAAACCTCG  TCCAAATTCG  CCCAAACCGG  CAATATGGAC  AAAATATTGT
851 CCCTGTTTTT  CTATATGGCG  ATCGCCACCT  CGTTTTTAGG  CGTAACGCTC
901 GGACTCTTCG  ACTACATCGC  CGACATCTTC  AAATGGAACG  ACAGCATCTC
951 CGGCCGACCC  AAAACCGCG  CGCTGACCTT  CCTGCCGCCC  CTGATTTCCT
1001 GCCTGCTCTT  CCCCACCGGC  TTCGTTACCG  CCATCGGCTA  CGTCGGCCTG
1051 GCGGCAACCG  TCTGGACAGG  CATCATCCCC  GCCATGCTGC  TCTACCGTTC
1101 GCGCAAAAAA  TTCGGCGCAG  GCAAACCTA  TAAAGTTTAC  GCGGCTTGT
1151 GGCTGATGGT  TTGGGTCTTC  CTTTTCGGCA  TCGTCAACAT  CGCCGCACAG
1201 GTATTGAGCC  AAATGGAAC  CGTCCCGTA  TTAAAGGAT  AA

```

This corresponds to the amino acid sequence <SEQ ID 360; ORF 102>:

```

m102.pep..
1  MPNKTPSLFG  GAMIAGTVI  GAGMLANPTA  TSGVWFTGSL  AVLLYTWFSM
51  LSSGLMILEV  NTHYPHGASF  DTMVKDLLGR  GWNIINGIAV  AFVLYLLTYA
101 YIFVGGDLTA  KGLGSAAGGD  VSLTVGQLVF  FGILAFVCWA  SARLVDREFTG
151 VLIGGMVLTF  IWAAGGLIAD  AKPSVLFDTQ  APAGTNYWIY  AATALPVCLA
201 SFGFHGNVSS  LLKYFKGDAP  KVAKSIWTGT  LIALVIYVLW  QTAIQSNLPR
251 NEFAPVIAAE  QQSVLIETL  SKFAQTGNMD  KILSLFSYMA  IATSFLGVTL
301 GLFDYIADIF  KWNDISISRT  KTAALTFLEP  LISCLLFTPG  FVTAIGYVGL
351 AATVWTGIIP  AMLLYRSRKK  FGAGKTYKVY  GGLWLMVWVF  LFGIVNIAAQ
401 VLSQMEVLPV  FRK*

```

m102/g102 86.0% identity in 415 aa overlap

```

          10      20      30      40      50      60
m102.pep  MPNKTPSLFGGAMI IAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g102       MSAKTPSLFGGAMI IAGKVIAGMFPNPTANLGDGLIGSLIVLLYTWFPFSSGALMILEV
          10      20      30      40      50      60

          70      80      90     100     110     120
m102.pep  NTHYPHGASFDTMVKDLLGRGWNIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGD
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g102       NTHNPRGASFDTMVKDLLGRGWNIINGIAVALVLYGSTYAYILVGGDLTAKGIGSAVGGK
          70      80      90     100     110     120

          130     140     150     160     170     180
m102.pep  VSLTVGQLVFFFGILAFVCWASARLVDREFTGVLIGGMVLTFIWAAGGLIADAKPSVLFDTQ
          : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g102       ISLTVGQLVFFFGILAFVCWASARLVDREFTGVLIGGMVLTFIWAATGGLVADAKPSVLFDTQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m102.pep  APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTIALVIYVLW

```

311

```

g102      ||:||:|||||
          APVGTGYWIIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWAGTLVALVIYVLW
          190      200      210      220      230      240

          250      260      270      280      290      300
m102.pep  QTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQTGNMDKILSLFSYMAIATSFLGVTL
          ||||:|||||
g102      QTAIQSNLPRNEFAPVIAAERQLSVLNETLSKFAQTGDMDKILSLFPYMAIATSFLGVTL
          250      260      270      280      290      300

          310      320      330      340      350
m102.pep  GLFDYIADIFKWNDSISGR-TKTAALTFLPPLISCLLFPTGFVTAIGYVGLAATVWT-GI
          |||| |||||:|||| |||:|||| ||:|||| |||| ||||| ||
g102      GLFDNIADIFKWNDSMSGRGKTVALNFLPPLISWLLPTGFFTAIGASGLAATVWDQGI
          310      320      330      340      350      360

          360      370      380      390      400      410
m102.pep  IPAMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGIVNIAAQVLSQMELVPVFKGX
          ||||| | :|||:|||||: |||||:|||||:|||||:|||||
g102      IPAMLLYVSPQKIGAGKTYKVYGGGLWML-VFLFGIANIAAQVLSQMELVPVFKGX
          370      380      390      400      410

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 361>:

a102.seq

```

1   ATGCCACCA AAACCCCTTC ACTGTTCCGC GCGCGATGA TTATCGCCGG
51  CACGNTCATC GCGCAGGTA TGCTCGCCAA CCCGACCGCC ACATCCGGCG
101 TATGGTTTAC CGGCTCGCTG GCCGTGTTGC TGTACACCTG GTTTTCCATG
151 CTCTCCAGCG GCCTGATGAT TTTGGAAGTC AACACCCACT ACCCCACGCG
201 CGCGANCTTC GACACCATGG TTAAAGACCT GCTCGGACGG AGCTGGAACA
251 TCATCAACGG CATCGCCGTC GCCTTCGTTT TATACCTGCT TACTTACGCT
301 TATATCTTCG TCGGCGGCGA CCTGACCGCC AAAGGCTTAG GCAGCGCGGC
351 AGGCGGCAAT GTTTCACCTCA CCGTCGGACA ACTCGTCTTC TTCGGCATTC
401 TCGCCTTTTG CGTATGGGCA TCCGCACGCT TGGTCGACCG ATTCACCAGC
451 GTCCTCATCG GCGGCATGGT ATTAACCTTT ATTTGGGCAA CCGCGGCCT
501 GATTGCCGAT GCCAACTGC CCGTCCTCTT CGACACCCAA GCCCCTACCG
551 GCACCAACTA CTGGATTTAT GTCGCCACCG CCCTGCCCCG CTGCCTTGCG
601 TCATTCGGTT TCCACGGCAA CGTCTCCAGC CTGCTCAAAT ACTTTAAAGG
651 CGACGCGCCC AAAGTGCTA AATCCATCTG GACGGGCACA CTGATTGCGC
701 TGGAATTTA CGTCTCTGG CAAACCGCCA TCCAANGCAA CCTGCCGCGC
751 AACGAGTTCG CCCCCGTGAT TGCCGCGCAA GGGCAAGTCT CCGTCNTGAT
801 TGAACCCCTG TCCAAATTCG CCAAACCGG CAATATGGAC AAAATATTGT
851 CCCTGTTTTT CTATATGGCG ATCGCCACCT CGTTTTTtagG CGTAACGCTC
901 GGA CTCTTCG ACTACATCGC CGACATCTTC AAATGGAACG ACAGCGTGTC
951 CGGCCGCACC AAAACCGCCG CGCTGACCTT CCTGCCGCTT NTAATTTCTT
1001 CGCTGCTCTT CCCCACCGGC TTTGTTACCG CCATCGGNTA CGTCGGCCTG
1051 GCGGCAACCG TCTGGACAGG CATCATCCCC GCCATGCTGC TNTACCGTTC
1101 GCGCAAAAAA TTCGGCGCAG GCAAAACCTA TAAAGTTTAC GCGGCTTGT
1151 GGCTGATGGT TTGGGTCTTC CTTTTCGGCA TCNTCAACAT CGCCGCACAN
1201 GTATTGAGCC AAATGGAAC TGTCCCGTA TTAAAGGAT AA
1202

```

This corresponds to the amino acid sequence <SEQ ID 362; ORF 102.a>:

a102.pep

```

1   MPTKTPSLFG GAMIIAGTXI GAGMLANPTA TSGVWFTGSL AVLLYTWFMS
51  LSSGLMILEV NTHYPHGAXF DTMVKDLLGR SWNIINGIAV AFVLYLLTYA
101 YIFVGGDLTA KGLGSAAGGN VSLTVGQLVF FGILAFVCWA SARLVDRTFS
151 VLIGGMVLTF IWATGGLIAD AKLPVLFDTQ APTGTNYWIY VATALPVCVA
201 SFGFHGNVSS LLKYFKGDAP KVAKSIWTGT LIALVIYVLW QTAIQXNLPR
251 NEFAPVIAAE GOVSVXIETL SKFAQTGNMD KILSLFSYMA IATSFLGVTL
301 GLFDYIADIF KWNDSVSGRT KTAALTFLPP XISCLLFPTG FVTAGYVGL
351 AATVWTGIIP AMLLYRSRKK FGAGKTYKVY GGLWLMVWVF LFGIXNIAAX
401 VLSQMELVPV FKG*

```

m102 / a102 95.9% identity in 413 aa overlap

312

m102.pep	10	20	30	40	50	60
	MPNKTPSLFGGAMIIAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
a102	MPTKTPSLFGGAMIIAGTXIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
	10	20	30	40	50	60
m102.pep	70	80	90	100	110	120
	NTHYPHGASFDTMVKDLLGRGWNIIINGIAVAFVLYLLTYAIFVGGDLTAKGLGSAAGGD					
a102	NTHYPHGAXFDTMVKDLLGRSWNIIINGIAVAFVLYLLTYAIFVGGDLTAKGLGSAAGGN					
	70	80	90	100	110	120
m102.pep	130	140	150	160	170	180
	VSLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFIWAAGGLIADAKPSVLFDTQ					
a102	VSLTVGQLVFFGILAFVCWASARLVDRFTSVLIGGMVLTFIWATGGLIADAKLPVLFDTQ					
	130	140	150	160	170	180
m102.pep	190	200	210	220	230	240
	APAGTNYWIYAATALPVCCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
a102	APTGTNYWIYVATALPVCCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
	190	200	210	220	230	240
m102.pep	250	260	270	280	290	300
	QTAIQGNLPRNEFAPVIAAEGQVSVLIELTSKFAQTGNMDKILSLFSYMAIATSFLGVTL					
a102	QTAIQXNLPRNEFAPVIAAEGQVSXLIETLSKFAQTGNMDKILSLFSYMAIATSFLGVTL					
	250	260	270	280	290	300
m102.pep	310	320	330	340	350	360
	GLFDYIADIFKWNDISGRKTAAALFLPPLISCLLFPTGFVTAIGYVGLAATVWTGIIP					
a102	GLFDYIADIFKWNDISVGRKTAAALFLPPXISCLLFPTGFVTAIGYVGLAATVWTGIIP					
	310	320	330	340	350	360
m102.pep	370	380	390	400	410	
	AMLLYRSRKKFGAGKTYKVYGGWLWMVWVFLFGIVNIAAQVLSQMELVPVFKGX					
a102	AMLLYRSRKKFGAGKTYKVYGGWLWMVWVFLFGIXNIAAXVLSQMELVPVFKGX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 363>:

g105.seq

1	Atgtccgcag	aaaCATACAc	acAAAAtcggc	tGGgtaggct	taggGcaaat
51	gGgtctgcct	atgGTAACGC	GGCTCTTGGA	CGGCGGCATC	GAAGTCGGCG
101	TATACAACCG	CTCGCCCGAC	AAAAC TGCCC	CCATCTCcgC	CAAAGGAGCA
151	AAAGTTTACG	GCagcACCGC	CGAACTCGTC	CGCGCCTGCC	CCGTCATTTT
201	CCTGATGGTT	TCCGACTATG	CCGCCGTGTG	CGACATCCTG	AACGGAGTCC
251	GCGACGGATT	GGCCGGCAAA	ATCATCGTCA	ACATGAGCAC	CATCTCCCCG
301	ACCGAAAACC	TCGCCGTCAA	AGCACTTGTC	GAAGCCGCAG	GCGGACAGTT
351	TGCCGAAGCA	CCCGTTTCCG	GATCGGTCGG	ACCCGCCACC	AACGGCACAC
401	TGCTGATTCT	GTTCGGCGGC	AGCGAAGCCG	TTTTAAACCC	GCTGCAAAAA
451	ATATTTTCCC	TTGTCGGCAA	AAAAACCTTC	CATTTTCGGCG	ATGTCGGCAA
501	AGGCTCGGGC	GCGAAACTCG	TCTTGAATCT	GCTCTTAGGC	ATTTTCGGCG
551	AAGCGTACAG	CGAAGCGATG	CTGATGGCGC	GGCAGTTCGG	CATCGATACC
601	GACACCATCG	TCGAAGCCAT	CGGCGGCTCG	GCAATGGACT	CGCCTATTGT
651	TCAAACAAAA	AAATCACTAT	GGGCAAACCG	TGAGTTCCCC	CCTGCCTTTG
701	CACTCAAAACA	CGCTTCCAAA	GAcctTAACC	TCGcgcgcAA	AGAGCTTGAA
751	CAGGCAGGCA	ACACCCTGCC	CGCCGTCGAA	ACCGTTGCTG	CCAGCTACCG
801	CAAAGCAGTT	GAAGCCGGCT	ACGGCGAACA	GGACGTTTCC	GGCGTTTACC
851	TGAAATTGGC	AGAACACTGA			

314

	190	200	210	220	230	240
g105.pep	IFGEAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK					
	: ::					
m105	AFSANVQRXXLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPXXFALKHASK					
	180	190	200	210	220	230
	250	260	270	280	289	
g105.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEH					
m105	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGTQDVSGVYLKLAEH					
	240	250	260	270	280	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 367>:

a105.seq

```

1  ATGTCCGCAA  ACGAATACAC  ACAAATCGGC  TGGATAGGCT  TAGGGCAAAT
51  GGGTCTGCCT  ATGGTAACGC  GGCTCTTGGA  CGGCGGCATC  GAAGTCGGCG
101 TATACAACCG  CTCGCCGAC  AAAACTGCCC  CCATCTCCGC  CAAAGGCGCA
151 AAAGTTTACG  GCAACACCGC  CGAACTCGTC  CGCGACTATC  CCGTCATTTT
201 CCTGATGGTT  TCCGACTATG  CCGCCGTGTG  CGACATCTGT  AACGGAGTCC
251 GCGACGGATT  GGCCGGCAAA  ATCATCGTCA  ACATGAGCAC  CATCTCCCGG
301 ACCGAAAACC  TCGCCGTCAA  AGCACTTGTC  GAAGCCGCAG  GCGGACAGTT
351 TGCCGAAGCA  CCCGTTTCCG  GATCGGTGCG  GCCCGCCACC  AACGGCACGC
401 TGCTGATTCT  GTTCGGCGGC  AGCGAAGCCG  TTTTAAACCC  GCTGCAAAAA
451 ATATTTTCCC  TCGTCGGCAA  AAAAACCTTC  CATTTCGGCG  ATGTCGGCAA
501 AGGTTTCGGC  GCGAAACTCG  TCTTGAATC  GCTCTTGGGC  ATTTTCGGCG
551 AAGCGTACAG  CGAAGCGATG  CTGATGGCGC  GGCAGTTCGG  CATCGATACC
601 GACACCATCG  TCGAAGCCAT  CGGCGGCTCG  GCAATGGACT  CGCCCATGTT
651 CCAAACCAA  AAATCCCTGT  GGGCAAACCG  CGAATTCCCA  CCCGCCTTCG
701 CCCTCAAACA  CGCTCCAAA  GACCTCAACC  TCGCCGTCAA  AGAGCTTGAA
751 CAGGCAGGCA  ACACCCTGCC  CGCCGTCGAA  ACCGTTGCTG  CCAGCTACCG
801 CAAAGCAGTC  GAAGCCGGCT  ACGGCGAACA  GGACGTTTCC  GCGGTTTACC
851 TGAAATTGGC  AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 368; ORF 105.a>:

a105.pep

```

1  MSANEYTQIG  WIGLGQMGLP  MVTRLLDGGI  EVGVYNRSPD  KTAPISAKGA
51  KVYGNTAELV  RDYPVIFLMV  SDYAAVCDIL  NGVRDGLAGK  IIVNMSTISP
101 TENLAVKALV  EAAGGQFAEA  PVSGSVGPAT  NGTLLILFGG  SEAVLNPLQK
151 IFSLVGKKT  FFGDVKGKSG  AKLVNLSLLG  IFGEAYSEAM  LMARQFGIDT
201 DTIVEAIGGS  AMDSPMFQTK  KSLWANREFP  PAFALKHASK  DLNLAVKELE
251 QAGNTLPAVE  TVAASYRKAV  EAGYGEQDVS  GVYLKLAEH*

```

m105/a105 96.5% identity in 289 aa overlap

	10	20	30	40	50	60
m105.pep	MSANEYAQIGWIGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
	:					
a105	MSANEYTQIGWIGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m105.pep	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISP TENLAVKALVEAAG-QFAEA					
a105	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISP TENLAVKALVEAAGGQFAEA					
	70	80	90	100	110	120
	120	130	140	150	160	179
m105.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVKGSGAKLVNLSLLG					
a105	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVKGSGAKLVNLSLLG					
	130	140	150	160	170	180
	180	190	200	210	220	230

315

```

m105.pep    IFGDV-QRXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPXAFALKHASK
|||::: :: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a105        IFGEAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
              190      200      210      220      230      240

m105.pep    240      250      260      270      280
DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a105        250      260      270      280      290
DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 369>:

g105-1.seq

```

1  ATGTCCGCAG AAACATACAC ACAAATCGGC TGGGTAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCCGAC AAAACTGCCC CCATCTCCGC CAAAGGAGCA
151 AAAGTTTACG GCAGCACC GC AACTCGTC CGCGCCTGCC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
301 ACCGAAACCG TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG ACCCGCCACC AACGGCACAC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAACCTTC CATTTCCGCG ATGTCGGCAA
501 AGGCTCGGGC GCGAAACTCG TCTTGAATC GCTCTTAGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCTATGTT
651 TCAAACAAAA AAATCACTAT GGGCAAACCG TGAGTTCCCC CCTGCCTTTG
701 CACTCAAACA CGCTTCCAAA GACCTTAACC TCGCCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTT GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAATTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 370; ORF 105-1.ng>:

g105-1.pep

```

1  MSAETYTOIG WVGLGQMGLP MVTRLDDGGI EVGVYNRSPD KTAPISAKGA
51  KVGNTAEVLV RACPVIFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP
101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLILIFGG SEAVLNPLQK
151 IFSLVGKKTF HFGDVGKGSG AKLVLSLLG IFGEAYSEAM LMARQFGIDT
201 DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 371>:

m105-1.seq

```

1  ATGTCCGCAA ACGAATACGC ACAAATCGGC TGGATAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCCGAC AAAACTGCCC CCATCTCCGC CAAAGGCGCA
151 AAAGTTTACG GCAACACC GC AACTCGTC CGCGACTATC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
301 ACCGAAACCG TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG GCCCGCCACC AACGGCACGC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TCGTCGGCAA AAAACCTTC CATTTCCGCG ATGTCGGCAA
501 AGGTTCGGGC GCGAAACTCG TCTTGAATC GCTCTGGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGSGACTCG GCAATGGACT CGCCCATGTT
651 CCAAACAAAA AAATCCCTGT GGGCAAACCG CGAATTCCCG CCGCCTTCG
701 CCCTCAAACA CGCCTCCAAA GACCTCAACC TCGCCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTC GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAACTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 372; ORF 105-1>:

m105-1.pep

```

1  MSANEYAQIG WIGLQGMGLP MVTRLDDGGI EVGVYNRSPD KTAPISAKGA
51  KVGNTAEVLV RDPVIFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP

```

316

101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK
 151 IFSLVGKKTFF HFGDVGKGS AKLVLSLLG IFGEAYSEXM LMARQFGIDT
 201 DTIVEAIGDS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
 251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

m105-1/g105-1 96.9% identity in 289 aa overlap

	10	20	30	40	50	60
m105-1.pep	MSANEYAQIGWIGLGQMG LPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
g105-1	MSAETYTQIGWVGLGQMG LPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGSTAELV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m105-1.pep	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA					
g105-1	RACPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m105-1.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGS GAKLVLSLLG					
g105-1	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGS GAKLVLSLLG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m105-1.pep	IFGEAYSEXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK					
g105-1	IFGEAYSEAMLARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK					
	190	200	210	220	230	240
	250	260	270	280	290	
m105-1.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX					
g105-1	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 373>:

a105-1.seq

1 ATGTCCGCAA ACGAATACAC ACAAATCGGC TGGATAGGCT TAGGGCAAAT
 51 GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGCGCGCATC GAAGTCGGCG
 101 TATACAACCG CTCGCCGAC AAAACTGCC CCATCTCCGC CAAAGCGCGA
 151 AAAGTTTACG GCAACACCGC CGAACTCGTC CGCGACTATC CCGTCATTTT
 201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
 251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCG
 301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGAG GCGGACAGTT
 351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG GCCCGCCACC AACGGCACGC
 401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
 451 ATATTTTCCC TCGTCGGCAA AAAAACCTTC CATTTCGGCG ATGTCGGCAA
 501 AGGTTCCGGG GCGAAACTCG TCTTGAACCT GCTCTTGGGC ATTTTCGGCG
 551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
 601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCCATGTT
 651 CCAAACCAAA AAATCCCTGT GGGCAAACCG CGAATTCCCA CCCGCCTCG
 701 CCCTCAAACA CGCCTCCAAA GACCTCAACC TCGCCGTCAA AGAGCTTGAA
 751 CAGGCAGGCA ACACCCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
 801 CAAAGCAGTC GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
 851 TGAAATTGGC AGAACACTGA

This corresponds to the amino acid sequence <SEQ ID 374; ORF 105-1.a>:

a105-1.pep

1 MSANEYTQIG WIGLGQMG LPMVTRLLDGGI EVGVYNRSPD KTAPISAKGA
 51 KVGYNTEALV RDYPVIFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP
 101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK
 151 IFSLVGKKTFF HFGDVGKGS AKLVLSLLG IFGEAYSEAM LMARQFGIDT
 201 DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
 251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

a105-1/m105-1 99.0% identity in 289 aa overlap

	10	20	30	40	50	60
a105-1.pep	MSANEYTQIGWIGLGQMG LPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					

m105-1	MSANEYAQIGWIGLGQMG LPMVTRLDDGGIEVGVYNRSPDKTAPISAKGAKVYGN TAE LV
	10 20 30 40 50 60
a105-1.pep	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPTENLAVKALVEAAGGQFAEA
m105-1	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPTENLAVKALVEAAGGQFAEA
	70 80 90 100 110 120
a105-1.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGSGAKLVLSLLG
m105-1	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGSGAKLVLSLLG
	130 140 150 160 170 180
a105-1.pep	IFGEAYSEAMLMARQFGIDTD TIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
m105-1	IFGEAYSEXMLMARQFGIDTD TIVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK
	190 200 210 220 230 240
a105-1.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
m105-1	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
	250 260 270 280 290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 375>:

```

g107.seq
1  ATGGTATTAA CCTTTATTTG GGCAACCGGC GGCCTGGTTG CCGATGCCAA
51  ACCGTCCGTC CTCTTCGACA CCCAAGCCCC CGTCGGCACC GGCTACTGGA
101 TTTACGCCGC CACCGCCCTG CCCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTTT CCAGCCTGCT CAAATACTTT AAAGGCGACG cgcCcaaagt
201 GgCGAaATCc atctggGcag gtacattggT TGCcttggtta atttacgtcc
251 TCTggcaaac cgccatCcaa agcaaccTGC cgcgcaacga gttcgcCCCC
301 gtgattgccg cggagaggca actCTCCGTC CTgaatgaaa cccTgtccaa
351 attcgcccaa accggcgata tggataAaat attgtcccta tttccctaca
401 tggcaatcgc cacctccttt ttaggcgTAA Ccttaggcct gtttgacaac
451 atcgccggac atcttcaaat ggaacgacag tatgtccggg cggcaccaaa
501 accgtcgcg tga

```

This corresponds to the amino acid sequence <SEQ ID 376; ORF 107.ng>:

```

g107.pep
1  MVLTFIWATG GLVADAKPSV LFDTQAPVGT GYWIYAATAL PVCLASFGEFH
51  GNVSSLLKYF KGDAPKVAKS IWAGTLVALV IYVLWQTAIQ SNLPRNEFAP
101 VIAAERQLSV LNETLSKFAQ TGDMDKILSL FPYMAIATSF LGVTGLGLFDN
151 IAGHLQMERQ YVRAAPKPSR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 377>:

```

m107.seq
1  ATGGTATTGA CCTTTATTTG GGCGGCCGCG GGGCTGATTG CCGATGCCAA
51  GCCGTCCGTC CTCTTCGATA CCCAAGCCCC CGCCGGCACA AACTACTGGA
101 TTTACGCCGs CACCGCCCTG CCCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTCT CCAGCCTGCT CAAATACTTT AAAGGCGACG CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGCGCTGGTA ATTTACGTCC
251 TCTGGCAAAC CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTCATCGCCG CCGAAGGGCA AGTCTCCGTC CTCATCGAAA CCCTGTCCAA
351 ATTCGCCCCA ACCGGCAATA TGGACAAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGGCGTAA CGCTCGGACT CTTCGACTAC
451 ATCGCCCATC TTCAAATGGA ACGACAGCAT CTCCGGgCCG CACCAAAACC
501 GCCGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 378; ORF 107>:

```

m107.pep..
1  MVLTFIWAAG GLIADAKPSV LFDTQAPAGT NYWIYAXTAL PVCLASFGEFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTLIALV IYVLWQTAIQ GNLPRNEFAP

```

101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTLGLFDY
 151 IAHLQMERQH LRAAPKPPR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 107 shows 89.4% identity over a 170 aa overlap with a predicted ORF (ORF 107.ng) from *N. gonorrhoeae*:

m107/g107

	10	20	30	40	50	60
m107.pep	MVLTFIWAAGGLIADAKPSVLFDTQAPAGTNYWIYAXTALPVCLASFGFHGNVSSLLKYF					
	: : : : : :					
g107	MVLTFIWATGGLVADAKPSVLFDTQAPVGTGYWIYAATALPVCLASFGFHGNVSSLLKYF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m107.pep	KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
	: : : : : :					
g107	KGDAPKVAKSIWAGTLVALVIYVLWQTAIQSNLPRNEFAPVIAAERQLSVLNETLSKFAQ					
	70	80	90	100	110	120
	130	140	150	160	170	
m107.pep	TGNMDKILSLFSYMAIATSF LGVTLGLFDYIA-HLQMERQHLRAAPKPPR					
	: : : : : :					
g107	TGDMDKILSLFPYMAIATSF LGVTLGLFDNIAGHLQMERQYVRAAPKPSR					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 379>:

a107.seq

```

1  ATGGTATTAA CCTTTATTTG GGCAACCGGC GGCCTGATTG CCGATGCCAA
51  ACTGCCCGTC CTCTTCGACA CCCAAGCCCC TACCGGCACC AACTACTGGA
101 TTTATGTCGC CACCGCCCTG CCCGTCTGCC TTGCGTCATT CGGTTTCCAC
151 GGCAACGTCT CCAGCCTGCT CAAATACTTT AAAGCGCAGC CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGCGCTGGTA ATTTACGTCC
251 TCTGGCAAAC CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTGATTGCCG CCGAAGGGCA AGTCTCCGTC CTGATTGAAA CCCTGTCCAA
351 ATTCGCCCCA ACCGGCAATA TGGACAAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGGCGTAA CGCTCGGACT CTTCGACTAC
451 ATCGCCGACA TCTTCAAATG GAACGACAGC GTGTCCGGCC GCACCAAAC
501 CGCCGCGCTG ACCTTCCTGC CGCCTCTAAT TTCCTGCCTG CTCTTCCCCA
551 CCGCTTTTGT TACCGCCATC GGCTACGTCG GCCTGGCGGC AACCGTCTGG
601 ACAGGCATCA TCCCCGCCAT GCTGCTCTAC CGTTCGCGCA AAAAATTTCG
651 CGCAGGCAAA ACCTATAAAG TTTACGGCGG CTTGTGGCTG ATGGTTTGGG
701 TCTTCCTTTT CGGCATCGTC AACATCGCCG CACAGGTATT GAGCCAAATG
751 GAACTCGTCC CCGTATTTAA AGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 380; ORF 107.a>:

a107.pep

```

1  MVLTFIWATG GLIADAKLPV LFDQTAPTGT NYWIYVATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTLIALV IYVLWQTAIQ GNLPRNEFAP
101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTLGLFDY
151 IADIFKWNDS VSGRTKTAAL TFLPPLISCL LFPTGFVTAI GYVGLAATVW
201 TGIIPAMLLY RSRKKFGAGK TYKVYGGWL MVWVFLFGIV NIAAQVLSQM
251 ELVPVFKG*

```

m107/a107 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m107.pep	MVLTFIWAAGGLIADAKPSVLFDTQAPAGTNYWIYAXTALPVCLASFGFHGNVSSLLKYF					
	: : : : : :					
a107	MVLTFIWATGGLIADAKLPVLFDTQAPTGTNYWIYVATALPVCLASFGFHGNVSSLLKYF					
	10	20	30	40	50	60

	70	80	90	100	110	120
m107.pep	KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
a107	KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
	70	80	90	100	110	120
	130	140	150	160	170	
m107.pep	TGNMDKILSLFSYMAIATSFLGVTGLGLFDYIAHLQMERQHLRAAPKPPRX					
a107	TGNMDKILSLFSYMAIATSFLGVTGLGLFDYIADIFKWNDSVSGRTKTAALTFLPPLISCL					
	130	140	150	160	170	180
a107	LFPTGFVTAIGYVGLAATVWTGIIIPAMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGIV					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 381>:

```

g108.seq
1   ATGttgccgg gCTTCAACCG GATATTCAaa cggTTTGCTC CAACACTCGG
51  AAcggCGCAT AAAACGCCgc ccTTCGCGTT ATCCCGAACG GGGCGGCTAA
101 TCAGATCCTA TCGCCATAAA AGGCGGGGTT TCAACCGAAA AGGAATTGAG
151 ATGAATAAAA CCTTGTCTAT TTTGCCGGCG GCAATCTTAC TCGGCGGGTG
201 CGCCGCCGGC GGCAACACAT TCGGCAGCTT AGACGGCGGC ACGGGTATGG
251 GTGGCAGCAT CGTCAAAATG ACGGTAGAAA gccAATGCCG TCGGGAATTG
301 GACAGGCGCA GCGAATGCCG TTTGACCGCG CTGGCGATGA GTGCCGAAAA
351 ACAGGCGGAA TGGGAAAACA AGATTTGCGG CTGCGCTACC GAAGAAGCAC
401 CTAACCAGCT GACCGGCAAC GATGTGATGC AGATGCTGaa ccagtccacG
451 CGCaatcagg cacTtgccgc CctgaccgTC AAAacggtTT CcgctgcTT
501 CAaacgcctg tACCGCTaa

```

This corresponds to the amino acid sequence <SEQ ID 382; ORF 108.ng>:

```

g108.pep
1   MLPGFNRIFK RFAPTLGTAH KTPPFALSRT GRLIRSYRHK RRGFNRKGIE
51  MNKTLSILPA AILLGGCAAG GNTFGSLDGG TGMGGSIVKM TVESQCRAEL
101 DRRSEWRLTA LAMSAEKQAE WENKICGCAT EEAPNQLTGN DVMQMLNQST
151 RNQALAAALTV KTVSACFKRL YR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 383>:

```

m108.seq
1   ATGTTGCCGG GCTTCAACCG GATATTCAAA CGGTTTGTTT CAACACTCGG
51  AACGGCGCAT AAAACGCCGC CCTTCGCGTT ATCCCGAACG GGGCGGCTAA
101 TCAGATTCTA TCGCCATAAA AGGCGGGGTT TCAACCGAAA AGGAATTGAG
151 ATGAATAAAA CCTTGTCTAT TTTGCCGGTG GCAATCTTAC TCGGCGGCTG
201 CGCCGCCGGA GGCGGTAACA CATTTCGGCAG CTTAGACGGT GGCACAGGCA
251 TGGGCGGCAG CATCGTCAAA ATGGCGGTTG GGAGCCAATG CCGTGCGGAA
301 TTGGACAAAC GCAGCGAATG GCGTTTGACC GCGCTGGCGA TGAGTGCCGA
351 AAAACAGGCG GAGTGGGAAA ACAAGATTG CGCTTGCGTC GCCCAAGAAG
401 CACCGAACG GATGACCGGC AACGATGTGA TGCAGATGCT GGCTCCGTCC
451 ACGCGCAATC AGGCACTTGC CGCCCTGACC GCCAAAACG TTTCCGCCTG
501 CTTCAAACAC CTGTACCGCT AA

```

This corresponds to the amino acid sequence <SEQ ID 384; ORF 108>:

```

m108.pep
1   MLPGFNRIFK RFVPTLGTAH KTPPFALSRT GRLIRFYRHK RRGFNRKGIE
51  MNKTLSILPV AILLGGCAAG GGNTFGSLDG GTGMGGSIVK MAVGSQCRAE
101 LDKRSEWRLT ALAMSAEKQA EWENKICACV AQEAPERMTG NDVMQMLAPS
151 TRNQALAAAL AKTVSACFKH LYR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 108 shows 89.6% identity over a 173 aa overlap with a predicted ORF (ORF 108.ng) from *N. gonorrhoeae*:

m108/g108

	10	20	30	40	50	60
m108.pep	MLPGFNRIFKRFVPTLGTAKHTPPFALSRTGRLIRFYRHKRRGFNRKGIEMNKTL SILPV					
	: :					
g108	MLPGFNRIFKRFAPLTGTAKHTPPFALSRTGRLIRSRYHKRRGFNRKGIEMNKTL SILPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m108.pep	AILLGGCAAGGGNTFGSLDGGTGMGGSIVKMAVG SQCRAELDKRSEWR L TALAMSAEKQA					
	: : : :					
g108	AILLGGCAAGG-NTFGSLDGGTGMGGSIVKMTVESQCRAELDR RSEWR L TALAMSAEKQA					
	70	80	90	100	110	
	130	140	150	160	170	
m108.pep	EWENKICACVAQEAPERMTGN DVMQMLAPSTRNQALAA LTAKTVSACFKHLYRX					
	: :: :: : :					
g108	EWENKICGCATEEAPNQLTGNDVMQMLNQSTRNQALAA LVKTVSACFKRLYRX					
	120	130	140	150	160	170

a108.seq

1	ATGTTGCCGG	GCTTCAACCG	GATATTCAA	CGGTTTGTT	CAACACTCG
51	AACGGCGCAT	AAAACGCCG	CCTTCGCGT	ATCCCGAAC	GGGCGGCTA
101	TCAGATTCTA	TCGCCATAA	AGGCGGGGT	TCAACCGAA	AGGAATTGAG
151	ATGAATAAAA	CCTTGTCTA	TTTGCCGGT	GCAATCTTA	TCCGCGGCTG
201	CGCGCCCGG	GGCGGTAA	CATTGGCGA	CTTAGACGC	GGCACAAGTA
251	TGGGCGGCAG	CATCGTCAA	ATGGCGGTAG	AAAGCCAAT	CCGTGCGGAA
301	TTGAACAAAC	GCAGCGAAT	GCGTTTGAC	GCGCTGGCG	TGAGTGCCGA
351	AAAACAGGCG	GAATGGGAA	ACAAGATTG	CGCTTGCGT	GCCCAAGAAG
401	CACCCAACCA	GCTGACCGC	AACGATGTG	TGCAGATGT	GGATCCGTCC
451	ACCGCAATC	AGGCACTTG	CGCCCTGAC	GCCAAAACG	TTTCCGCGTG
501	CTTCAAACAC	CGTACCGCT	AA		

a108.pep

1 MLPGFNRIKF RVVPTLGTAH KTPPFALSRT GRLIRFYRHK RRGFNKRGIE
51 MNKTLSILPV AILLGGCAAG GGNTFGSLDG GTGMGGSIVK MAVESQCRAE
101 LNKRSWRLT ALAMSAEKQA EWENKICACV AQEAPNQLTG NDVMQMLDPS
151 TRNOALAALT AKTVSACFKH Lyr*

		10	20	30	40	50	60
m108.pep		MLPGFNRI	FKRFVPTL	GTAHKTPP	FALSRTGR	LIRFYRHK	RGRGFNRK
a108		MLPGFNRI	FKRFVPTL	GTAHKTPP	FALSRTGR	LIRFYRHK	RGRGFNRK
		10	20	30	40	50	60
		70	80	90	100	110	120
m108.pep		AILLGGCA	AAGGGNTF	GSLDGGT	GMGGSIVK	MAVGSQC	RAELDKR
a108		AILLGGCA	AAGGGNTF	GSLDGGT	GMGGSIVK	MAVESQC	RAELNKR
		70	80	90	100	110	120
		130	140	150	160	170	
m108.pep		EWENKIC	ACVAQE	APERMT	GNQDVM	QMLAPST	RNQALA
a108		EWENKIC	ACVAQE	APNQLT	GNQDVM	QMLDPST	RNQALA
		130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 387>:

g109.seq

```

1  ATGTATTATC GCCGGGTTGT GGGGCTATCC GATGGACTTG GCGATTGCGC
51 AGCCGGTATT GATCGTAGGC GTATGCTTAC CGCTTTTGGA AGCGGGCATG
101 GAAATGACGC GCAAAGGCAA AACCACCCAA TCCGCCGCCA TCGTGGTGTT
151 CTCTTCCGTC TGGTCAATCC GGTTTTCGGC TGGGCGTTGA CGATGCTGTT
201 GGATAATTTG GGCTTAATCG GCTGCAAAGA ACGCAGCGCG CAATTAGGTT
251 TTGTCGGACG AGTATTGATA CCCGCACTAG GTTTCTTAAT CTTGTGTGTG
301 GCGATGGGTG CGGTCGGGAT GCTGCCCCGT ATCCCTCCGT TTTTGGAGCA
351 GTTCAAATCT TTGGGCTAG

```

This corresponds to the amino acid sequence <SEQ ID 388; ORF 109.ng>:

g109.pep

```

1  MYRVRVGLS DGLGDLAAGI DRRRMLTAFG SHHGNDQRQ NHPIRRHRGV
51 LFRVLPVFG WALTMLLDNL GLIGCKERSA QLGFGVRLI PAVGFLILCV
101 AMGAVGMLPG IPPFLEQFKS LG

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 389>:

m109.seq

```

1  ATGTATTATC GCCGGGTTAT GGGGCTATCC GATGGACTTG GCGATTGCGC
51 AGCCGGTATT GAGCGTAGCC TTGGTCGTAG GCGTATACTT ACCGCTTTTG
101 GAAGCGGGCA TGGAAATGAC GCGCAAAGGC AAAACCACCC AATCCGCCGC
151 CATCGTGGTG TTCTCTTCCG CCTTGTCATC CCGGTTTTTCG GCTGGGCGTT
201 GACGATGCTG TTGGATAATT TGGGCTTAAT CGGCTGCAA GAGCGCAGTG
251 CGCAATTAGG TTTCGCCGGA CGCGTGTGA TACCCGAGT AGGTTTCTTG
301 ATCTTGTTG TGGCGATGGG TCGGTCGGG ATGCTGCCCG GTATCCCGCC
351 GTTTTTGGA CACTTCAAAT CTTTGGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 4; ORF 109>:

m109.pep

```

1  MYRVRVMGLS DGLGDLAAGI ERSLGRRRIL TAFSGHGND AQRQNHPIRR
51 HRGVLFRLVN PVFGWALTML LDNLGLIGCK ERSAQLGFAG RVLIPAVGFL
101 ILCVAMGAVG MLPGIPPFLE HFKSLG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 109 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 109.ng) from *N. gonorrhoeae*:

m109/g109

	10	20	30	40	50	60
m109.pep	MYRVRVMGLSDGLGDLAAGIERSLGRRIILTAFGSHHGNDQRQNHPIRRHRGVLFRLVN					
	: : :					
g109	MYRVRVGLSDGLGDLAAGIDR---RRMLTAFSGSHHGNDQRQNHPIRRHRGVLFRLVN					
	10	20	30	40	50	
	70	80	90	100	110	120
m109.pep	PVFGWALTMLLDNLGLIGCKERSAQLGFAGRVLIPAVGFLILCVAMGAVGMLPGIPPFLE					
	:					
g109	PVFGWALTMLLDNLGLIGCKERSAQLGFVGRVLIPAVGFLILCVAMGAVGMLPGIPPFLE					
	60	70	80	90	100	110
m109.pep	HFKSLGX					
	:					
g109	QFKSLGX					
	120					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 391>:

a109.seq

```

1  ATGTATTATC GCCGGGTTGT GGGGCTATCC GATGGACTTG GCGATTGCGC
51 AGCCGGTATT GAGCGTAGCC TTGGTCGTAG GCGTATACTT ACCGCTTTTG
101 GAAGCGGGCA TGGAAATGAC GCGCAAAGGC AAAACCACCC AATCCGCCGC
151 CACCGTGGTG TTCTCTTCCG CTTGGTCAAT CCGGTTTTTCG GCTGGGCGTT

```

322

```

201 GACGATGCTG TTGGATAATT TGGGCTTAAT CGGCTGCAAA GAGCGCAGCG
251 CGCAATTAGG TTTCACCGGA CGCGTATTGA TACCCGTAGT AGGTTTCTTG
301 ATCTTGTGTG TGGCGATGGG TGCGGTCGGG ATGCTGCCCC GTATCCCGCC
351 GTTTTGGAG CACTTCAAAT CTTTGGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 392; ORF 109>:

a109.pep

```

1 MYYRRVVGLS DGLGDLAAGI ERSLGRRRIL TAFSGSHGND AQRQNHPIRR
51 HRGVLFRVLN PVFGWALTML LDNLGLIGCK ERSAGLGFTG RVLIPVVGFL
101 ILCVAMGAVG MLPGIPPFLE HFKSLG*

```

m109/a109 97.6% identity in 126 aa overlap

	10	20	30	40	50	60
m109.pep	MYYRRVMGLSDGLGDLAAGIERSLGRRRILTAFSGSHGND AQRQNHPIRRHRGVLFRVLN					
	:					
a109	MYYRRVVGLSDGLGDLAAGIERSLGRRRILTAFSGSHGND AQRQNHPIRRHRGVLFRVLN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m109.pep	PVFGWALTMLLDNLGLIGCKERSAQLGFAGRVLIPAVGFLILCVAMGAVGMLPGIPPFLE					
	:					
a109	PVFGWALTMLLDNLGLIGCKERSAQLGFTGRVLIPVVGFLILCVAMGAVGMLPGIPPFLE					
	70	80	90	100	110	120
m109.pep	HFKSLGX					
a109	HFKSLGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 393>:

g111.seq

```

1 ATGCCGTCTG AAACACGCCT GCCGAACCTT ATCCGCGCCT TGATATTTGC
51 CCTGGGTTTC ATCTTCCTGA ACGCCTGTTC GGAacaaac GCGCAaacg
101 TTACCCTGCA AGGCGAAACG ATGGGTACGA CcTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCCCCT GCCAAAATAC AAAAGCGCAT
201 TGATGATGCG CTAAAGAAG TCAACCGGCA GATGtccaCC TACCAGACCG
251 ATTCCGAAAT CAGCCGGTt atacagacan atgctggaga gctcttcgcg
301 tntcatgcag nttctataac tgattccgcc gaagactgtc tgcctaatac
351 gcctatctca tcggcgctct ga

```

This corresponds to the amino acid sequence <SEQ ID 394; ORF 111.ng>:

g111.pep

```

1 MPSETRLPNL IRALIFALGF IFLNACSEQT AQTVTLOGET MGTYYTVKYL
51 SNNRDKLPSF AKIQKRIDDA LKEVNRQMSY YQTDSEISRF IQTAGELFAH
101 ASITDSAEDC LPNTPISSAL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 395>:

m111.seq

```

1 ATGCCGTCTG AAACACGCCT GCCGAACCTT ATCCGCGTCT TGATATTTGC
51 CCTGGGTTTC ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCCTGCA AGGCGAAACG ATGGGCACGA CCTATAYCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AWAACGCAT
201 CGATGACGCG CTAAAGAAG TCAACCGGyA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCTCCGC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC GCCTGAACCG
351 CCTGACACAC GGCGCGCTGG ACGTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTCGG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAGG CGGCATCTTA TACGGGCATA GACAAAATCA TTTTGAACAA
501 AGGCAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCAAG GCCTATTTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TGCGGGCGAA

```

```
m111.pep
1  MPSETRLPNF IRVLIFALGF IFLNACSEQT AQTVTLQGET MGTTYXVKYL
51  SNNRDKLPSP AEIXKRIDDA LKEXNRXMST YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPK VNLWGF GPDK SVTREPSPEQ
151 IKQAASYTGI DKII LKQKG D YASLSKTHPK AYLDLSSIAK GFGVDK VAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGE PWR IGIEQPNIVQ GGNTQI IVPL
251 NNRSLATSGD YRIFHVDKNG KRLSHIINPN NKRPI SHNLA SISV VADSAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*
```

m111.pep/g111.pep

	10	20	30	40	50	60
m111.pep	MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLQGETMGTTYXVKYLSNNRDKLPSP					
	: :					
g111	MPSETRLPNLIRALIFALGFIFLNACSEQTAQTVTLQGETMGTTYTVKYLSNNRDKLPSP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m111.pep	AEIXKRIDDALKEXNRXMSQPDSEISRNFQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
	: : :					
g111	AKIQKRIDDALKEVNRQMSQYQTDSEISRFIQTXAGELFAXHAXSITDSAEDCLPNTPI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m111.pep	GALDVTVGPLVNLWGFQDPKSVTREPSPEQIKQAASYTGIDKIILKQKDYASLSKTHPK					
g111	SALX					

a111.seq

1	ATGCCGCTCTG	AAACACGCCT	GCCGAACTTT	ATCCGCACCT	TGATATTTGC
51	CCTGAGTTTT	ATCTTCTCTA	ACGCCTGTTC	GGAAACAAAC	GCGCAAAACG
101	TTACCTGCA	AGGTGAAACG	ATGGGACGA	CTTATACCGT	AAAATACCTT
151	TCAAATAATC	GGGACAAACT	CCCTCACCT	GCCGAAATAC	CAAAAGCGCAT
201	CGATGACGCG	CTTAAAGAAG	TCAACCGGCA	GATGTCCACC	TATCAGCCCG
251	ACTCGGAAAT	CAGCGGTTTC	AACCAACACA	CAGCCGGCAA	GCCCCCTCCG
301	ATTTCAAGCG	ACTTCGCACA	CGTTACTGCC	GAAGCGCTGC	ACCTGAACCG
351	CCTGACACAC	GGCGCGCTGG	ACGTAACCGT	GGCCCCCTTG	GTC AACCTTT
401	GGGGATTTCG	CCCCGACAAA	TCCGTTACCC	GTGAACCGTC	GCCGGAACAA
451	ATCAAACAAG	CAGACTCTTA	TACGGGCATA	GACAAAAATCA	TTTTGAAACA
501	AGGCAAGAT	TACGCTTCCT	TGAGCAAAAC	CCACCCCAG	GCCATTTTGG
551	ATTTATCTTC	GATTGCCAAA	GGCTTCGGCG	TTGTATAAAGT	TGCGGGCGAA
601	CTGGA AAAAT	ACGGCATTCA	AAATTATCTG	GTGAAATCG	GCGGCGAGTT
651	GCACGGCAA	GGCAAAAAAC	GCGCGGCGGA	ACCTTGGGCG	ATCGGCATCG
701	AACAGCCCAA	CATCGTCCAA	GGCGGCAATA	CGCAGATTAT	CGTCCCGCTG
751	AACAACCGTT	CGCTTGCCAC	TTCCGGCGAT	TACCGTATTT	TCCACGTCG

```

801 TAAAAGCGGC AAACGCCTCT CCCATATCAT TAATCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCGATG
901 ACGGCGGACG GCTTGTCCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAAGCTCG TGTTCCTG ATTGTCAGGG
1001 ATAAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTTGA AAAAGTCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 398; ORF 111.a>:

a111.pep

```

1 MPSETRLPNF IRTLIFALSF IFLNACSEQT AQTVTLOGET MGTITYTVKYL
51 SNNRDKLPSP AEIQKRIDDA LKEVNRQMSY YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTAE EAVHLNRLTH GALDVTVGPL VNLWGFDPK SVTREPSPEQ
151 IKQAASYTGI DKIIILKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPRW IGIEQPNIVQ GGNTQIIIVPL
251 NNRSLATSGD YRIFHVDKSG KRLSHIINPN NKRPIHNLAS SISVVDASAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

m111/a111 97.7% identity in 351 aa overlap

m111.pep	10	20	30	40	50	60
	MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLQGETMGTITYXVKYLSNNRDKLPSP					
a111	MPSETRLPNFIRTLIFALSFIFLNACSEQTAQTVTLQGETMGTITYTVKYLSNNRDKLPSP					
	10	20	30	40	50	60
m111.pep	70	80	90	100	110	120
	AEIXKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
a111	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISSDFAHVTAEAVHLNRLTH					
	70	80	90	100	110	120
m111.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFDPKSVTREPSPEQIKQAASYTGIDKIIILKQKDYASLSKTHPK					
a111	GALDVTVGPLVNLWGFDPKSVTREPSPEQIKQAASYTGIDKIIILKQKDYASLSKTHPK					
	130	140	150	160	170	180
m111.pep	190	200	210	220	230	240
	AYLDLSSIAKGFVGVKAGELEKYGIQNYLVEIGGELHGKGNARGEPRWIGIEQPNIVQ					
a111	AYLDLSSIAKGFVGVKAGELEKYGIQNYLVEIGGELHGKGNARGEPRWIGIEQPNIVQ					
	190	200	210	220	230	240
m111.pep	250	260	270	280	290	300
	GGNTQIIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNNKRPIHNLASISVVDASAM					
a111	GGNTQIIIVPLNNRSLATSGDYRIFHVDKSGKRLSHIINPNNKRPIHNLASISVVDASAM					
	250	260	270	280	290	300
m111.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
a111	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 399>:

g111-1.seq

```

1 ATGCCGCTCTG AAACACGCCT GCCGAACCTT ATCCGCGCCT TGATATTTGC
51 CCTGGGTTTC ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAaCCG
101 TTACCCTGCA AGGCGAAACG ATGGGTACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCCCCT GCCAAAATAC AAAAGCGCAT
201 TGATGATGCG CTTAAGAAG TCAACCGCA GATGTCCACC TACCAGACCG

```



```

251 ATTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ATTTGCGACA CGTTACCGCC GAAGCCGTCC GCCTGAACCG
351 CCTGACTCAC GCGCGACTGG ACGTAACCGT CGGCCCTTTG GTCAACCTTT
401 GGGGGTTCGG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAGG CGGCATCTTA TACGGGCATA GACAAAATCA TTTTGCAACA
501 AGGCAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAA GCCTATTGCG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGGCGAA
601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCggcGAGTT
651 GCACGGCAAA GGCAAAAATG CGCACGGCGA ACCGTGGCGC ATCGGTATAG
701 AGCAACCCAA TATcatccaa ggcggcaata cgcAGattat cgtcccgtg
751 aaCaaccgtt cgcttgccac ttccggcgat taccgtaTTT tccacgtcgA
801 TAAAAACGGC Aaacgccttt cccacATCAT CAATCCCAAC AACAAACGAC
851 CCATCAGcCA CAacctcgcc tcCATCagCg TGGTCTCAGA CAGTGCAATG
901 ACGGCGGACG GTTTATCCAC AGGATTATTT GTTTTAGGCG AAACCGAAGC
951 CTTAAGGCTG GCAGAACAAG AAAAATCTCG TGTTCCTTA ATTGTCCGGG
1001 ATAAGGACGG CTACCGCACC GCCATGTCTT CCGAATTGTC CAAGCTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 400; ORF 111-1.ng>:

```

g111-1.pep
1  MPSETRLPNL IRALIFALGF IFLNACSEQT AQTVTLOGET MGTITYVKYL
51  SNNRDKLPSP AKIQKRIDDA LKEVNRQMSY YQTDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWGFPGDK SVTREPSPEQ
151 IKQAASVTGI DKIIKQGGK YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHKG GKNAGPEPWR IGIEQPNIIQ GGNTQIIIVPL
251 NNRSLATSGD YRIFHVDKNG KRLSHIINPN NKRPIHNLA SISVVSDSAM
301 TADGLSTGLF VLGETEALRL AEQEKLAFLV IVRDKDGYRT AMSSEFAKLL
351 R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 401>:

```

m111-1.seq
1  ATGCGCTCTG AAACACGCCT GCCGAACCTT ATCCGCGTCT TGATATTGCG
51  CCTGGGTTTC ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCCCTGCA AGGCGAAACG ATGGGACGCA CCTATACCGT CAAATACCTT
151 TCAATAAGAT GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAACGCAT
201 CGATGACGCG CTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC GCCTGAACCG
351 CCTGACACAC GCGCGCTGG ACGTAACCGT CGGCCCTTTG GTCAACCTTT
401 GGGGATTCGG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAGG CGGCATCTTA TACGGGCATA GACAAAATCA TTTTGAAACA
501 AGGCAAAAGT TACGCTTCCT TGAGCAAAAC CCACCCCAAG GCCTATTGCG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGGCGAA
601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCGTGGCGC ATCGGTATCG
701 AGCAGCCCAA TATCGTCCAA GCGCGCAATA CGCAGATTAT CGTCCCGCTG
751 AACAACCGTT CGCTTGCCAC TTCCGGCGAT TACCGTATT TCCACGTCGA
801 TAAAAACGGC AAACGCCTCT CCCATATCAT CAACCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGAGA CAGTGCATG
901 ACGGCGGACG GCTTGTCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAGGCTG GCAGAGCGCG AAAAATCTCG TGTTCCTTG ATTGTCAGGG
1001 ATAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTGTA AAAATGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 402; ORF 111-1>:

```

m111-1.pep
1  MPSETRLPNF IRVLIFALGF IFLNACSEQT AQTVTLOGET MGTITYVKYL
51  SNNRDKLPSP AEIQKRIDDA LKEVNRQMSY YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWGFPGDK SVTREPSPEQ
151 IKQAASVTGI DKIIKQGGK YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHKG GKNARGEPR IGIEQPNIVQ GGNTQIIIVPL
251 NNRSLATSGD YRIFHVDKNG KRLSHIINPN NKRPIHNLA SISVVSADAM
301 TADGLSTGLF VLGETEALKL AEREKLAFLV IVRDKGGYRT AMSSEFEKLL
351 R*

```

m111-1/g111-1 96.6% identity in 351 aa overlap

```

          10      20      30      40      50      60
m111-1.pep MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLOGETMGTITYVKYLSNNRDKLPSP
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g111-1      MPSETRLPNLIRALIFALGFIFLNACSEQTAQTVTLOGETMGTITYVKYLSNNRDKLPSP

```

326

	10	20	30	40	50	60
m111-1.pep	70	80	90	100	110	120
	AEIQKRIDDALKEVNRQMSTYQPDSEISRFNQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
	: : : :					
g111-1	70	80	90	100	110	120
	AKIQKRIDDALKEVNRQMSTYQTDSEISRFNQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
m111-1.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFGPKSVTREPSPEQIKQAASYTGIDKIILKQKDYASLSKTHPK					
	: : :					
g111-1	130	140	150	160	170	180
	GALDVTVGPLVNLWGFGPKSVTREPSPEQIKQAASYTGIDKIILQQKDYASLSKTHPK					
m111-1.pep	190	200	210	220	230	240
	AYLDLSSIAGFGVDKVGAGELEKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIVQ					
	: : :					
g111-1	190	200	210	220	230	240
	AYLDLSSIAGFGVDKVGAGELEKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIIQ					
m111-1.pep	250	260	270	280	290	300
	GGNTQIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNNKRPISHNLASISVVADSAM					
	: : :					
g111-1	250	260	270	280	290	300
	GGNTQIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNNKRPISHNLASISVVSDSAM					
m111-1.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAFLIVRDKGGYRTAMSSEFEKLLRX					
	: : :					
g111-1	310	320	330	340	350	
	TADGLSTGLFVLGETEALRLAEQEKLAFLIVRDKDGYRTAMSSEFAKLLRX					

g111-1/p44550

sp|P44550|YOJL_HAEIN HYPOTHETICAL LIPOPROTEIN HI0172 PRECURSOR >gi|1074292|pir||C64144
 hypothetical protein HI0172 - Haemophilus influenzae (strain Rd KW20) >gi|1573128 (U32702)
 lipoprotein, putative [Haemophilus influenzae Rd] Length = 346
 Score = 349 bits (885), Expect = 2e-95
 Identities = 177/328 (53%), Positives = 240/328 (72%), Gaps = 4/328 (1%)

Query: 23 LNACSEQTAQTVTLQGETMGTTYXVKYLSNNRDKLPSPAEIXKRIDDALKEYNRMSTYQ 82
 L AC ++T + ++L G+TMGTTY VKYL + S + + I+ LK+ N MSTY+
 Sbjct: 17 LAACQKET-KVISLSGKTMGTTYHVYKLDGDSITATS-EKTHEEIEAILKDVNAKMSTYK 74

Query: 83 PDSEISRFNQHT-AGKPLRISSDFAHVTAEAVRLNRLTHGALDVTVGPLVNLWGFGPKS 141
 DSE+SRFNQ+T P+ IS+DFA V AEA+RLN++T GALDVTVG+VNLWGFGP+K
 Sbjct: 75 KDSELSRFNQNTQVNTPIEISADFAKVLAEAIRLNKVTEGALDVTVGPPVNLWGFGPEKR 134

Query: 142 VTREPSPEQIKQAASYTGIDKIILKQKDYASLSKTHPKAYLDLSSIAGFGVDKVGAGEL 201
 ++P+PEQ+ + ++ GIDKI L K+ A+LSK P+ Y+DLSSIAGFGVD+VA +L
 Sbjct: 135 PEKQPTPEQLAERQAWVGIDKITLDTNKEKATLSKALPQVYVDLSSIAGFGVDQVAEKL 194

Query: 202 EKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIVQGGNTQIIVPLNNRSLATSGDY 261
 E+ QNY+VEIGGE+ KGKN G+PW+I IE+P + ++ LNN +A+SGDY
 Sbjct: 195 EQLNAQNYMVEIGGEIRAKGNIEGKPWQIAIEKPTTGERAVEAVIGLNNMGMASGDY 254

Query: 262 RIFHVDKNGKRLSHIINPNNKRPISHNLASISVVADSAMTADGLSTGLFVLGETEALKLA 321
 RI+ ++NGKR +H I+P PI H+LASI+V+A ++MTADGLSTGLFVLGE +AL++A
 Sbjct: 255 RIY-FEENGKRFAHEIDPKTGYPYIQQHHLASITVLAPTSMTADGLSTGLFVLGEDKALEVA 313

Query: 322 EREKLAVFLIVRDKGGYRTAMSSEFEKL 349
 E+ LAV+LI+R G+ T SS F+KL
 Sbjct: 314 EKNLAVYLIIRTNDNGFVTKSSSAFKKL 341

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 403>:

a111-1.seq

```

1  ATGCCGCTCTG  AAACACGCCT  GCCGAACCTT  ATCCGCACCT  TGATATTTCG
51  CCTGAGTTTT  ATCTTCCTGA  ACGCCTGTTC  GGAACAAACC  GCGCAAACCG
101  TTACCCTGCA  AGGTGAAACG  ATGGGCACGA  CCTATACCGT  CAAATACCTT
151  TCAAATAATC  GGGACAAACT  CCCCTCACCT  GCCGAAATAC  AAAAGCGCAT
201  CGATGACGCG  CTTAAGAAG  TCAACCGGCA  GATGTCCACC  TATCAGCCCG
251  ACTCCGAAAT  CAGCCGGTTC  AACCAACACA  CAGCCGGCAA  GCCCTCCCG
301  ATTTCAAGCG  ACTTCGCACA  CGTTACTGCC  GAAGCCGTCC  ACCTGAACCG

```

```

351 CCTGACACAC GGC GCGCTGG ACCTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTCGG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAAG CAGCATCTTA TACGGGCATA GACAAAATCA TTTTGAAACA
501 AGGCAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAAG GCCTATTGTT
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGGCGAA
601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGCGCA ACCTTGGCGC ATCGGCATCG
701 AACAGCCCAA CATCGTCCAA GCGGCAATA CGCAGATTAT CGTCCCGCTG
751 AACAAACGTT CGTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA
801 TAAAGCGGCG AAACGCCTCT CCCATATCAT TAATCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCCGAGA CAGTGCAGTG
901 ACGGCGGACG GCTTGTCCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAAGCTCG TGTTCCTCTG ATTGTCAGGG
1001 ATAAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTGTA AAAAGTCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 404; ORF 111-1.a>:

a111-1.pep

```

1  MPSETRLPNF IRTLIFALSF IFLNACSEQT AQTVTLOGET MGTITYTVKYL
51  SNNRDKLPSP AEIQKRIDDA LKEVNRQMST YQPDSEISRF NOHTAGKPLR
101 ISSDFAHVTA EAVHLNRLTH GALDVTVGPL VNLWGFPGDK SVTREPSPEQ
151 IKQAASYTGI DKIIILKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHKG KGNARGEPWR IGIEQPNIVQ GGNTQIIVPL
251 NNRLATSGD YRIFHVDKSG KRLSHIINPN NKRPIHNLAS SISVVDASAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

a111-1/m111-1 98.9% identity in 351 aa overlap

	10	20	30	40	50	60
a111-1.pep	MPSETRLPNFIRTLIFALSFIFLNACSEQTAQTVTLOGETMGTITYTVKYLNNRDKLPSP					
m111-1	MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLOGETMGTITYTVKYLNNRDKLPSP					
	10	20	30	40	50	60
a111-1.pep	AEIQKRIDDALKEVNRQMSTYQPDSEISRFNOHTAGKPLRISSDFAHVTA EAVHLNRLTH					
m111-1	AEIQKRIDDALKEVNRQMSTYQPDSEISRFNOHTAGKPLRISSDFAHVTA EAVRLNRLTH					
	70	80	90	100	110	120
a111-1.pep	AEIQKRIDDALKEVNRQMSTYQPDSEISRFNOHTAGKPLRISSDFAHVTA EAVHLNRLTH					
m111-1	AEIQKRIDDALKEVNRQMSTYQPDSEISRFNOHTAGKPLRISSDFAHVTA EAVRLNRLTH					
	70	80	90	100	110	120
a111-1.pep	GALDVTVGPLVNLWGFPGDKSVTREPSPEQIKQAASYTGIDKIIILKQKDYASLSKTHPK					
m111-1	GALDVTVGPLVNLWGFPGDKSVTREPSPEQIKQAASYTGIDKIIILKQKDYASLSKTHPK					
	130	140	150	160	170	180
a111-1.pep	GALDVTVGPLVNLWGFPGDKSVTREPSPEQIKQAASYTGIDKIIILKQKDYASLSKTHPK					
m111-1	GALDVTVGPLVNLWGFPGDKSVTREPSPEQIKQAASYTGIDKIIILKQKDYASLSKTHPK					
	130	140	150	160	170	180
a111-1.pep	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHKGKGNARGEPWRIGIEQPNIVQ					
m111-1	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHKGKGNARGEPWRIGIEQPNIVQ					
	190	200	210	220	230	240
a111-1.pep	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHKGKGNARGEPWRIGIEQPNIVQ					
m111-1	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHKGKGNARGEPWRIGIEQPNIVQ					
	190	200	210	220	230	240
a111-1.pep	GGNTQIIVPLNNRSLATSGDYRIFHVDKSGKRLSHIINPNKRPIHNLASISVVDASAM					
m111-1	GGNTQIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPIHNLASISVVDASAM					
	250	260	270	280	290	300
a111-1.pep	GGNTQIIVPLNNRSLATSGDYRIFHVDKSGKRLSHIINPNKRPIHNLASISVVDASAM					
m111-1	GGNTQIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPIHNLASISVVDASAM					
	250	260	270	280	290	300
a111-1.pep	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
m111-1	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
	310	320	330	340	350	
a111-1.pep	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
m111-1	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 405>:

g114.seq

```

1  ATGGCTTCCA TCACTTCGCC GCTGCACGGG GCGCAGCAGG AATGCAGCAA
51  GACTTTTTTA TGTCCGCCGG GCGGACGAG TATGGGGCGG TCAATGTCGG

```

This corresponds to the amino acid sequence <SEQ ID 406; ORF 114.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 407>:

This corresponds to the amino acid sequence <SEQ ID 408; ORF 114>:

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 409>:

```

a114.seq
1  ATGCCGGAGG CAAGCATCGC CTCCATCACT TCGCCGCTGC ACGGGGCGCA
51  ACAGGAATGC AGCAAGACTT TTTTATGTCC GCCGGGCGGG ACGAGTATGG
101 GCGCGTCAAT GTCGGTAACG GTAGGTTTGT TTTGTGTTTC CATTAACTTA
151 ACGATATCTG TCGAATACGG TTGAAGCGGC TATTTTATCA GAGCCGCCGC
201 ATGTAAACA GGGTGTCAAG GCATCAGCCC GAGCTGCCTG AACGAACGGA
251 CGGTTTGC GC GTTACGATA AAATGGTCTG GCAGCGACAC ATCGACCAGC
301 GACATTGCCT GTGCCAGCCG CCTTGTGAAC ATGATGTCCT CCTGCGAAGG
351 TTCGGGGCAG CCGCCCGGAT GGTGTGTCGC GATAATCAGG CTGTCGGCAT
401 ATTCGTCCAA TGCCAGTTTG ACAATTTTCA CGATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 410; ORF 114.a>:

a114.pep

```

1  MPEASIASIT SPLHGAQQEC SKTFLCPPGG TSMGRSMSVT VGLFCVSINL
51  TISVEYG*SG YFIRAAACKT GCQGISPSCL NERTVCAVTI KWSSSDTSTS
101 DIACASRLVN MMSSCEGSGE PPGWLCAIIR LSAYSSNASL TISRM*

```

m114/a114 92.9% identity in 140 aa overlap

```

              10      20      30      40      50
m114.pep      MASITSPLHGAHRECSKTFLCPPGGTSIGRSMSTVGLFCVSINLTISVEYGXSG
              :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114           MPEASIASITSPLHGAQQECSKTFLCPPGGTSMGRSMSTVGLFCVSINLTISVEYGXSG
              10      20      30      40      50      60

              60      70      80      90      100     110
m114.pep      YFIRAAACKTECQGINPSCLEQTLXVTIKWSSSDTSTSDIACASRLVNMSSCEXSSE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114           YFIRAAACKTGCQGISPSCLNERTVCAVTIKWSSSDTSTSDIACASRLVNMSSCEGSSE
              70      80      90      100     110     120

              120     130     140
m114.pep      PPGWLCAIIRLSAYSSNASLTISRMX
              |||||:|||||:|||||:|||||:|||||
a114           PPGWLCAIIRLSAYSSNASLTISRMX
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 411>:

g117.seq

```

1  atggtcgacg aactcgacCT GCTGCCCGAT GCCGTCGCCG CCACCCTGCT
51  TGCCGACATC GGACGCTACG TCCCCGATTG GAACCTATTG GTTTCCGAGC
101 GCTGCAACAG CACCGTCGCC GAGCTGGTCA AAGGTGtgga CGAAGTGCAG
151 AAACCTACCC ACTTCGCCCC GGTGGACAGC CTCGCCACGC CGGAAGAACG
201 CGCACAGCAA GCGGAAACCA TCGGAAAAT GCTGCTGGCg atggttaccg
251 Acatccgcgt cgtatTAATC AAACCTGGCGA TCGGTacgcg caccCTGcta
301 ttTTtaagCA ACGCCCCCGA CAGCCCTGAA AAACGcgccg TCgcaaaAga
351 aaccctCGAC ATCTTCGCCC CGCTCGCCA CCGCTTGGGc GTGTGGCAGC
401 TCAAATGGCA GCTCGAAGAT TTGGGCTTCC GCCATCAAGA ACCCGAAAAA
451 TACCGCGAAA TCGCCCTGCT TTTGGACGAA AAACGCACCG AACGCCTCGA
501 ATACATCGAA AACTTCCTCG ATATCCTGCG TACGGAATC AAAAAATACA
551 ATATCCACTT TGAAGTCGCC GGCCGTCCGA AACACATCTA CTCCATTTAC
601 AAAAAAATGG TGAAGAAAAA ACTCAGCTTC GACGgccTGT TCGACATCCG
651 CGCCGTGCGG ATTCTGGTCG ATACCGTCCC CGaGTGTTAC ACCACGCTGG
701 gcatCGTCCA CAGCCTCTGG CAGCCCATTc CCGGCGagtt CGAcgactAC
751 ATCGCCAACC CCAAAGgcaa CGgttATAAA AGtTTGCACA CCGTCATCGT
801 cggcccGGAA gacaaaggtg tggaaGtgCA AATCCGCACC TTCGAtatGC
851 accAATTcAa CgaatTcggT gtcgcccGCC ACTGGCGtta caaagaaggc
901 ggcaaaggcg attccGCcTA cgaacaaAAA ATcgccTggt TGCgcaaACT
951 CTTGGACTGG CGCGAAAATA TGGCGGAAAG CGGCAAGGAA GACCTCGCCG
1001 CCGCCTTCAA AACCGAGCTT TTCAACGACA CGATTATGT TTTGACCCCG
1051 CACGGCAAAG TCCTCTCTCT GCCAACGGGC GCAACCCCA TCgACTTCGC
1101 CTACGCCCTG CACAGCAGCA TcggCGACCG CTGCCGGGGC GCGAAAGTCG
1151 AaggGCAGAT TGTGCCGCTG TCCACCCCGC TCGAAAACGG ACAGCGCGTC
1201 GAAATcatta cCGCcaaAGA AGGGCATCCT TCCGTCAACT GGCTTTACGA
1251 AGGctgGGtc aaATCCGGCA AGGCCATCGG caaAATCCG GCCTAcacCC
1301 CCCAGcaaAa cgCgaCACC GTGCGCGAAG AAGGCCGTGT CCAACTCGAC
1351 AAGCAGCTTG CCAAACCTCAC GCCCAAACCC AACCTGCAAG AGCTTgcca
1401 aaATCTCGGC tacaaAAAGC cagaagacct ctacacCGCc gtcggacaag
1451 gcgaaatttc caaccgcgcc atCcaaaaag cctgcggcac GCTgaacgaa
1501 ccgccccCCG TGCCCGTCAG CGCAACCACC ATCGTCAAAC AGTCCAAAAT

```

```

1551 CAAAAAAGGT GGCAAAACCG GCGTGCTCAT CGACGGCGAA GACGGCCTTGA
1601 TGACCACGCT TGCCAAATGC TGCAAACCCG CGCCGCCCGA CGATATTGCC
1651 GGCTTCGTTA CCCGCGAGCG CGGCATTTC GTCCACCGCA AAACCTGCCC
1701 CTCTTTCCGA CACCTTGCCG AACACGCGCC CGAAAAAGTA CTGGACGCAA
1751 GTTGGGCGGC GTTGCAGGAA GGGCAAGTGT TCGCCGTCGA TATCGAAATC
1801 CGCGCCCAAG ACCGCTCCGG GCTTTTGCGC GACGTATCCG ACGCGCTCGC
1851 CCGCCACAAA CTCAACGTTA CCGCCGTGCA AACCAGTCC CGCGACTTGG
1901 AAGCCAGCAT GAGGTCACG CTCGAAGTCA AACAAgTCAA CGacCTCCCG
1951 CGCGTCCTCG CCGGCCTCGG CGATGTCAAA GGCGTATTGA GCGTTACCCG
2001 GCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 412; ORF 117.ng>:

g117.pep

```

1 MVDELDDLDPD AVAATLLADI GRYVPDWNLL VSERCNSTVA ELVKGVDDEVQ
51 KLTHFARVDS LATPEERAQQ AETMRKMLLA MVTDIRVVLI KLAMRTRTLL
101 FLSNAPDSPE KRAVAKETLD IFAPLANRLG VWQLKWQLED LGFRHQEPEK
151 YREIALLLDE KRTERLEYIE NFLDILRTEL KKYNIHFEDA GRPKHIYSIY
201 KKMVKKKLSF DGLFDIRAVR ILVDTVPECY TTLGIVHSLW QPIPGFDDY
251 IANPKGNGYK SLHTVIVGPE DKGVEVQIRT FDMHQFNEFG VAAHWRYKEG
301 GKGDSEYEQK IAWLRQLLDW RENMAESGKE DLAAAFKTEL FNDTIYVLTTP
351 HGKVLSLPTG ATPIDFAYAL HSSIGDRCRG AKVEGQIVPL STPLENGQRV
401 EIITAKEGHP SVNWLYEGWV KSGKAIGKIR AYIRQONADT VREEGRVQLD
451 KQLAKLTPKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTLNE
501 PPPVPVSATT IVKQSKIKKG GKTGVLIDGE DGLMTTLAKC CKPAPPDDIA
551 GFVTRERGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GQVFAVDIEI
601 RAQDRSGLLR DVSDALARHK LNVTAVQTQS RDLEASMRFT LEVKQVNDLP
651 RVLAGLGDKV GVLVSVTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 413>:

m117.seq (partial)

```

1 ..GTGAAACTCA AGAAATACAA TGTCCATTTC GAAGTCGCCG GCCGCCCGAA
51 ACACATCTAC TCCATTTACA AAAAAATGGT GAAGAAAAAA CTCAGCTTCG
101 ACGGCCTCTT TGACATCCGC GCCGTGCGAA TTCTGGTTGA TACCGTCCCC
151 GAGTGTTACA CCACGCTGGG TATCGTCCAC AGCCTCTGGC AGCCCATTC
201 CGGCGAGTTC GACGACTACA TCGCCAATCC CAAAGGCAAC GGCTATAAAA
251 GTTTGCACAC CGTCATCGTC GGCCCGGAAG ACAAAGGCGT GGAAGTACAA
301 ATCCGCACCT TCGATATGCA CCAATTCAAC GAATTCCGTG TCGCCGCCCA
351 CTGgCGTTAC AAAGAGGGCG GCAAGGGCGA TTCCGCCTAC GAACAGAAAA
401 TCGCCTGGTT GCGCCAACTC TTGGACTGGC GCGAAAACAT GCGGAAAGC
451 GGCAAGGAAG ACCTCGCCGC CGCCTTCAAA ACCGAGCTTT TCAACGACAC
501 GATTTATGTT TTGACCCCGC ACGGCAAAGT CCTCTCCCTG CCCACGGGCG
551 CGACCCCAT CGACTTCGCC TACGCCCTGC ACAGCAGCAT CGGCGACCGT
601 TGCCGCGGTG CGAAAGTCGA AGGGCAGATT GTGCCGCTGT CCACCCGCT
651 CGAAAACGGA CAGCGCGTCG AAATCATTAC CGCCAAAGAA GGGCATCCTT
701 CCGTCAACTG GCTTTACGAA GGCTGGGTCA AATCCAACAA GGCAATCGGC
751 AAAATCCGCG CCTACATCCG CCAGCAAAAC GCCGACACCG TGCGCGAAGA
801 AGGCCGCGTC CAACTCGACA AACAGCTTGC CAAACTCAGC CCCAAACCCA
851 ACCTGCAAGA GCTTGCCGAA AATCTCGGCT AAAAAAGCC AGAAGACCTC
901 TACACCGCCG TCGGACAAGG CGAAATTTCC AACCGCGCCA TCCAAAAAGC
951 CTGCGGCACg CTGAACGAAC CGCCGCCCGT ACCCGTCAGC GAAACCACCA
1001 TCGTCAAACA GTCCAAAATC AAAAAAGGCG GCAAAAACGG CGTGCTCATC
1051 GACGGCGAAG ACGGTCTGAT GACCACGCTT GCCAAATGCT GCAAACCCGC
1101 GCCGCGCGAC GATATTATCG GCTTCGTTAC CCGCGAGCGC GgCATTTTCAg
1151 TGCACCGCAA AwyyTkCyCG TCTTTCCAAC ACCTCGCCGA ACACGCGCCC
1201 GAWAAAGTGC TGGACGCAAG CTGGGCGGCA TTGCAGGAAG GACAAGTATT
1251 CGCCGTCGAT ATCGAAATCC GCGCCCAAGA CCGCTCCGGG CTTTTGCGCG
1301 ACGTATCCGA CGCGCTCGCC CGCCACAAAC TCAACGTTAC CGCCGTGCAA
1351 ACCCAGTCCC GCGACTTGGA AGCCAGCATG AGGTTACGCG TCGAAGTCAA
1401 ACAAGTCAAC GACCTCCCGC GCGTCCTCGC CAGCCTCGGC GACGTCAAAG
1451 GCGTATTGAG CGTTACCCGG CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 414; ORF 117>:

m117.pep (partial)

```

1....VKLKKYNVHF EVAGRPKHIY SIYKKMVKKK LSF DGLFDIR AVRILVDTVP
51 ECYTTLGIVH SLWQIPGGEF DDYIANPKGN GYKSLHTVIV GPEDKGVEVQ
101 IRTFDMHQFN EFGVAAHWRY KEGGKGSAY EQKIAWLRQL LDWRENMAES
151 GKEDLAAAFK TELFNDTIYV LTPHGKVLSL PTGATPIDFA YALHSSIGDR
201 CRGAKVEGQI VPLSTPLENG QRVEIITAKE GHPSVNWLYE GWVKSNAIG
251 KIRAYIRQN ADTVREEGRV QLDKQLAKLT PKPNLQELAE NLGYKKPEDL
301 YTAVGQGEIS NRAIQACGT LNEPPVPVVS ETTIVKQSKI KKGKNGVLI
351 DGEDGLMTTL AKCKPAPPD DIIGFVTRER GISVHRKXXX SFQHLAEHAP
401 XKVLDASWAA LQEGQVFAVD IEIRAQDRSG LLRDVSDALA RHKLNVTAVQ
451 TQSRDLEASM RFTLEVQVN DLPRVLASLG DVKGVLSVTR L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 117 shows 97.6% identity over a 490 aa overlap with a predicted ORF (ORF 117.ng) from *N. gonorrhoeae*:

m117/g117

m117.pep				10	20	30
				VKLKKYNVHFEVAGRPKHIYSIYKKMVKKKL		
g117	EKYREIALLLDEKRTERLEYIENFLDILRTELKKYNHFEVAGRPKHIYSIYKKMVKKKL					
	150	160	170	180	190	200
m117.pep		40	50	60	70	80
		SFDGLFDIRAVRILVDTVPECYTTLGIHSLWQIPGGEFDDYIANPKGN				
g117		SFDGLFDIRAVRILVDTVPECYTTLGIHSLWQIPGGEFDDYIANPKGN				
	210	220	230	240	250	260
m117.pep		100	110	120	130	140
		PEDKGVEVQIRTFDMHQFNEFGVAAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESG				
g117		PEDKGVEVQIRTFDMHQFNEFGVAAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESG				
	270	280	290	300	310	320
m117.pep		160	170	180	190	200
		KEDLAAAFKTELFNDTIYVLTTPHGKVLSLPTGATPIDFAYALHSSIGDR				
g117		KEDLAAAFKTELFNDTIYVLTTPHGKVLSLPTGATPIDFAYALHSSIGDR				
	330	340	350	360	370	380
m117.pep		220	230	240	250	260
		PLSTPLENGQRVEIITAKEGHPSVNWLYEGWVKSNAIGKIRAYIRQNADTVREEGRVQ				
g117		PLSTPLENGQRVEIITAKEGHPSVNWLYEGWVKSNAIGKIRAYIRQNADTVREEGRVQ				
	390	400	410	420	430	440
m117.pep		280	290	300	310	320
		LDKQLAKLTPKPNLQELAENLGYKKPEDLYTAVGQGEISNRAIQACGT				
g117		LDKQLAKLTPKPNLQELAENLGYKKPEDLYTAVGQGEISNRAIQACGT				
	450	460	470	480	490	500
m117.pep		340	350	360	370	380
		TTIVKQSKI KKGKNGVLIDGEDGLMTTLAKCKPAPPDDIIGFVTRERGISVHRKXXXS				
g117		TTIVKQSKI KKGKNGVLIDGEDGLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPS				
	510	520	530	540	550	560
m117.pep		400	410	420	430	440
		FQHLAEHAPXKVLDASWAAALQEGQVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAQT				
		400	410	420	430	440
		FQHLAEHAPXKVLDASWAAALQEGQVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAQT				
		400	410	420	430	440
		FQHLAEHAPXKVLDASWAAALQEGQVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAQT				

332

g117	FRHLAEHAPEKVLDSWAALQEGQVFAVDIEIRAQDRSGLLRDVSALARHKLNVTAQT
	570 580 590 600 610 620
m117.pep	QSRDLEASMRFTLEVQVNDLPRVLASLGDVKGVLSVTRLX
g117	QSRDLEASMRFTLEVQVNDLPRVLAGLGDVKGVLSVTRLX
	630 640 650 660

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 415>:

a117.seq

```

1  ATGGTTCATG  AACTCGACCT  GCTCCCCGAT  GCCGTCGCCG  CCACCCTGCT
51  TGCCGACATC  GGACGCTACG  TCCCCGACTG  GAACCTATTG  GTTTCGGAAC
101 GCTGCAACAG  TACCGTCGCC  GAGCTGGTCA  AAGGTGTGGA  CGAAGTGCAG
151 AAACTCACCC  ACTTCGCCCG  GGTGGACAGC  CTCGCCACGC  CGGAAGAACC
201 CGCCAGCAG  GCAGAACTA  TGCGGAAAT  GCTGCTGGCG  ATGGTTACCG
251 ACATCCGCGT  CGTGTTAATC  AAATGGCGA  TGCGTACGCG  CACCCTGCAA
301 TTTTAAAGCA  ACGCCCCGGA  CAGCCCCGAA  AAACGCGCCG  TCGCCAAAGA
351 AACCCTCGAC  ATCTTCGCCC  CGCTCGCCAA  CCGTTTGGGC  GTGTGGCAGC
401 TCAAATGGCA  GCTCGAAGAT  TTGGGCTTCC  GCCATCAAGA  ACCCGAAAAA
451 TACCGCGAAA  TCGCCCTGCT  TTTGGACGAA  AAACGCACCG  AACGCCTCGA
501 ATACATCGAA  AACTTCCTTA  ATATCCTGCG  TACGGAATC  AAAAAATACA
551 ATATCCACTT  TGAAGTCGCC  GGCCGTCGCA  AACACATCTA  CTCCATTTAC
601 AAAAAATGG  TGAAGAAAAA  ACTCAGCTTC  GACGGGTGT  TCGACATCCG
651 CGCCGTGCGG  ATTCTGGTTG  ATACCGTCCC  CGAGTGTTAC  ACCACACTGG
701 GCATTGTCCA  CAGCCTCTGG  CAGCCCATTC  CCGGCGAGTT  CGACGACTAC
751 ATCGCCAACC  CGAAAGGCAA  CGGCTATAAA  AGTTTGCACA  CCGTCATCGT
801 CGGCCCGGAA  GACAAAGGCG  TGGAAGTGCA  AATCCGCACC  TTCGATATGC
851 ACCAATTCAA  CGAATTCGGT  GTCGCCGCGC  ACTGGCGTTA  CAAAGAGGGC
901 GGCAAAGCG  ATTCCGCCTA  CGAACAAAAA  ATCGCCTGGT  TACGCCAACT
951 TTTGGACTGG  CGCGAAAACA  TGGCGGAAAG  CGGCAAGGAA  GACCTCGCCG
1001 CCGCCTTCAA  AACCAGGCTT  TTCAACGACA  CGATTTATGT  TTTGACCCCG
1051 CACGGCAAAG  TCCTCTCCCT  GCCACAGGC  GCGACCCCA  TCGACTTCGC
1101 CTACGCCCTG  CACAGCAGCA  TCGGCGACCG  TTGCCGCGGT  GCGAAAGTCG
1151 AAGGGCAGAT  TGTGCCGTG  TCCACCCCGC  TCGAAAACGG  ACAGCGTGTC
1201 GAAATCATTA  CCGCCAAAGA  AGGCATCCT  TCCGTCAACT  GGCTTTACGA
1251 AGGCTGGGTC  AAATCCAACA  AGGCAATCGG  CAAAATCCGC  GCCTACATCC
1301 GCCAGCAAAA  CGCCGACACC  GTGCGCGAAG  AAGGCCGCGT  CCAACTCGAC
1351 AAACAGCTTG  CCAAACAC  GCCCAAACCC  AACCTGCAAG  AGCTTGCCGA
1401 AAATCTCGGC  TACAAAAAGC  CAGAAGACCT  CTACACCGCC  GTCGGAACAG
1451 GCGAAATTTC  CAACCGCGCC  ATCCAAAAAG  CCTGCGGCAC  GCTGAACGAA
1501 CCGCCGCCCG  TACCCGTCAG  CGAAACCACC  ATCGTCAAAC  AGTCCAAAAT
1551 CAAAAAAGGC  GGCAAAAACG  GCGTGCTCAT  CGACGGCGAA  GACGGTCTGA
1601 TGACCACGCT  TGCCAAATGC  TGCAAACCCG  CGCCGCCCGA  CGACATTGTC
1651 GGCTTCGTTA  CCCGCGATCG  CGGCATTTTC  GTACACCGCA  AAACCTGCCC
1701 CTCTTTCCGA  CACCTCGCCG  AACACGCGCC  CGAAAAAGTA  CTGGACGCAA
1751 GTTGGGCGGC  GTTGCAAGAA  GGACAAGTGT  TCGCCGTCGA  TATCGAAATC
1801 CGCGCCCAAG  ACCGCTCCGG  GCTTTTGCGC  GACGTATCCG  ACGCGCTCGC
1851 CCGCCACAAA  CTCAACGTTA  CCGCCGTGCA  AACCAGTCC  CGCGACTTGG
1901 AAGCCAGCAT  GAGGTTACG  CTCGAAGTCA  AACAAGTTAC  CGACCTCCCA
1951 CGCGTCCTCG  CCAGCCTCGG  CGACGTCAAA  GGCGTATTGA  GCGTTACCCG
2001 GCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 416; ORF 117.a>:

a117.pep

```

1  MVHELDLLPD  AVAATLLADI  GRYVPDWNLL  VSERCNSTVA  ELVKGVDEVQ
51  KLTHFARVDS  LATPEERAQQ  AETMRKMLLA  MVTDIRVLI  KLAMRTRTLQ
101  FLSNAPDSPE  KRAVAKETLD  IFAPLANRLG  VWQLKWQLED  LGFRHQEPEK
151  YREIALLLDE  KRTERLEYIE  NFLNILRTEL  KKYNIHFEVA  GRPKHIYSIY
201  KKMVKKKLSF  DGLFDIRAVR  ILVDTVPECY  TTLGIVHSLW  QPIPGFEDDY
251  IANPKGNGYK  SLHTVIVGPE  DKGVEVQIRT  FDMHQFNEFG  VAAHWRYKEG
301  GKGDSAYEQK  IAWLRQLLDW  RENMAESGKE  DLAAAFKTEL  FNDTIYVLTP
351  HGKVLSLPTG  ATPIDFAYAL  HSSIGDRCRG  AKVEGQIVPL  STPLENGQRV

```


333

401 EIITAKEGHP SVNWLYEGWV KSNKAIGKIR AYIRQQNADT VREEGRVQLD
 451 KQLAKLTPKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTLNE
 501 PPPVPVSETT IVKQSKIKKG GKNGVLIDGE DGLMTTLAKC CKPAPPDDIV
 551 GFVTRDRGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GQVFAVDIEI
 601 RAQDRSGLLR DVSDALARHK LNVTAQTQS RDLEASMRFT LEVKQVTDLP
 651 RVLASLGDVK GVLSVTRL*

m117/a117 98.0% identity in 490 aa overlap

m117.pep				10	20	30
				VKLKKYNVHFEVAGRPKHIYSIYKKMVKKKL		
a117	EKYREIALLLDEKRTERLEYIENFLNIRTELKKYNHFEVAGRPKHIYSIYKKMVKKKL			: : : : :		
	150	160	170	180	190	200
m117.pep		40	50	60	70	80
		SFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQPIPGEFDDYIANPKGNGYKSLHTVIVG				
a117		: : : :				
		SFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQPIPGEFDDYIANPKGNGYKSLHTVIVG				
	210	220	230	240	250	260
m117.pep		100	110	120	130	140
		PEDKGVEVQIRTFDMHQFNEFGVAAHWRYKEGGKGD SAYEQKIAWLRLDWRNMAESG				
a117		: : : :				
		PEDKGVEVQIRTFDMHQFNEFGVAAHWRYKEGGKGD SAYEQKIAWLRLDWRNMAESG				
	270	280	290	300	310	320
m117.pep		160	170	180	190	200
		KEDLAAAFKTELFNDTIYVLTTPHGKVLSPGTGATPIDFAYALHSSIGDRCRGAKVEGQIV				
a117		: : : :				
		KEDLAAAFKTELFNDTIYVLTTPHGKVLSPGTGATPIDFAYALHSSIGDRCRGAKVEGQIV				
	330	340	350	360	370	380
m117.pep		220	230	240	250	260
		PLSTPLENGQ RVEIITAKEGHPSVNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQ				
a117		: : : :				
		PLSTPLENGQ RVEIITAKEGHPSVNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQ				
	390	400	410	420	430	440
m117.pep		280	290	300	310	320
		LDKQLAKLTPKPNLQELAENLG YKKPEDLYTAVGQGEISNRAIQKACGTLNEPPPVPVSE				
a117		: : : :				
		LDKQLAKLTPKPNLQELAENLG YKKPEDLYTAVGQGEISNRAIQKACGTLNEPPPVPVSE				
	450	460	470	480	490	500
m117.pep		340	350	360	370	380
		TTIVKQSKIKKGGKNGVLIDGEDGLMTTLAKCKPAPPDDIIGFVTRERGISVHRKXXXS				
a117		: : : :				
		TTIVKQSKIKKGGKNGVLIDGEDGLMTTLAKCKPAPPDDIIGFVTRDRGISVHRKTCPS				
	510	520	530	540	550	560
m117.pep		400	410	420	430	440
		FQHLAEHAPXKVLDA SWAALQEGQVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAVQT				
a117		: : : :				
		FRHLAEHAPEKVLDA SWAALQEGQVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAVQT				
	570	580	590	600	610	620
m117.pep		460	470	480	490	
		QSRDLEASMRFTLEVKQVNDLPRVLASLGDVKGVLSVTRLX				
a117		: : : :				
		QSRDLEASMRFTLEVKQVTDLPRVLASLGDVKGVLSVTRLX				
	630	640	650	660		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 417>:

g117-1.seq

```

1   ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CCCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCGC CGCTCTGCCG GACAACGATA
101 AAAAAGCTCAT CGGTACCGCA TGGTCGCTGG CGCAGGAACA TTATCCTGCC
151 GATGCCGCCA CGCCGTATGG CGAGCCGCTG CCCGACCACT TCCTCGGCGC
201 GGCAGCAATG GTCGACGAAC TCGACCTGCT GCCCGATGCC GTCGCGGCCA
251 CCCTGCTTGC CGACATCGGA CGCTACGTCC CCGATTGGAA CCTATTGGTT
301 TCCGAGCGCT GCAACAGCAC CGTCGCGGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAGAAA CTTACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401 AAGAACGCGC ACAGCAAGCG GAAACCATGC GGAAATGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCGT ATTAATCAAA CTGGCGATGC GTACGCGCAC
501 CCTGCAATTT TTAAGCAACG CCCCCGACAG CCCTGAAAAA CGCGCCGTCG
551 CCAAGAAAC CCTCGACATC TTCGCCCCGC TCGCCAACCG CTGGGCGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCGCC ATCAAGAACC
651 CGAAAAATAC CGCGAAATCG CCCTGCTTTT GGACGAAAAA CGCACCGAAC
701 GCCTCGAATA CATCGAAAAC TTCCTCGATA TCCTGCGTAC GGAACATAAA
751 AAATACAATA TCCACTTTGA AGTCGCGCGC CGTCCGAAAC ACATCTACTC
801 CATTACAAA AAAATGGTGA AGAAAAAACT CAGCTTCGAC GGCGTGTTCG
851 ACATCCGCGC CGTGCGGATT CTGGTCGATA CCGTCCCCGA GTGTTACACC
901 ACGCTGGGCA TCGTCCACAG CCTCTGGCAG CCCATTCCCG GCgagttCGA
951 cgactACATC GCCAACCCCA AAGgcaACGg ttATAAAAGt TTGCACACCG
1001 TCATCGTcgg cccGGAagaa aaaggtgtgg aagtgcAAAT CCGCACCTTC
1051 GATATGCacc AATTcAaCga ATTcGGTgTC GCCGCCCACT GGCGTTACAA
1101 AGAAGGCGGC AAAGGCGATT CCGCTACGA ACAAAAAATC GCCTGGTTGC
1151 GCCAACTCTT GGACTGGCGC GAAAATATGG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCCGCCG CCTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAAGTCC TCTCTCTGCC AACGGGCGCA ACCCCCATCG
1301 ACTTCGCCTA CGCCCTGCAC AGCAGCATCG GCGACCGCTG CCGGGGCGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCGCTCG AAAACGGACA
1401 GCGCGTCGAA ATCATTACCG CCAAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAAA TCCGGCAAGG CCATCGGCAA AATCCGCGCC
1501 TACATCCGCG AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGTGTCCA
1551 ACTCGACAAG CAGCTTGCCA AACTCACGCC CAAACCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCCGTC
1651 GGACAAGGCG AAATTTCGAA CCGCGCCATC CAAAAAGCCT GCGGCACGCT
1701 GAACGAACCG CCGCCCGTGC CCGTCAGCGC AACCACCATC GTCAAACAGT
1751 CCAAAATCAA AAAAGGTGGC AAAACCGGCG TGCTCATCGA CGGCGAAGAC
1801 GGCTTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 TATTGCCGCG TTCTGTACCC GCGAGCGCGG CATTTCGCTC CACCGCAAAA
1901 CCTGCCCTC TTTCCGACAC CTTGCCGAAC ACGCGCCCGA AAAAGTACTG
1951 GACGCAAGTT GGGCGGCGTT GCAGGAAGGG CAAGTGTTCT CCGTCGATAT
2001 CGAAATCCGC GCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAACTC AACGTTACCG CCGTGCAAAC CCAGTCCCGC
2101 GACTTGGAAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTCAACGA
2151 CCTCCGCGC GTCCCTCGCG GCCTCGGCGA TGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 418; ORF 117-1.ng>:

g117-1.pep

```

1   MTAISPIQDT QSATLQELRE WFDSYCAALP DNDKNLIGTA WSLAQEHYPA
51  DAATPYGEPL PDHFLGAAQM VDELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLDILRTELK
251 KYNIHFEVAG RPKHIYSIYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKNGYKYS LHTVIVGPPE KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLLDWR ENMAESGKED
401 LAAAFKTELF NDTIYVLTPH GKVLSLPTGA TPIDFAYALH SSIGDRRCRA
451 KVEGQIVPLS TPLENGQVRE IITAKEGHPS VNWLYEGWVK SGKAIGKIRA
501 YIRQONADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSATTI VKQSKIKKGG KTGVLIDGED
601 GLMTTLAKCC KPAPPDDIAG FVTRERGISV HRKTCPSFRH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRETL EVKQVNDLPR VLAGLGDVKG VLSVTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 419>:

m117-1.seq

```

1   ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA

```

```

51  ATTGCGCGAA  TGGTTCGACA  GCTACTGCGC  CGCTCTGCCG  GACAACGATA
101 AAAACCTCAT  CGGTACCGCA  TGGTTGCTGG  CGCAGGAACA  TTACCCCGCC
151 GATGCCGCCA  CGCCGTATGG  CGAGCCGCTG  CCCGACCACT  TCCTCGGCGC
201 GGCAGCAATG  GTTCATGAAC  TCGACCTGCT  CCCCAGTGCC  GTCGCCGCCA
251 CCCTGCTTGC  CGACATCGGA  CGCTACGTCC  CCGACTGGAA  CCTATTGGTT
301 TCCGAACGCT  GCAACAGTAC  CGTCGCCGAG  CTGGTCAAAG  GTGTGGACGA
351 AGTGCAGAAA  CTCACCCACT  TCGCCCGGGT  GGACAGCCTC  GCCACGCCGG
401 AAGAACGCGC  CCAGCAGGCA  GAAACTATGC  GGAAAATGCT  GCTGGCGATG
451 GTTACCAGCA  TCCGCGTCGT  GTTAATCAAA  CTGGCGATGC  GTACGCGCAC
501 CCTGCAATTT  TTAAGCAACG  CCCCCGACAG  CCCCAGAAAA  CGCGCCGTCG
551 CCAAAGAAAC  CCTCGACATC  TTCGCCCCGC  TCGCCAACCG  TTTGGGCGTG
601 TGGCAGCTCA  AATGGCAGCT  CGAAGATTG  GGCTTCCGCC  ATCAAAAGCC
651 CGAAAAATAC  CGCGAAATCG  CGCTGCTTTT  GGACGAAAAA  CGCACCGAAC
701 GCCTCGAATA  CATCGAAAC  TTCTCAACA  TCCTGCGCGG  TGAACCAAG
751 AAATACAATG  TCCATTTTCA  AGTCGCCGGC  CGCCGAAAC  ACATCTACTC
801 CATTTCACAA  AAAATGGTGA  AGAAAAAAT  CAGCTTCGAC  GGCTCTTTG
851 ACATCCGCGC  CGTGCGAAT  CTGGTTGATA  CCGTCCCGCA  GTGTTACACC
901 ACGCTGGGTA  TCGTCCACAG  CCTCTGGCAG  CCCATTCCCG  GCGAGTTTCA
951 CGACTACATC  GCCAATCCCA  AAGGCAACGG  CTATAAAAGT  TTGCACACCG
1001 TCATCGTCGG  CCCGGAAGAC  AAAGGCGTGG  AAGTACAAAT  CCGCACCTTC
1051 GATATGCACC  AATTC AACGA  ATTCCGGTGC  GCCGCCCACT  GGCGTTACAA
1101 AGAGGCGCGC  AAGGCGGATT  CCGCCTACGA  ACAGAAAATC  GCCTGGTTGC
1151 GCCAACTCTT  GGACTGGCGC  GAAAACATGG  CGGAAAGCGG  CAAGGAAGAC
1201 CTCGCCGCCG  CCTTCAAAAC  CGAGCTTTTC  AACGACACGA  TTTATGTTTT
1251 GACCCCGCAC  GGCAAAGTCC  TCTCCCTGCC  CACGGGCGCG  ACCCCCATCG
1301 ACTTCGCCTA  CGCCTGCAC  AGCAGCATCG  GCGACCGTTG  CCGCGGTGCG
1351 AAAGTCGAAG  GGCAGATTGT  GCCGTGTCC  ACCCGCTCG  AAAACGGACA
1401 GCGCGTCGAA  ATCATTACCG  CCAAAGAAGG  GCATCCTTCC  GTCAACTGGC
1451 TTTACGAAGG  CTGGGTCAA  TCCAACAAGG  CAATCGGCAA  AATCCGCGCC
1501 TACATCCGCC  AGCAAAACGC  CGACCCGTG  CGCGAAGAAG  GCCCGTCCA
1551 ACTCGACAAA  CAGCTTGCCA  AACTCACGCC  CAAACCAAC  CTGCAAGAGC
1601 TTGCCGAAAA  TCTCGGCTAC  AAAAAGCCAG  AAGACCTCTA  CACCGCGTTC
1651 GGACAAGGCG  AAATTTCCAA  CCGCGCCATC  CAAAAGCCT  CCGGCACGCT
1701 GAACGAACCG  CCGCCCGTAC  CCGTCAGCGA  AACCACCATC  GTCAAAACAGT
1751 CCAAAATCAA  AAAAGGCGGC  AAAACGGCG  TGCTCATCGA  CGGCGAAGAC
1801 GGTCTGATGA  CCACGCTTGC  CAAATGCTGC  AAACCCGCGC  CGCCCGACGA
1851 TATTATCGGC  TTCGTTACCC  GCGAGCGCGG  CATTTACGTG  CACCGCAAAA
1901 CCTGCCCGTC  TTTCCAACAC  CTCGCCGAAC  ACGCGCCCGA  AAAAGTGCTG
1951 GAGCGAAGCT  GGGCGGCATT  GCAGGAAGGA  CAAGTATTTC  CCGTCGATAT
2001 CGAAATCCGC  GCCCAAGACC  GTCGCGGCT  TTTGCGCGAC  GTATCCGACG
2051 CGCTCGCCCG  CCACAAACTC  AACGTTACCG  CCGTGCAAA  CCAGTCCCGC
2101 GACTTGAAG  CCAGCATGAG  GTTCACGCTC  GAAGTCAAAC  AAGTCAACGA
2151 CCTCCGCGC  GTCCTCGCCA  GCCTCGGCGA  CGTCAAAGGC  GTATTGAGCG
2201 TTACCCGGCT  TTAA

```

This corresponds to the amino acid sequence <SEQ ID 420; ORF 117-1>:

m117-1.pep

```

1  MTAISPIQDT  QSATLQELRE  WFDSYCAALP  DNDKNLIGTA  WLLAQEHYPA
51  DAATPYGEPL  PDHFLGAAQM  VHELDLLPDA  VAATLLADIG  RYVPDWNLLV
101 SERCNSTVAE  LVKGVDEVOK  LTHFARVDSL  ATPEERAQQA  ETMRKMLLAM
151 VTDIRVVLIK  LAMRTRTLQF  LSNAPDSPEK  RAVAKETLDI  FAPLANRLGV
201 WQLKWQLEDL  GFRHQKPEKY  REIALLLDEK  RTERLEYIEN  FLNILRGELK
251 KYNVHFEVAG  RPKHIYSIYK  KMKVKKLSFD  GLFDIRAVRI  LVDTVPECYT
301 TLGIVHSLWQ  PIPGEFDDYI  ANPKNGYKYS  LHTVIVGPED  KGVEVQIRTF
351 DMHQFNEFGV  AAHWRYKEGG  KGDSAYEQKI  AWLRQLLDWR  ENMAESGKED
401 LAAAFKTELF  NDTIYVLTPL  GKVLSLPTGA  TPIDFAYALH  SSIGDRCRGA
451 KVEGQIVPLS  TPLENGQORVE  IITAKEGHPS  VNWLVEGWVK  SNKAIGKIRA
501 YIRQQNADTV  REEGRVQLDK  QLAKLTPKEN  LQELAENLGY  KKPEDLYTAV
551 GQGEISNRAI  QKACGTLNEP  PPVPVSETTI  VKQSKIKKGG  KNGVLIDGED
601 GLMTTLAKCC  KPAPDDIIG  FVTRERGISV  HRKTCPSFOH  LAEHAPEKVL
651 DASWAALQEG  QVFAVDIEIR  AQDRSGLLRD  VSDALARHKL  NVTAVQTQSR
701 DLEASMRFTL  EVKQVNDLPR  VLASLGDVKG  VLSVTRL*

```

m117-1/g117-1 98.2% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFSYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
g117-1	MTAISPIQDTQSATLQELREWFSYCAALPDNDKNLIGTAWSLAQEHYPADAATPYGEPL					
	10	20	30	40	50	60
	70	80	90	100	110	120

m117-1.pep	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK
g117-1	PDHFLGAAQMVDELDDLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK
	70 80 90 100 110 120
m117-1.pep	130 140 150 160 170 180
	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKLAMRTRTLQFLSNAPDSPEK
g117-1	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKLAMRTRTLQFLSNAPDSPEK
	130 140 150 160 170 180
m117-1.pep	190 200 210 220 230 240
	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQKPEKYREIALLLDEKRTERLEYIEN
g117-1	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQEPEKYREIALLLDEKRTERLEYIEN
	190 200 210 220 230 240
m117-1.pep	250 260 270 280 290 300
	FLNILRGELKKYNVHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT
g117-1	FLDILRTELKKYNIHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT
	250 260 270 280 290 300
m117-1.pep	310 320 330 340 350 360
	TLGIVHSLWQPIPGEFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV
g117-1	TLGIVHSLWQPIPGEFDDYIANPKNGYKSLHTVIVGPEEKGVEVQIRTFDMHQFNEFGV
	310 320 330 340 350 360
m117-1.pep	370 380 390 400 410 420
	AAHWRYKEGGKGSAYEQKIAWLRLQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPH
g117-1	AAHWRYKEGGKGSAYEQKIAWLRLQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPH
	370 380 390 400 410 420
m117-1.pep	430 440 450 460 470 480
	GKVLSTLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS
g117-1	GKVLSTLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS
	430 440 450 460 470 480
m117-1.pep	490 500 510 520 530 540
	VNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY
g117-1	VNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY
	490 500 510 520 530 540
m117-1.pep	550 560 570 580 590 600
	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKIKKGGKNGVLIDGED
g117-1	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSATTIVKQSKIKKGGKTGVLIDGED
	550 560 570 580 590 600
m117-1.pep	610 620 630 640 650 660
	GLMTTLAKCCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDAASWAALQEG
g117-1	GLMTTLAKCCKPAPPDDIAGFVTRERGISVHRKTCPSFRHLAEHAPEKVLDAASWAALQEG
	610 620 630 640 650 660
m117-1.pep	670 680 690 700 710 720
	QVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAQTQSRDLEASMRFTLEVQVNDLPR
g117-1	QVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAQTQSRDLEASMRFTLEVQVNDLPR
	670 680 690 700 710 720
m117-1.pep	730
	VLASLGDVKGVLSTRLX
g117-1	VLAGLGDVKGVLSTRLX
	730

m117-1/RelA

sp|P55133|RELA_VIBSS GTP PYROPHOSPHOKINASE (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) >gi|537617 (U13769) ppGpp synthetase I [Vibrio sp.] Length = 744
Score = 536 bits (1366), Expect = e-151
Identities = 288/685 (42%), Positives = 432/685 (63%), Gaps = 31/685 (4%)

Query: 74 LDLLPDAVAATLLADI---GRYVPDWNLLVSERCNSTVAELVKGVDVQKLTHFARVDSL 130
L + D + A LL + G Y D + E + T+ LV+GV+++ ++ ++ S
Sbjct: 68 LSMADTLIAALLYPLVEGGCYSTD---ALKEEYSGTILHLVQGVQMC AIS---QLKST 121

Query: 131 ATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEKRAVAKETLDI 190
A +A Q + +R+MLL+MV D R V+IKLA R L+ + + PD +RA A+E +I
Sbjct: 122 AEETAQAAQVDNIRRMLLSMVDDFRCVVIKLAERICNLREVKDQDPDEV-RRAAQECANI 180

Query: 191 FAPLANRLGVWQLKWQLEDLGRHQKPEKYREIALLLDEKRTERLEYIENFLNIRGELK 250
+APLANRLG+ QLKW++ED FR+Q P+ Y++IA L E+R +R +YI +F++ L +K
Sbjct: 181 YAPLANRLGIGQLKWEIEDYAFRYQHPDITYKQIAKQLSERRIDREDYITHFVDDLS DAMK 240

Query: 251 KYNVHFEVAGRPKHIYSIYKKMVKKKLSFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQ 310
N+ EV GRPKHIYSI++KM KK L FD LFD+RAVRI+ + + +CY LG+VH+ ++
Sbjct: 241 ASNIRAEVQGRPKHIYSIWRKMQKKSLEFDELFDVRAVRIVAEELQDCYAALGVVHTKYR 300

Query: 311 PIPGEFDDYIANPKNGYKSLHTVIVGPEDKGVQVQIRTFDMHQFNEFGVAAHWRYKEG- 369
+P EFDDY+ANPK NGY+S+HTV++GPE K +E+QIRT MH+ +E GVAAHW+YKEG
Sbjct: 301 HLPKEFDDYVANPKNGYQSIHTVVLGPEGKTIEIQIRTKMHHESELGVAAHWKYKEGT 360

Query: 370 --GKGDSAYEQIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLT PHGKVL SLP 427
G SAY++KI WLR+LL W+E M++SG ++ ++++F+D +Y TP G V+ LP
Sbjct: 361 ASGGAQSAYDEKINWLRKLLAQEEMSDSG--EMLDELRSQVFD RRYAFTPKGDVVDLP 418

Query: 428 TGATPIDFAYALHSSIGDRRCRAKVEGQIVPLSTPLENGQRVEIITAKEGHPNVNWL YE- 486
+ ATP+DFAY +HS +G RC GAKVEG+IVP + L+ G +VEIIT KE +PS +WL
Sbjct: 419 SNATPLDFAYHIHSEVGHRCIGAKVEGRIVPFTYHLQMGDQVEIITQKEPNPSRDWLNPN 478

Query: 487 -GWVKSNAIGKIRAYIRQQNADTVREGRVQLDKQLAKL--TPKPNLQELAENLGYKKP 543
G+V S++A K+ A+ R+Q+ D G+ L+ +L K+ T K A+ K P
Sbjct: 479 LGFVTSSRARAKVHAWFRKQDRDKNIIAGKEILEAELVKIATLKDAQYAAKRFNVKSP 538

Query: 544 EDLYTAVGQGEIS-NRAIQKACGTLEPPPPVPVSETTIVKQSKI-----KKGKNGV 594
E+LY +G G++ N+ I +N+P + + K S+ KK ++ V
Sbjct: 539 EELYAGTSGDLRINQVINHINALVNKPTAEEDQQLLEKLSEASNQATSHKKPQRDAV 598

Query: 595 LIDGEDGLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDSW 654
+++G D LMT LA+CC+P P DDI GFVT+ RGISVHR C + L HAPE+++D W
Sbjct: 599 VVEGVNDLNMTHLARCCQPIPGDDIIGFVTQGRGISVHRMDCEQLEELRHHAPERIIDTVW 658

Query: 655 AALQEGQVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQ--SRDLEASMRFTLEV 712
G + + + + A +R+GLL++++ L K+ V ++++ + + M F LE+
Sbjct: 659 GGGFVGN-YTITVRVTASERNGLKELTNLMNEKVKVAGMKSRVDYKKQMSIMDFE L 717

Query: 713 KQVNDLPRVLASLGDVKGVLSVTRL 737
+ L RVL + VK V RL
Sbjct: 718 TDLEVLGRVLKRIEQVKDVAEAKRL 742

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 421>:

all17-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCAC CGCGCTGCCG AACAACGATA
101 AAAAATTGT CTAGCCGCC CGTTCGCTGG CGGAAGCACA TTACCCCGCC
151 GATGCCGCCA CGCCGTATGG CGAACCGCTG CCCGACCACT TCCTCGGCGC
201 GCGCAAATG GTTCATGAAC TCGACCTGCT CCCCGATGCC GTCGCGGCCA
251 CCCTGCTTGC CGACATCGGA CGCTACGTCC CCGACTGGAA CCTATTGGTT
301 TCCGAACGCT GCAACAGTAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAGAAA CTCACCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401 AAGAAGCGCG CCAGCAGGCA GAAACTATGC GGAATATGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCGT GTAATCAAA CTGGCGATGC GTACGCGCAC
501 CCTGCAATTT TTAAGCAACG CCCCCGACAG CCCCCGAAAA CGCGCCGTCG
551 CCAAAGAAAC CCTCGACATC TTCGCCCGCG TCGCCAACCG TTTGGGCGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCCGCC ATCAAGAACC
651 CGAAAAATAC CGCGAAATCG CCCTGCTTTT GGACGAAAAA CGCACCGAAC
701 GCCTCGAATA CATCGAAAC TTCCTTAATA TCCTGCGTAC GGAAC TCAA
751 AAATACAATA TCCACTTTGA AGTCGCCGGC CGTCCGAAAC ACATCTACTC
801 CATTTACAAA AAAATGGTGA AGAAAAAACT CAGCTTCGAC GGGTTGTTCTG

```

```

851 ACATCCGCGC CGTGGCGATT CTGGTTGATA CCGTCCCCGA GTGTTACACC
901 ACATCTGGGCA TTGTCCACAG CCTCTGGCAG CCCATTCCCC GCGAGTTTCGA
951 CGACTACATC GCCAACCCGA AAGGCAACGG CTATAAAAGT TTGCACACCG
1001 TCATCGTCGG CCCGGAAGAC AAAGGCGTGG AAGTGCAAAT CCGCACCTTC
1051 GATATGCACC AATTCAACGA ATTCGGTGTG GCCGCGCACT GGCGTTACAA
1101 AGAGGGCGGC AAAGGCGATT CCGCTACGA AAAAAAATC GCCTGGTTAC
1151 GCCAATTTT GGA CTGGCGC GAAAACATGG CGGAAAGCG CAAGGAAGAC
1201 CTCGCCGCG CCTTCAAAC CGAGCTTTT AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAAGTCC TCTCCCTGCC CACAGCGCG ACCCCCATCG
1301 ACTTCGCCTA CGCCCTGCAC AGCAGCATCG GCGACCGTTG CCGCGGTGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCGCTCG AAAACGGACA
1401 GCGTGTGCAA ATCATTACCG CCAAAGAAG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAG CTGGGTCAA TCCAACAAG CAATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGCGTCCA
1551 ACTCGACAAA CAGCTTGCCA AACTCACGCC CAAACCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCGCTC
1651 GGACAAGCG AAATTTCCAA CCGCGCCATC CAAAAGCCT GCGGCACGCT
1701 GAACGAACCG CCGCCCGTAC CCGTCAGCGA AACCACCATC GTCAAAACAGT
1751 CCAAAATCAA AAAAGGCGGC AAAAACGGCG TGCTCATCGA CGCGGAAGAC
1801 GGTCTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCGACGA
1851 CATTGTGCGG TTCGTTACCC GCGATCGCG CATTTGCGTA CACCGCAAAA
1901 CCTGCCCTC TTTCCGACAC CTCGCCGAAC ACGCGCCCGA AAAAGTACTG
1951 GACGCAAGTT GGGCGGCGTT GCAGGAAGGA CAAGTGTTTC CCGTCGATAT
2001 CGAAATCCGC GCCAAGACC GCTCCGGGCT TTTGCGGAC GTATCCGACG
2051 CGCTCGCCCG CCACAACTC AACGTTACCG CCGTGCAAAC CCAGTCCCGC
2101 GACTTGAAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTTACCGA
2151 CCTCCACGC GTCCTCGCCA GCCTCGGCGA CGTCAAAGGC GTATTAGCG
2201 TTACCCGCT TAA

```

This corresponds to the amino acid sequence <SEQ ID 422; ORF 117-1.a>:

a117-1.pep

```

1  MTAISPIQDT QSATLQELRE WFD SYCTALP NNDKKLVLA RSLAEAHYPA
51  DAATPYGEPL PDHFLGAAQM VHELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLNLRTELK
251 KYNIHFVAVG RPKHIYSIYK KMKVKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKNGYKS LHTVIVGPED KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLLDWR ENMAESGKED
401 LAFAFKTELF NDTIYVLTPL GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGQVRE IITAKEGHPS VNWLVEGWVK SNKAIGKIRA
501 YIRQONADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSETTI VKQSKIKKGG KNGVLIDGED
601 GLMTTLAKCC KPAPPDDIVG FVTRDRGISV HRKTCPSFRH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVTDLPR VLASLGDVKG VLSVTRL*

```

a117-1/m117-1 97.7% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFD SYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
a117-1	MTAISPIQDTQSATLQELREWFD SYCTALPNNDKKLVLAARSLAEAHYPADAATPYGEPL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m117-1.pep	PDHFLGAAQM VHELDLLPDAVAATLLADIGRYVPDWNLLV SERCNSTVAELVKGVDEVQK					
a117-1	PDHFLGAAQM VHELDLLPDAVAATLLADIGRYVPDWNLLV SERCNSTVAELVKGVDEVQK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m117-1.pep	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLK LAMRTRTLQFLSNAPDSPEK					
a117-1	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLK LAMRTRTLQFLSNAPDSPEK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m117-1.pep	RAVAKETLDI FAPLANRLGVWQLKWQLEDL GFRHQKPEKYREIALLLDEK RTERLEYIEN					
a117-1	RAVAKETLDI FAPLANRLGVWQLKWQLEDL GFRHQEPEKYREIALLLDEK RTERLEYIEN					
	190	200	210	220	230	240

m117-1.pep	250	260	270	280	290	300
	FLNILRGELKKYNVHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT					
a117-1	FLNILRTELKKYNIHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT					
	250	260	270	280	290	300
m117-1.pep	310	320	330	340	350	360
	TLGIVHSLWQPIPGEFDDYIANPKGNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV					
a117-1	TLGIVHSLWQPIPGEFDDYIANPKGNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV					
	310	320	330	340	350	360
m117-1.pep	370	380	390	400	410	420
	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPH					
a117-1	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPH					
	370	380	390	400	410	420
m117-1.pep	430	440	450	460	470	480
	GKVLSTPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS					
a117-1	GKVLSTPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS					
	430	440	450	460	470	480
m117-1.pep	490	500	510	520	530	540
	VNWLYEGWVKSNAIGKIRAYIROQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY					
a117-1	VNWLYEGWVKSNAIGKIRAYIROQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY					
	490	500	510	520	530	540
m117-1.pep	550	560	570	580	590	600
	KKPEDLYTAVGQGEISNRAIQKACGTLINEPPVPVSETTIVKQSKIKKGGKNGVLIDGED					
a117-1	KKPEDLYTAVGQGEISNRAIQKACGTLINEPPVPVSETTIVKQSKIKKGGKNGVLIDGED					
	550	560	570	580	590	600
m117-1.pep	610	620	630	640	650	660
	GLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDAASWAALQEG					
a117-1	GLMTTLAKCKPAPPDDIIGFVTRDRGISVHRKTCPSFRHLAEHAPEKVLDAASWAALQEG					
	610	620	630	640	650	660
m117-1.pep	670	680	690	700	710	720
	QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQSRDLEASMRFTLEV KQVNDLPR					
a117-1	QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQSRDLEASMRFTLEV KQVNDLPR					
	670	680	690	700	710	720
m117-1.pep	730					
	VLASLGDVKGVL SVTRLX					
a117-1	VLASLGDVKGVL SVTRLX					
	730					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 423>:

```

g118.seq
  1  ATGTGCGAGT  TCAAGGATTT  TAGAAGAAAC  ATCCCTTGTT  TTGAAGAGTA
 51  TGACGAAAAT  TCATTTATTG  GCAAATGGTA  TGATGACGGG  GTGTGGGATG
101  ATGAAGAATA  TTGGAAGCTG  GAGAAATGAT  TAATcgaGGT  TAGGAGAAAA
151  TATCCTTATC  CGATGGATAT  ACCAAGGGAT  ATTGTGATTG  GAATCGGTAC
201  CATTATTGAT  TTTTAAATGG  TTCCAAATTG  GGAGCTTTTT  GAAATTAAG
251  CTTCCCCTTG  GTTGCCTGAT  AGCGTGGGAA  TTCATGAACG  TTATGAAAGA
301  TTCACAACGA  TGCTCCGTTA  TATTTTACC  GAGAAAGACA  TAGTCAACGT
351  GCGATTTGAT  TATTACAaCA  AAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 424; ORF 118.ng>:

```

g118.pep
  1  MCEFKDFRRN  IPCFEEYDEN  SFIGKWYDDG  VWDDEEYWK  LENDLIEVRRK
 51  YPYPM DIPRD  IVIGIGTIID  FLMV PNWELF  EIKAS PWLPD  SVGIHERYER
101  FTTMLRYIFT  EKDIVNVRFD  YYNKK*

```

340

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 425>:

```
m118.seq
  1  ATGTGTGAGT TCAAGGATAT TATAAGAAAC GTTCCTTATT TTGAGGGGTA
 51  TGACGAAAAT TCATTTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101  ATGAAGAATA TTGGAAGTTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151  TATCCTTATC CGATGGACAT ACCAAGATAT GTTGTCAATT GAATCGGTAC
201  CATTATTGAT TTCTTAATGG TTCCAAATTG GAAACTTTTT GAAATTAAG
251  CTTCCCCTTG GTTGCCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301  TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351  GCGATTTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 426; ORF 118>:

```
m118.pep
  1  MCEFKDIIRN VPFEGYDEN SFIGKYYDDG VWDDEEYWKL ENDLIEVRKK
 51  YPYPM DIPRY VVIGIGTIID FLMVPNWKLF EIKAS PWLPD SVGIHERYER
101  FTTMLRYIFT EKDIVNVRFD YYNKK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 118 shows 92.8% identity over a 125 aa overlap with a predicted ORF (ORF 118.ng) from *N. gonorrhoeae*:

```
m118/g118

          10      20      30      40      50      60
m118.pep  MCEFKDIIRNVPYFEGYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRY
          |||||: ||:| || |||||:|||||:|||||:|||||:|||||:|||||:|||||
g118       MCEFKDFRRNIPCFEEYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRD
          10      20      30      40      50      60

          70      80      90      100     110     120
m118.pep  VVIGIGTIIDFLMVPNWKLF EIKAS PWLPDSVGIHERYERFTTMLRYIFTEKDIVNVRFD
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g118       IVIGIGTIIDFLMVPNWKLF EIKAS PWLPDSVGIHERYERFTTMLRYIFTEKDIVNVRFD
          70      80      90      100     110     120

m118.pep  YYNKKX
          |||||
g118       YYNKKX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 427>:

```
a118.seq
  1  ATGTGTGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
 51  TGACGAAAAT TCATTTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101  ATGAAGAATA TTGGAATTTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151  TATCCTTATC CGATGGATAT ACCAAGGGAT ATTGTGATTG GAATCGGTAC
201  CATTATTGAT TTTTAAATGG TTCCAAATTG GGAGCTTTTT GAAATTAAG
251  CTTCCCCTTG GTTGCCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301  TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351  GCGATTTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 428; ORF 118.a>:

```
a118.pep
  1  MCEFKDFRRN IPCFEEYDEN SFIGKYYDDG VWDDEEYWKL ENDLIEVRKK
 51  YPYPM DIPRD IVIGIGTIID FLMVPNWELE EIKAS PWLPD SVGIHERYER
101  FTTMLRYIFT EKDIVNVRFD YYNKK*
```

m118/a118 93.6% identity in 125 aa overlap

```
m118.pep  MCEFKDIIRNVPYFEGYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRY
          |||||: ||:| || |||||:|||||:|||||:|||||:|||||:|||||
a118       MCEFKDFRRNIPCFEEYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRD
          10      20      30      40      50      60
```


		70	80	90	100	110	120
m118.pep		VVIGIGTIIDFLMVPNWKLFEIKAS	PWLPDSVGIHERYERFTT	MLRYIFTEK	DIVNVRFD		
		:					
a118		IVIGIGTIIDFLMVPNWELFEIKAS	PWLPDSVGIHERYERFTT	MLRYIFTEK	DIVNVRFD		
		70	80	90	100	110	120
m118.pep	YYNKKX						
a118	YYNKKX						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 429>:

g120.seq

1	ATGATGAAGA	CTTTTAAAAA	TATATTTTCC	GCCGCCATT	TGTCCGCCGC
51	CCTGCCGTGC	GCGTATCGGC	CAAGGCTACC	CCAATCCGCG	GTGCTGCACT
101	ATTCCGGCAG	CTACGGCATT	CCCGCACGA	TGACATTGA	ACCGACGCGC
151	AATGCTTACA	AAATCGTTTC	GACGATTAAG	GTGCCGCTAT	ACAATATCCG
201	TTTCGAATCC	GGCGGTACGG	TTGTCGGCAA	TACCTTGCAC	CCTGCCTACT
251	ATAAAGACAT	ACGCAGGGGC	AAACTGTATG	CGGAAGCCAA	ATTGCGCGAC
301	GGCAGCGTAA	CCTACGGCAA	AGCGGGCGAG	AGCAAAACCG	AGCAAAGCCC
351	CAAGGCTATG	GATTTGTTCA	CGCTTGCTGT	GCAGTTGGCG	GCAATATGAC
401	CGAAACTCCC	CCCGGTCTGT	AAAATCACCA	ACGGCAAAAA	ACTTTATTCC
451	GTCGCGCGCC	TGAATAAGGC	GGGTACGGGA	AAATACAGCA	Taggcggcgt
501	gGAAACCGAA	GTCGTCAAAT	ATCGGGTGCG	GCGCGGCCAC	GATACGGTAA
551	CGTATTCTT	CGCACCGTCC	CTGAACAATA	TTCCGGCACA	AATCGGCTAT
601	ACCGACgaCG	GCAAAACCTA	TACGCTGAAG	CTCAAATCGG	TGCAGATCAA
651	CGGACAGGCC	GCCAAACCGT	AA		

This corresponds to the amino acid sequence <SEQ ID 430; ORF 120.ng>:

```
g120.pep
1  MMKTFKNIFS AAILSAAALPC AYAARLPQSA VLHYSGSYGI PATMTFERSG
51 NAYKIVSTIK VPLYNRFES GGTVVGNTLH PAYYKDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DTVTYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSGVQINGQA AKP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 431>:

```
m120.seq
1  ATGATGAAGA CTTTTAAAAA TATATTTTCC GCCGCCATT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCC GTGCTGmACT
101 ATTCCGGCAG CTACGGCATT CCGGCCACGA TGACATTGTA ACGCAGCGCG
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAGTCC GCGGTACGG TTGTCGGCAA TACCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AAACGTGTAT CGGAAGcCA ATTCGCCGAC
301 GGCAGCGTAA CTTACGGCAA AGCGGGCGAG AGCAAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTGTGTCA CGCTTGCTG CGAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGCGTG AAAATCACA ACGGCAAAAA ACTTTATTCC
451 GTCGGCGGTT TGAATAAGGC GGGTACAGGA AAATACAGCA TAGGCGGCGT
501 GGAACCGAA GTCGTCAAAT ATCGGGTGCG GCGCGGCGAC GATGCGGTAA
551 TGTATTTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAACCTA TACGTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAAACCG
```

This corresponds to the amino acid sequence <SEQ ID 432; ORF 120>:

m120.pep	1	MMKTFKNIFS	AAILSAAALPC	AYAAGLPQSA	VLXYSGSYGI	PATMTFERSG
	51	NAYKIVSTIK	VPLYNIRFES	GGTVVGNTLH	PTYYRDIRRG	KLYAEAKFAD
	101	GSVTYKGAGE	SKTEQSPKAM	DLFTLAWQLA	ANDAKLPPGL	KITNGKKLYS
	151	VGGLNKAGTG	KYSIGGVETE	VVKYRVRRGD	DAVMYFFAPS	LNNIPAQIGY
	201	TDDGKTYTLK	LKSIVINGOA	AKP		

342

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 120 shows 97.3% identity over a 223 aa overlap with a predicted ORF (ORF 120.ng) from *N. gonorrhoeae*:

m120/g120

	10	20	30	40	50	60
m120.pep	MMKTFKNIFSAAILSAALPCAYAAGLPQSAVLXYSYGI PATMTFERSGNAYKIVSTIK					
g120	MMKTFKNIFSAAILSAALPCAYAARLPQSAVLHYSYGI PATMTFERSGNAYKIVSTIK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m120.pep	VPLYNIRFESGGTVVGNTLHPTYYRDIRRGKLYAEAKFADGSVTYKGAGESKTEQSPKAM					
g120	VPLYNIRFESGGTVVGNTLHPAYYKDIRRGKLYAEAKFADGSVTYKGAGESKTEQSPKAM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m120.pep	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE VKYRVRGD					
g120	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE VKYRVRGD					
	130	140	150	160	170	180
	190	200	210	220		
m120.pep	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQA AKP					
g120	DTVTYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQA KPX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 433>:

a120.seq

1	ATGATGAAGA	CTTTTAAAAA	TATATTTTCC	GCCGCCATTT	TGTCCGCCGC
51	CCTGCCGTGC	GCGTATGCGG	CAGGGCTGCC	CCAATCCGCC	GTGCTGCACT
101	ATTCCGGCAG	CTACGGCATT	CCCGCCACGA	TGACATTGTA	ACGCAGCGGC
151	AATGCTTACA	AAATCGTTTC	GACGATTAAA	GTGCCGCTAT	ACAATATCCG
201	TTTCGAGTCC	GGCGGTACGG	TTGTCGGCAA	TACCCTGCAC	CCTACCTACT
251	ATAGAGACAT	ACGCAGGGGC	AAACTGTATG	CGGAAGCCAA	ATTCCGCCGAC
301	GGCAGCGTAA	CCTACGGCAA	AGCGGGCGAG	AGCAAAACCG	AGCAAAGCCC
351	CAAGGCTATG	GATTTGTTCA	CGCTTGCTG	GCAGTTGGCG	GCAAATGACG
401	CGAAACTCCC	CCCGGGGCTG	AAAATCACCA	ACGGCAAAAA	ACTTTATTCC
451	GTCGGCGGTT	TGAATAAGGC	GGGTACAGGA	AAATACAGCA	TAGGCGGCGT
501	GGAAACCGAA	GTCGTCAAAT	ATCGGGTGCG	GCGCGGCGAC	GATGCGGTAA
551	TGTATTTCTT	CGCACCGTCC	CTGAACAATA	TTCCGGCACA	AATCGGCTAT
601	ACCGACGACG	GCAAAACCTA	TACGCTGAAA	CTCAAATCGG	TGCAGATCAA
651	CGGCCAGGCA	GCCAAACCGT	AA		

This corresponds to the amino acid sequence <SEQ ID 434; ORF 120.a>:

a120.pep

1	MMKTFKNIFS	AAILSAALPC	AYAAGLPQSA	VLHYSYGI	PATMTFERSG
51	NAYKIVSTIK	VPLYNIRFES	GGTVVGNTLH	PTYRDIRRG	KLYAEAKFAD
101	GSVTYKGAGE	SKTEQSPKAM	DLFTLAWQLA	ANDAKLPPGL	KITNGKKLYS
151	VGGLNKAGTG	KYSIGGVETE	VVKYRVRRGD	DAVMYFFAPS	LNNIPAQIGY
201	TDDGKTYTLK	LKSVQINGQA	AKP*		

m120/a120 99.6% identity in 223 aa overlap

	10	20	30	40	50	60
m120.pep	MMKTFKNIFSAAILSAALPCAYAAGLPQSAVLXYSYGI PATMTFERSGNAYKIVSTIK					
a120	MMKTFKNIFSAAILSAALPCAYAAGLPQSAVLHYSYGI PATMTFERSGNAYKIVSTIK					

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	10	20	30	40	50	60
	70	80	90	100	110	120
m120.pep	VPLYNIRFESGGTVVGNTLHPTYYRDIRRGKLYAEAKFADGSVTYKGAGESKTEQSPKAM					
a120	VPLYNIRFESGGTVVGNTLHPTYYRDIRRGKLYAEAKFADGSVTYKGAGESKTEQSPKAM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m120.pep	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETEYVVKYRVRRGD					
a120	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETEYVVKYRVRRGD					
	130	140	150	160	170	180
	190	200	210	220		
m120.pep	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAPX					
a120	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAPX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 435>:

g121.seq

```

1  ATGGAACAC  AGCTTTACAT  CGGCATTATG  TCGGGAACCA  GTATGGACGG
51  GCGGATGCC  GTGCTGGTAC  GGATGGACGG  CGGCAAATGG  CTGGGCGCGG
101 AAGGGCACGC  CTTTACCCCC  TACCGTGACC  GGTGCGCCG  CAAATTGCTG
151 GATTTCAGG  ACACAGGCAC  AGACGAAGTG  CACCGCAGCA  GGATGTTGTC
201 GCAAGAACTC  AGCCGCCTGT  ACGCGCAAAC  CGCCGCCGAA  CTGCTGTGCA
251 GTCAAAACCT  CGCTCCGTGC  GACATTACCG  CCCTCGGCTG  CCACGGGCAA
301 ACCGTCCGAC  ACGCGCCGGA  ACACGGTtac  AGCATACAGC  TTGCCGATTT
351 GCCGCTGCTG  GCGGAAGTga  cgcggatttt  TACCGTCggc  gacttcCGCA
401 GCCGCGACCT  TGCTGCCGGC  GGacaAGGTG  CGCCGCTCGT  CCCCgcCTTT
451 CACGAAGCCC  TGTTCCGCGA  TGACAGGGAA  ACACGCGTGG  TACTGAACAT
501 CGGCGGGATT  GCCAACATCA  GCGTACTCCC  CCCCgcCGCA  CCCGcCTTCG
551 GCTTCGACAC  AGGGCCGGGC  AATATGCTGA  TGGAcgcgtg  gacgcaggca
601 cactGGcagc  TGCCTTACGA  CAAAaacggt  gcAAAGgcg  cacAAGGCAA
651 catatTGCcg  cAACTGCTCG  gcaggctGCT  CGCCcaccCG  TATTTCTCAC
701 AACCCcacc  aaAAAGCACG  GGgcGCGaac  TgtttgcccT  AAattggctc
751 gaaacctAcc  ttgacggcgg  cgaaaaccga  tacgacgtat  tgccgacgct
801 ttcccgattc  accgcgcaaa  ccgTttggga  cgccgtctca  CACGCAGCGG
851 CAGATGCCCG  TCAAATGTAC  ATTTGCGGCG  GCGGCATCCG  CAATCTGTT
901 TTAATGGCGG  ATTTGGCAGA  ATGTTTCGGC  ACACGCGTTT  CCCTGCACAG
951 CACCGCCGAA  CTGAACCTCG  ATCCTCAATG  GGTGGAGGCG  gccgCATTtg
1001 cgtggttgC  GGCGTGTGG  ATTAACCGCA  TCCCGGTAG  TCCGCACAAA
1051 GCGACCGCG  CATCAAACC  GTGTATTCTG  GGCGCGGGAT  ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 436; ORF 121.ng>:

g121.pep

```

1  METQLYIGIM  SGTSMDGADA  VLVRMDGGKW  LGAEGHAFTP  YPDLRRLKLL
51  DLQDTGTDEL  HRSRMLSQEL  SRLYAQTAAE  LLCSQNLAPC  DITALGCHGQ
101 TVRHAPEHGY  SIQLADLPLL  AELTRIFTVG  DFRSRDLAAG  GQGAPLVPAP
151 HEALFRDDRE  TRVVLNIGGI  ANISVLPPGA  PAFGFDTPG  NMLMDAWTQA
201 HWQLPYDKNG  AKAAQGNILP  QLLGRLLAHP  YFSQPHPKST  GRELFALNWL
251 ETYLDGGENR  YDVLRTLRF  TAQTVWDAVS  HAAADARQMY  ICGGGIRNPV
301 LMADLAECFG  TRVSLHSTAE  LNLDPQWVEA  AAFAWLAACW  INRIPGSPHK
351 ATGASKPCIL  GAGYYY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 437>:

m121.seq

```

1  ATGGAACAC  AGCTTTACAT  CGGCATCATG  TCGGGAACCA  GCATGGACGG
51  GCGGATGCC  GTACTGATAC  GGATGGACGG  CGGCAAATGG  CTGGGCGCGG
101 AAGGGCACGC  CTTTACCCCC  TACCCCGGCA  GGTACGCCG  CCAATTGCTG

```

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```

151 GATTTCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTG
201 GCAAGAACTC AGCCGCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
401 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
451 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
501 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
551 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
601 XXXXXxCAGC TTCCTTACGA CAAAACCGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTGCGAC
701 AACGCCACCC TAAAAGCAGC GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGTTTT ACCGCGCAA CCGTTTGCGA CGCCGTCTCA CACGACGCG
851 CAGATGCCCG TCAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACGGCG CATCCAAACC GTGTATTCTG AnCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 438; ORF 121>:

m121.pep

```

1 METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRQLL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL AXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
151 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
201 xxQLPYDKNG AKSAQGNILP QLLDRLLAHP YFAQRHPKST GRELFAINWL
251 ETYLDGGENR YDVLRTLRF TAQTVCDAYS HAAADARQMY ICDGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 121 shows 73.5% identity over a 366 aa overlap with a predicted ORF (ORF121.ng) from *N. gonorrhoeae*:

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTYPGRLLRQLLDLQDTGADEL					
g121	METQLYIGIMSGTSMGDADAVLVRMDGGKWLGAEGHAFTYPDRLLRKLDDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAAELLCSONLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
g121	HRSRMLSQELSRLYAQTAAELLCSONLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121.pep	AXXX					
g121	AELTRIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDDRETRVVLNIGGIANISVLPPGA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121.pep	XXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
g121	PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLRFRTAQTVCDAVSHAAADARQMYICDGGIRNPV					
g121	GRELFALNWLETYLDGGENRYDVLRTLRFRTAQTVWDAVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m121.pep	LMADLAECFGTRVSLHSTADLNLDLPQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
g121	LMADLAECFGTRVSLHSTAE LNLDLPQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYYX					
g121	GAGYYYYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 439>:

```

a121.seq
1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCGC GGACGAAGTG CACCGCAGCA GGATGTTGTC
201 GCAAGACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGCGCCGCG GGACAAGGCG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCACGCA CCCGCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCGG TATTTGCGAC
701 AACCCACCCC TAAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGATTG ACCGCGCAAA CCGTTTTCGA CGCCGTCTCA CACGACGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCG
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 440; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPEHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPFAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AFAWMAACW VNRI PGSPHK
351 ATGASKPCIL GAGYYY*

```

m121/a121 74.0% identity in 366 aa overlap

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPPYGRLLRRQLDLQDTGADEL					
a121	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPPYGRLLRRQLDLQDTGADEL					
	10	20	30	40	50	60
m121.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
a121	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPEHSYSVQLADLPLL					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m121.pep	XX					
a121	AERTQIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121.pep	XXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
a121	PAFGFDTGPGNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLRSRFTAQTVCDVSHAAADARQMYICDGGIRNPV					
a121	GRELFALNWLETYLDGGENRYDVLRTLRSRFTAQTVFCDVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m121.pep	LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
a121	LMADLAECFGTRVSLHSTAE LNLDPOWVEAAAFWMAACWVNRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYY					
a121	GAGYYYY					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 441>:

m121-1.seq

```

1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGAACCA GCATGGACGG
51  GCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTACGCCG CCAATTGCTG
151 GATTTGCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCGCTGCTG GCGGAACGGA CGCGGATTTT TACCGTCGGC GACTTCCGCA
401 GCGCGACCTT TGCGGCCGGC GGACAAGGCG CGCCACTCGT CCCCCTTT
451 CACGAAGCCC TGTTCGCGA CAACAGGGA ACACGCGCGG TACTGAACAT
501 CGCGGGGATT GCCAACATCA GCGTACTCCC CCCCACGCA CCGCCTTCG
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGACGCGTG GACGAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCCG TATTTCGCAC
701 AACCCACCC TAAAGCACG GGGCGCAAC TGTTCGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGTTTT ACCGCGCAA CCGTTGCGA CGCGTCTCA CACGAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGNATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGCGC CATCAAACC GTGTATTCTG ANCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 442; ORF 121-1>:

m121-1.pep

```

1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGLRRQLL
51  DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPHEGY SIQLADLPLL AERTRIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDNRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLRSR TAQTVCDVSH HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

m121-1/g121 95.6% identity in 366 aa overlap

10 20 30 40 50 60

a121-1.seq

This corresponds to the amino acid sequence <SEQ ID 444; ORF 121-1.a>:

a121-1.pap

1	METQLYIGIM	SGTSMGDADA	VLIRMDGGKW	LGAEGHAFTP	YPGRLRRKLL
51	DLQDTGADEL	HRSRLMSQEL	SRLYAQTAEE	LLCSQNLAPE	DITALGHCHGQ
101	TVRHAPDESL	SVQLADLP LL	AERTQIFTVV	DFRSRD LAAG	GOGAPLPVPAF
151	HEALFRDDRE	TRAVLNI GGI	ANISVLPPDA	PAFGFDLTGP	NMLMDAWMWA

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201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
 251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
 301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK
 351 ATGASKPCIL GAGYYY*

m121-1/a121-1 96.4% identity in 366 aa overlap

m121-1.pep	10	20	30	40	50	60
	METQLYIGIMSGTSM	GADAVLIRMDGGKWL	GAEGHAFTPYPGRLRR	QLLDLQDTGADEL		
a121-1	10	20	30	40	50	60
	METQLYIGIMSGTSM	GADAVLIRMDGGKWL	GAEGHAFTPYPGRLRR	KLLDLQDTGADEL		
m121-1.pep	70	80	90	100	110	120
	HRSRILSQELSR	LYAQTAELLCSQNL	APSDITALGCHGQT	VRHAPEHGYSIQL	ADLPLL	
a121-1	70	80	90	100	110	120
	HRSRILSQELSR	LYAQTAELLCSQNL	APSDITALGCHGQT	VRHAPEHSYSVQL	ADLPLL	
m121-1.pep	130	140	150	160	170	180
	AERTRIFTVGDF	RSRDLAAGGQGAP	LVPAFHEALFRDN	RETRAVLNIGGIAN	ISVLPPDA	
a121-1	130	140	150	160	170	180
	AERTQIFTVGDF	RSRDLAAGGQGAP	LVPAFHEALFRDD	RETRAVLNIGGIAN	ISVLPPDA	
m121-1.pep	190	200	210	220	230	240
	PAFGFDTGPGNML	DAWTOAHWQLPYD	KNGAKAAQGNILP	QLLDRLLAHPYFA	QPHPKST	
a121-1	190	200	210	220	230	240
	PAFGFDTGPGNML	DAWMQAHWQLPYD	KNGAKAAQGNILP	QLLDRLLAHPYFA	QPHPKST	
m121-1.pep	250	260	270	280	290	300
	GRELFALNWLE	TYLDGGENRYDVL	RRTLSRFTAQTV	CDVSHAAADARQ	MYICGGGIRNPV	
a121-1	250	260	270	280	290	300
	GRELFALNWLE	TYLDGGENRYDVL	RRTLSRFTAQTV	FDAVSHAAADARQ	MYICGGGIRNPV	
m121-1.pep	310	320	330	340	350	360
	LMADLAECFG	TRVSLHSTADL	NLDLPQWVEAAX	FAWLAACWINRI	PGSPHKATGASK	PCIL
a121	310	320	330	340	350	360
	LMADLAECFG	TRVSLHSTAE	LNLDPQWVEA	AAFAWMAACW	VNRIPGSPHKAT	GASKPCIL
m121-1.pep					XAGYYYY	
a121					GAGYYYY	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 445>:

g122.seq

1	ATGGCTTTAC	TGAGCATCCG	CAAGCTGCAC	AAACAATACG	GCAGCGTAAC
51	CGCCATCCAA	TCCTTAGACT	TGGACTTGGA	AAAAGCGCAA	GtcacCGTAC
101	TGCTGGGCCC	gTccggctgc	ggCAAATCCA	CCCTectgcg	ctgcgtcaaC
151	GGTTTGGAGC	CGCACC Aagg	cgGCAGCATC	GTGATGGACG	GTgtcgGCCA
201	ATTGcg AAA	GACGTTTCCT	GGCAAACCGC	CCGGCAAAAa	gtcggatatgg
251	tctttcaaag	taacgAactg	Tttgcccaca	tgaccgtcat	cgAaaacatc
301	ttcttAggcC	CGGTAAagga	aCAAAACGc	gaccgtgccg	aagcaGAGGC
351	gCAAGCCGCG	AAactGttgg	aacgcgTCGG	actgctAGAC	CGCAAAAACG
401	CCTATCCGCG	CGAACTTTCC	GGCGGTCAGA	AACAGCGCAT	CGCCATTGTC
451	CGCGCCCTGT	GCCTGAATCC	GGAAGTCATC	CTGCTGGACG	AAATCACC GC
501	CGCACTTGAC	CCCGAAATGG	TGCGCGAAGT	CTTGGAAGTG	GTTTGGAAAC
551	TCGCCCCGGA	AGGGATGAGT	ATGCTCATCG	TAACCCACGA	AATGGGGTTC
601	GCACGCAAAG	TTGCCGACCG	CATCGTCTTT	ATGGACAAAG	GCGGCATCGT
651	CGAATCGTCC	GACCCCGAAA	CCTTTTTTTC	CGCACCAAAA	AGCGAACGCG
701	CCCGCCAATT	TCTGGCAGGT	ATGGACTACT	GA	

This corresponds to the amino acid sequence <SEQ ID 446; ORF 122.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 447>:

m122.seq

This corresponds to the amino acid sequence <SEQ ID 448; ORF 122>:

m122.pap

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 122 shows 47.2% identity over a 246 aa overlap with a predicted ORF (ORF 122.ng) from *N. gonorrhoeae*:

m122/g122

		10	20	30	40	50	60
m122.pep		VVMIKIRNIHKTFGENTILRGIDLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQI					
		::::: ::: : :::: ::: ::: ::: ::: ::: ::: ::: : :					
g122		MALLSIRKLHKQYGSVTAIQSLDLLEKGEVIVLLGPSGCGKSTLLRCVNGLEPHQGGSI					
		10	20	30	40	50	60
		70	80	90	100	110	120
m122.pep		EFDNERPLKIDFSKKPSKHDILALRRKSMVFQQYNLFPHKTALENVMEGPVAVQGKPAA					
		: : : : : : : ::: ::: ::: :::					
g122		VMDGVGEFGKDVSWQTA-----RQKVGVMVFQSNELFAHMTVIENIFLGPVKEQNRDRA					
		70	80	90	100	110	
		130	140	150	160	170	180
m122.pep		QAREEALKLLEKVGLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSA LDPEL					
		: : : :: : : : :: :: : :: ::					
g122		EAEAQAGKLLERVLGDRKNAYPRELSSGGQKQRIATVRALCLNPEVILLDEITAA LDPEM					
		120	130	140	150	160	170
		190	200	210	220	230	240
m122.pep		VQDVLDXMKELAQEGWTMVVVTHEIKFALEVATTXVMDXGVIVEQGSQD LFDHPKHER					
		:: ::: : :: ::: :: : :: ::: :					
g122		VREVLEVVLLELAREGMSMLIVTHEMGFARKVADRI VFMDKGGIVESDPETFFSAPKSEI					

350

	180	190	200	210	220	230
	250					
m122.pep	TRRFLSQIQSTKIX					
	: : : :					
g122	ARQFLAGMDYX					
	240					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 449>:

```
a122.seq
1  GTTGTTCATGA  TTAAATCCG  CAATATCCAT  AAGACCTTCG  GCAAAAATAC
51  CATTTTGCGC  GGCATCAATT  TGGATGTGTG  CAAAGGGCAG  GTGGTCGTCA
101 TCCTCGGGCC  TTCCGGCTCA  GGCAAAACGA  CGTTTCTGCG  ATGCCTAAAC
151 GCGTTGGAAG  TGCCCGAAGA  CGGACAAATC  GAGTTCGACA  ACGAGCGACC
201 GCTGAAAATC  GATTTTCTTA  AAAAACCAAG  CAAACACGAT  ATTTTGGCAC
251 TGCGCCGCAA  ATCAGGCATG  GTGTTTCAAC  AATACAACCT  CTTTCCGCAC
301 AAAACCGCCT  TGGAAAACGT  GATGGAAGGA  CCGGTTGCCG  TACAGGGCAA
351 GCCTGCCGCC  CAAGCGCGCG  AAGAGGCTCT  GAAACTGCTG  GAAAAAGTCG
401 GCTTGGGCGA  CAAAGTGGAT  TTGTATCCCT  ACCAGCTTTC  CGGCGGTCAG
451 CAGCAGCGCG  TCGGCATTGC  CCGAGCATTG  GCGATTACAG  CCGAGCTGAT
501 GTTGTGTTGAC  GAACCCACTT  CCGCGCTTGA  CCCCAGATTG  GTGCAAGACG
551 TGTTGAACGC  CATGAAGGAA  TTGGCGCGGG  AAGGTTGGAC  GATGTCGTC
601 GTTACCCACG  AAATCAAGTT  CGCGCTGGAA  GTTGCCACGA  CCGTTGTCGT
651 GATGGACGGC  GCGGTTATCG  TAGAGCAGGG  CAGCCCGAAA  GAGTTGTTTC
701 ACCACCCCAA  ACACGAACGG  ACGCGGAGAT  TTTTAAGCCA  AATCCAATCT
751 ACCAAGATTT  GA
```

This corresponds to the amino acid sequence <SEQ ID 450; ORF 122.a>:

```
a122.pep
1  VVMIKIRNIH  KTFGKNTILR  GINLDVCKGQ  VVILGPSGS  GKTTFRLCLN
51  ALEMPEDGQI  EFDNERPLKI  DFSKKPSKHD  ILALRRKSGM  VFQYNLFPH
101 KTALENVMEG  PVAVQGKPAA  QAREEALKLL  EKVGLGDKVD  LYPYQLSGGQ
151 QQRVGIARAL  AIQPELMLFD  EPTSALDPEL  VQDVLNAMKE  LAREGWTMVV
201 VTHEIKFALE  VATTVVVMDG  GVIVEQGSPK  ELFDHPKHER  TRRFLSQIQS
251 TKI*
```

m122/a122 96.0% identity in 253 aa overlap

	10	20	30	40	50	60
m122.pep	VVMIKIRNIHKTFTGENTILRGIDLVDCKGQVVILGPSGSGKTTFRLCLNALEMPEDGQI					
a122	VVMIKIRNIHKTFTGKNTILRGINLDVCKGQVVILGPSGSGKTTFRLCLNALEMPEDGQI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m122.pep	EFDNERPLKIDFSKKPSKHDILALRRKSXMFQQYNLFPHKTALENVMEGPVAVQGKPAA					
a122	EFDNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPVAVQGKPAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m122.pep	QAREEALKLLEKVGLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSALDPEL					
a122	QAREEALKLLEKVGLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSALDPEL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m122.pep	VQDVLDXMKELAQEGWTMVVVTHEIKFALEVATTXVVMGXGVIVEQGSPQDLFDHPKHER					
a122	VQDVLNAMKELAREGWTMVVVTHEIKFALEVATTVVVMDGGVIVEQGSPKELFDHPKHER					
	190	200	210	220	230	240
	250					
m122.pep	TRRFLSQIQSTKIX					

351

a122 |||||
 TRRFLSQIQSTKIX
 250

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 451>:

g122-1.seq

```

1  ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA ACACCATTTT
51  GCGCGGCATC GATTTGGATG TGGGCAAAGG GCAGGTGGTC GTCATCCTCG
101 GGCCTTCCGG CTCGGGTAAA ACAACATTTC TCGCTGCCT AAACGCGTTG
151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGCGC GGCCGTTACG
201 CATTGATTTT TCCAAAAAAA CAAGCAAACA CGATATTTTG GCACTGCGCC
251 GCAAGTCCGG AATGGTATTC CAACAATACA ACCTCTTCCC GCATAAAACC
301 GTGTTGGAAA ACGTGATGGA AGGCGCGGTT GCCGTACAGG GCAAGCCTGC
351 CGCCCAAGCG CGCGAAGAGG CTTTGAAACT GCTGGAAAAA GTCGGCTTGG
401 GCGATAAAGT GGATTTGTAT CCCTACCAGC TTTCCGCGCG TCAGCAGCAG
451 CGTGTCGGTA TCGCCCGCGC ACTGGCGATT CAGCCTGAAT TGATGCTGTT
501 TGACGAACCC ACTTCCGCGC TGGACCCCGA GTTGGTGCAA GACGTGTTGG
551 ACGCCATGAA GGAATTGGCG CGGGAAGGTT GGACGATGGT CGTCGTTACC
601 CACGAAATCA AGTTCACGCT GGAAGTTGCC ACGAACGTCG TCGTGATGGA
651 CGGCGGCGTT ATCGTAGAGC AGGCGAGCCC GAAAGAGTTG TTCGACCACC
701 TCAAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTGCCAAG
751 ATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 452; ORF 122-1.ng>:

g122-1.pep

```

1  MIKIRNIHKT FGENTILRGI DLDVKGQVQV VILGPSGSGK TTFLRCLNAL
51  EMPEDGQIEF DNARPLRIDF SKKTSKHDIL ALRRKSGMVF QQYNLFPHKT
101 VLENVMEGPV AVQGKPAAQA REEALKLLEK VGLGDKVDLY PYQLSGGQQQ
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDMKELA REGWTMVVVT
201 HEIKFTLEVA TNVVVMDGGV IVEQGSPEL FDHLKHERTR RFLSQIQSAK
251 I*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 453>:

m122-1.seq

```

1  ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA ACACTATTTT
51  GCGCGGCATC GATTTGGATG TGTGCAAAGG GCAGGTGGTC GTCATCCTCG
101 GGCCTTCCGG CTCAGGCAAA ACGACGTTTC TCGATGCCT AAACGCGTTG
151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGAGC GACCGCTGAA
201 AATCGATTTT TCTAAAAAAC CAAGCAAACA CGATATTTTG GCACTGCGCC
251 GCAAATCAGG CATGGTGTTT CAACAATACA ACCTCTTCCC GCACAAAACC
301 GCCTTGAAAA ACGTAATGGA AGGACCGGTT GCCGTACAGG GCAAGCCTGC
351 CGCCCAAGCG CGCGAAGAGG CTCTGAAACT GCTGGAAAAA GTCGGCTTGG
401 GCGACAAAGT GGATTTGTAT CCCTACCAGC TTTCCGCGCG TCAGCAGCAG
451 CCGCTCGGCA TTGCCCGCGC ATTGGCGATT CAGCCTGAAC TGATGCTGTT
501 TGACGAACCG ACTTCCGCGC TCGATCCTGA ATTGGTGCAA GATGTTTGG
551 ATACCATGAA GGAATTGGCG CAAGAAGGCT GGACCATGGT TGTCGTTACG
601 CATGAAATCA AGTTCGCCTT AGAAGTGGCA ACCACCGTCG TCGTGATGGA
651 CGGCGGCGTT ATTGTCAAC AAGGCAGCCC GCAAGATTTG TTCGACCACC
701 CCAAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTACCAAG
751 ATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 454; ORF 122-1>:

m122-1.pep

```

1  MIKIRNIHKT FGENTILRGI DLDVCKGQVQ VILGPSGSGK TTFLRCLNAL
51  EMPEDGQIEF DNERPLKIDF SKKPSKHDIL ALRRKSGMVF QQYNLFPHKT
101 ALENVMEGPV AVQGKPAAQA REEALKLLEK VGLGDKVDLY PYQLSGGQQQ
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDTMKELA QEGWTMVVVT
201 HEIKFALEVA TTVVVMDGGV IVEQGSQDL FDHPKHERTR RFLSQIQSTK
251 I*

```

m122-1/g122-1 94.8% identity in 251 aa overlap

```

10      20      30      40      50      60
m122-1.pep  MIKIRNIHKTFGENTILRGIDLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF
          |||||
g122-1      MIKIRNIHKTFGENTILRGIDLDVKGQVQVILGPSGSGKTTFLRCLNALEMPEDGQIEF

```

352

	10	20	30	40	50	60
m122-1.pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPPVAVQGKPAAQA					
g122-1	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTVLENVMEGPPVAVQGKPAAQA					
	70	80	90	100	110	120
m122-1.pep	130	140	150	160	170	180
	REEALKLLEKVGGLGDKVDLYPYQLSGGQQQQRVGIARALAIQPELMLFDEPTSLDPELVQ					
g122-1	REEALKLLEKVGGLGDKVDLYPYQLSGGQQQQRVGIARALAIQPELMLFDEPTSLDPELVQ					
	130	140	150	160	170	180
m122-1.pep	190	200	210	220	230	240
	DVLDTMKELAQEGWTMVVVTHEIKFALEVATTVVVMDGGVIVEQGSPPQLDFDHPKHERTR					
g122-1	DVLDTMKELAREGWTMVVVTHEIKFTLEVATNVVMDGGVIVEQGSPPKELFDHLKHERTR					
	190	200	210	220	230	240
m122-1.pep	250					
	RFLSQIQSTKIX					
g122-1	RFLSQIQSAKIX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 455>:

a122-1.seq

```

1  ATGATTAAAA TCCGCAATAT CCATAAGACC TTCGGCAAAA ATACCATTTT
51  GCGCGGCATC AATTTGGATG TGTGCAAAGG GCAGGTGGTC GTCATCCTCG
101 GGCCTTCCGG CTCAGGCAAA ACGACGTTTC TGCGATGCCT AAACGCGTTG
151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGAGC GACCGCTGAA
201 AATCGATTTT TCTAAAAAAC CAAGCAAACA CGATATTTTG GCACTGCGCC
251 GCAATCAGG CATGGTGTTC CAACAATACA ACCTCTTTCC GCACAAAACC
301 GCCTTGGAAA ACGTGATGGA AGGACCGGTT GCCGTACAGG GCAAGCCTGC
351 CGCCCAAGCG CGCGAAGAGG CTCTGAAACT GCTGGAAAAA GTCGGCTTGG
401 GCGACAAAGT GGATTGTGAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG
451 CGCGTCGGCA TTGCCCGAGC ATTGGCGATT CAGCCCGAGC TGATGTTGTT
501 TGACGAACCC ACTTCCGCGC TTGACCCCGA GTTGGTGCAA GACGTGTGTA
551 ACGCCATGAA GGAATTGGCG CGGGAAGGTT GGACGATGGT CGTCGTTACC
601 CACGAAATCA AGTTCGCGCT GGAAGTTGCC ACGACCGTTG TCGTGATGGA
651 CGGCGGCGTT ATCGTAGAGC AGGGCAGCCC GAAAGAGTTG TTCGACCACC
701 CCAACACGTA ACGGACGCGG AGATTTTTAA GCCAAATCCA ATCTACCAAG
751 ATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 456; ORF 122-1.a>:

a122-1.pep

```

1  MIKIRNIHKT FGKNTILRGI NLDVCKGQVV VILGPSGSGK TFLRCLNAL
51  EMPEDGQIEF DNERPLKIDF SKKPSKHDIL ALRRKSGMVF QQYNLFPHKT
101 ALENVMEGPV AVQGKPAAQA REEALKLLEK VGLGDKVDLY PYQLSGGQQQ
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLNAMKELA REGWTMVVVT
201 HEIKFALEVA TTVVVMDGGV IVEQGSPEL FDHPKHERTR RFLSQIQSTK
251 I*

```

a122-1/m122-1 97.2% identity in 251 aa overlap

	10	20	30	40	50	60
a122-1.pep	MIKIRNIHKTFGKNTILRGINLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
m122-1	MIKIRNIHKTFGENTILRGIDLVDCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
	10	20	30	40	50	60
a122-1.pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPPVAVQGKPAAQA					
m122-1	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPPVAVQGKPAAQA					
	70	80	90	100	110	120
a122-1.pep	130	140	150	160	170	180
	REEALKLLEKVGGLGDKVDLYPYQLSGGQQQQRVGIARALAIQPELMLFDEPTSLDPELVQ					
m122-1	REEALKLLEKVGGLGDKVDLYPYQLSGGQQQQRVGIARALAIQPELMLFDEPTSLDPELVQ					

	130	140	150	160	170	180
a122-1.pep	190	200	210	220	230	240
	DVLNAMKELAREGWTMVVVTHEIKFALEVATTVVVMDGGVIVEQGGSPKELFDHPKHHERTR					
m122-1	::					
	DVLDTMKELAQEGWTMVVVTHEIKFALEVATTVVVMDGGVIVEQGGSPQDLFDHPKHHERTR					
	190	200	210	220	230	240
a122-1.pep	250					
	RFLSQIQSTKIX					
m122-1						
	RFLSQIQSTKIX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 457>:

g125.seq

1	ATGTCGGGCA	ATGCCTCCTC	TCCTTCATCT	TCCGCCGCCA	TCGGGCTGGT
51	TTGGTTCGGC	GCGGCGGTAT	CGATTGCCGA	AATCAGCACG	GGTACGCTGC
101	TCGCCCCCTG	GGGCTGGCAG	CGCGGTCTGG	CGGCCCTGCT	TTTGGGTCA
151	GCCGTCGGCG	GCGCGCTGTT	TTTGGCGGCG	GCTGATATCG	CGCGCATGAC
201	CGGACGCAGC	TCGATGAAAA	GTGTGCGCCT	GTCTGTCGGC	AAATGCGGTT
251	CAGTGCTGTT	TTCCGTGGCG	AATATGCTGC	AACTGGCCGG	CTGGACGGCG
301	GTGATGATTT	ACGTCGGCGC	AacggTCAGC	TCCGCTTTGG	GCAAAGTGTT
351	GTGGGACgyc	gaATCCTTTG	TCTGGTGGCG	ATTGGCAAA	GGCGCACTGA
401	TCGTGCTGTG	GCTGCTTTTT	GGCGCACGCA	GAACGGGCGG	GCTGAAAAAC
451	GTTTCGATGC	TGCTGATGCT	GCTTGCCGTG	TGTGGTTGA	GCTGCGAAGT
501	GTTTCGCTTCG	TCCGGCACAA	ACGCCGCGCC	CGCCGTTTCA	GACGGCATGA
551	CCTTCGGAAC	GGCAGTCGAA	CTGTCCGCGC	TCATGCCGCT	TTCTTGGCTG
601	CCGCTGGCCG	CCGACTACAC	GCGCCAAGCA	CGCCGCCCGT	TTGCGGCAAC
651	CCTGACGGCA	ACGCTCGCCT	ATACGCTGAC	GGGCTGCTGG	ATGATGCTCT
701	TGGGTTTTGGC	GCGGCTCTGT	TTTACC GGAG	AAACCGACGT	GGCGAAAATC
751	CTGTTGGGCG	CGGGCTTGGG	CATAACGGGC	ATTCTGGCAG	TCGTCTCTCT
801	CACCGTTACC	ACAACGTTTC	TCGATACCTA	TTCCGCCGGC	GCGAGTGC GA
851	ACAACATTTC	CGCGCGTTTT	GCGGAAATAC	CCGTCGCTGT	CGGCGTTACC
901	CTGatccgca	ccgtgcttgc	cgtcattgtg	cccgttaccg	aatataaaaa
951	cttctctgctg	cttatccgtc	cggatatttg	gccgatggcg	gggtggttttg
1001	attqccgaCT	TTTttqtctt	AAAACGGCGT	GA	

This corresponds to the amino acid sequence <SEQ ID 458; ORF 125.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 459>:

```

m125.seq
1  ATGTCGGGCA  ATGCCTCCTC  TCCTTCATCT  TCCTCCGCCA  TCGGGCTGAT
51  TTGGTTCGGC  GCGGCGGTAT  CGATTGCCGA  AATCAGCACG  GGTACGCTGC
101 TTGCGCCTTT  GGGCTGGCAG  CGCGGTCTGG  CGGCTCTACT  TTTGGGTCA
151 GCCGTCGGCG  GCGCGCTGTT  TTTTGCGGCG  GCGTATATCG  CGCCACTGAC
201 CGGACGCAGC  TCGATGGAAG  GCGTGCGCCT  TCGTTTCGGC  AAACGCGGTT
251 CAGTGCTGTT  TTCCGTGGCG  AATATGCTGC  AACTGGCCGG  CTGGACGGCG
301 GTGATGATTT  ACGCCGGCGC  AACGGTCAGC  TCCGCTTTGG  GCAAAGTGTT
351 GTGGGACGCG  GAATCTTTTG  TCTGGTGGGC  ATTGGCAAAC  GGCGCGCTGA
401 TTGTGCTGTG  GCTGGTTTTT  GGCGCACGCA  AAACAGCGCG  GCTGAAAACC
451 GTTTCGATGC  TGCTGATGCT  GTTGGCGGTT  CTGTGGCTGA  GTGCCGAAGT
501 CTTTTCCACG  GCAAGCAGCA  CGCCCGCACA  GGTTCAGAG  GGCAATGAGT
551 TCGGAACGGC  AGTCGAGCTG  TCCGCCGTGA  TGCCGCTTTC  CTGGCTGCCG
601 CTGCGCGCCG  ACTACACGCG  CCACGCGCGC  CGCCCGTTTG  CGGCAACCCT
651 GACGGCAACG  CTCGCCTACA  CGCTGACCGG  CTGCTGGATG  TATGCCCTGG
701 GTTTGGCAGC  GGGCTTGTTT  ACCGGAGAAA  CCGACGTGGC  AAAAAATCCG
751 CTGGGCGCAG  GCTTTGgTGC  GGCAGGCATT  TTGGCGGTGC  TCCTCTCCAC
801 CGTTACCAAC  ACGTTTCTCG  ATGCCTATTC  GCGCGGTCG  ATGTGCAAC

```

851 ACATTTCCTG GCGTTTTGCG GAAACACCCG TCGCTGTCrG CGTTACCCCTG
 901 ATCGGCACGG TACTTGCCGT CATGCTGCCC GTTACCGAAT ATGAAAACCTT
 951 CCTGCTGCTT ATCGGCTCGG TATTTGCGCC GATGGCGGgC GGTTTTGATT
 1001 GCCGACTTTT TCGTCTTGAA ACGGCGTGA

This corresponds to the amino acid sequence <SEQ ID 460; ORF 125>:

m125.pep
 1 MSGNASSPSS SSAIGLIWFG AAVSIAEIST GTLLAPLGWQ RGLAALLLGH
 51 AVGGALFFAA AYIGALTGRS SMESVRLSFG KRGSVLFSVA NMLQLAGWTA
 101 VMIYAGATVS SALGKVLWDG ESFVWWALAN GALIVLWLVF GARKTGGLKT
 151 VSMLLMLLAV LWLSAEVFST AGSTAAQVSD GMSFGTAVEL SAVMPLSWLP
 201 LAADYTRHAR RPFATLTAT LAYTLTGCM YALGLAAALF TGETDVAKIL
 251 LGAXLGAAGI LAVVLSTVTT TFLDAYSAGA SANNISARFA ETPVAVXVTL
 301 IGTVLAVMLP VTEYENFLLI IGSVFAPMAG GFDCRLFRLE TA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 125 shows 92.1% identity over a 343 aa overlap with a predicted ORF (ORF 125.ng) from *N. gonorrhoeae*:

m125/g125

	10	20	30	40	50	60
m125.pep	MSGNASSPSSSSAIGLIWFGAAVSIAEISTGTLLAPLGWQORGLAALLLGHAVGGALFFAA					
	: : : : : : : : : :					
g125	MSGNASSPSSAAIGLVWFGAAVSIAEISTGTLLAPLGWQORGLAALLLGHAVGGALFFAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m125.pep	AYIGALTGRSSMESVRLSFGKRGSVLFSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG					
	: : : : : : : : :					
g125	AYIGALTGRSSMESVRLSFGKCGSVLFSVANMLQLAGWTAVMIYVGVATVSSALGKVLWDG					
	70	80	90	100	110	120
	130	140	150	160	170	179
m125.pep	ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQ-VS					
	: : : : : : : : :					
g125	ESFVWWALANGALIVLWLVFGARRTGGLKTVSMLLMLLAVLWLSVEVFASSGTNAAPAVS					
	130	140	150	160	170	180
	180	190	200	210	220	230
m125.pep	DGMSFGTAVELSAVMPLSWPLAADYTRHARRPFAATLTATLAYTLTGCMYALGLAAAL					
	: : : : : : : : :					
g125	DGMTFGTAVELSAVMPLSWPLAADYTRQARRPFAATLTATLAYTLTGCMYALGLAAAL					
	190	200	210	220	230	240
	240	250	260	270	280	290
m125.pep	FTGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVT					
	: : : : : : : : :					
g125	FTGETDVAKILLGAGLGITGILAVVLSTVTTTFLDTYSAGASANNISARFAEIPVAVGVT					
	250	260	270	280	290	300
	300	310	320	330	340	
m125.pep	LIGTVLAVMLPVTEYENFLLIIGSVFAPMAGGFDCRLFRLETAX					
	: : : : : : : : :					
g125	LIRTVLAVMLPVTEYKNFLLIIRSVFGPMAGGFDCRLFCLKTAX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 461>:

a125.seq
 1 ATGTCGGGCA ATGCCTCCTC TCCTTCATCT TCCGCCGCCA TCGGGCTGAT
 51 TTGGTTCGGC GCGGCGGTAT CGATTGCCGA AATCAGCACG GGTACACTGC
 101 TTGCGCCTTT GGGCTGGCAG CGCGGTCTGG CGGCTCTGCT TTTGGGTCAT

al25.pep					
1	MSGNASSPSS	SA AIGLIWFG	AAVSIAEIST	GTLLAPLGWQ	RGLAALLLGH
51	AVGGALFFAA	AYIGALTGRS	SMESVRLSFG	KRGSVFLSVA	NMLQLAGWTA
101	VMIYAGATVS	SALGKVLWDG	ESFVWWALAN	GALIVLVLFV	GARKTGGLKT
151	VSMLLMLLAV	LWLSAEVFST	AGSTAAQVSD	GMSFGTAVEL	SAVMPLSWLP
201	LAADYTRHAR	RPFATLTALT	LAYTLTGCMW	YALGALAAFL	TGETDVAKIL
251	LGAGLGAAGI	LAVVLSTVTT	TFLDAYSAGV	SANNISAKLS	EIPIAVAVAV
301	VGTLGLVLLP	VTEYENFLLL	IGSVFAPMAX	GFDCRLFRLE	TA*

	10	20	30	40	50	60
m125.pep	MSGNASSPSSSSAIGLIWFGAAV	SI AEISTGTLLAPLQWQRGLAALL	LGHAVGGALFFAA			
a125	MSGNASSPSSSSAIGLIWFGAAV	SI AEISTGTLLAPLQWQRGLAALL	LGHAVGGALFFAA			
	10	20	30	40	50	60
m125.pep	AYIGALTGRSSMESVRLSFGKRG	SVLFSVANMLQLAGWTAVMIYAGAT	VSSALGKVLWDG			
a125	AYIGALTGRSSMESVRLSFGKRG	SVLFSVANMLQLAGWTAVMIYAGAT	VSSALGKVLWDG			
	70	80	90	100	110	120
m125.pep	ESFVWWALANGALIVLWL	LVFGARKTGGLKTVSMLLM	LAVLWLSAEVFSTAGSTAAQVSD			
a125	ESFVWWALANGALIVLWL	LVFGARKTGGLKTVSMLLM	LAVLWLSAEVFSTAGSTAAQVSD			
	130	140	150	160	170	180
m125.pep	GMSFGTAVELSAVMPLSWL	PLAADYTRHARRPFAATLTAT	LAYTLTGCMYALGLAAALF			
a125	GMSFGTAVELSAVMPLSWL	PLAADYTRHARRPFAATLTAT	LAYTLTGCMYALGLAAALF			
	190	200	210	220	230	240
m125.pep	TGETDVAKILLGAXLGAAGI	LAVVLSTVTTTFLDAYSAGAS	ANNISARFAETPVAVXVTL			
a125	TGETDVAKILLGAXLGAAGI	LAVVLSTVTTTFLDAYSAGV	SANNISAKLSEIPIAVAVAV			
	250	260	270	280	290	300
m125.pep	IGTVLAVMLPVTEYENFLL	LIGSVFAPMAGGFDCR	LFLETAX			
a125	VGTLLAVLLPVTEYENFLL	LIGSVFAPMAXGFDCR	LFLETAX			
	310	320	330	340		

310 320 330 340

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 463>:

```
g126.seq
1   AtgccgctcTG AAaccCcaaaa ggcACGCCGC CGGCTTTTCAG ACGGCATCGC
51  GTCCGACAAC CATACCAAAG AATCCATCAT GCTCACCctg tacggcGAAA
101 CTTTCCCTTC GCGGCTGCTg ctcggcacgG cggcctacCC GACCCCTGAA
151 ATCCTCAAAC AATCCGTCCG AACCGCCCGG CCCGCGATGA ttaccGTCTC
201 GCTGCGCCGC ACGGGATGCG GCGGCGAGGC GCACGGTCAG GGGTTTTGGT
251 CGCTGCTTCA AGAAACCGGC GTTCCCGTCC TGCCGAACAC GGCAGGCTGC
301 CAAAGCGTGC AGGAAGCGGT AACGACGGCG CAAATGGCGC GCGAAGTGTT
351 TGAAACCGAT TGGATAAAAT TGGAACTCAT CGGCGACGAC GACACCTTGC
401 AGCCGGACGT GTTCCAACCTC GTCGAAGCGG CGGAAATCCT GATTAAAGAC
451 GGCTTCAAAG TGCTGCCTTA TTGCACCGAA GACCTGATTG CCTGCCGCCG
501 CCTGCTCGAT GCGGGCTGTC AGGCGTTGAT GCCGTGGGCG GCTCCCATCG
551 GCACGGGTTT GGGGGCGGTT CACGCCTATG CGTCAAAAT CCTGCGCGAA
601 CGCCTGCCCG ACACGCCGCT GATTATCGAC GCGGGCTTGG GTTTGCCTTC
651 CCAAGCGGCA CAAGTGATGG AATGGGGTTT TGACGGCGTA TTGTTAAACA
701 CCGCCGTTTC CCGCAGCGGC GACCCCGTCA ACATGGCGCG CGCCTTCGCA
751 CTCGCCGTCG AATCCGACG GCTGGCATT GAAGCCGGGC CGGTCGAAGC
801 GCGAACCAA GCCCAAGCCA GCACGCCGAC AGTCGGACAA CCGTTTTTGC
851 ATTCGGCGGA ATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 464; ORF 126.ng>:

```
g126.pep
1   MPSETPKARR RLSDGIASDN HTKESIMLTL YGETFPSRL LGTAAYPTPE
51  ILKQSVRTAR PAMITVSLRR TCGGGEAHGQ GFWSLQETG VPVLPNTAGC
101 QSVQEAHTTA QMAREVFETD WIKLELIGDD DTLQPDVFQL VEAEEILIKD
151 GFKVLPYCTE DLIACRRLD AGCQALMPWA APIGTGLGAV HAYALKILRE
201 RLPDTPLIID AGLGLPSQAA QVMEWGFDGV LLNTAVSRSG DPNVMARAFA
251 LAVESGR LAF EAGPVEARTK ACASTPTVGQ PFWHSAEY*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 465>:

```
m126.seq (partial)
1   ..CACTATACAA AGGAACCCAT TATGCTCACC CTATACGGCG AAACCTTTCCC
51  CTCGCGGCTG CTGCTCGGCA CGGCTGCCTA CCCGACCCCC GAAATCCTCA
101 AACAATCCAT CCAAACCGCC CAGCCTGCGA TGATTACCGT CTCGCTGCGC
151 CGCGCGGGAA GCGGCGGCGA GGCGCACGGT CAGGGGTTTT GGTGCTGCTG
201 TCAAGAAACC GCGGTTCCCG TCCTGCCGAA CACGGCAGG TGCCAAAGCG
251 TGCAGGAAGC GGTAACGACG GCGCAAATGG CGCGCGAAGT GTTTGAAACC
301 GATTGGATAA AATTGGAACCT CATCGGAGAT GACGACACCT TGCAGCCGGA
351 TGTGTTCCAG CTTGTCGAAG CGGCGGAAAT CCTGATTAAA GACGGCTTCA
401 AAGTGCTGCC TTATTGCACC GAAGACCTGA TTGCCTGCCG CCGCTGCTC
451 GACGCGGGCT GTCAGGCGTT GATGCCGTGG GCGGCCCGGA TCGGCACGGG
501 TTTGGGCGCG GTTCACGCCT ACGCGTTGAA CGTCCTGCGC GAACGCCTGC
551 CCGACACGCC GCTGATTATC GACGCGGGCT TGGGTTTGCC CTCACAGGCG
601 GCACAAGTGA TGGAATGGGG CTTTGACGGC GTGCTTTTGA ATACTGCCGT
651 TTCCCGCAGC GGCGATCCGG TCAATATGGC ACGCGCCTTC GCACTCGCCG
701 TCGAATCCGG ACGGCTGGCA TTTGAAGCCG GACCGGTCGA AGCACGCGAC
751 AAAGCGCAAG CCAGCACGCC GACAGTCGGA CAACCGTTTT GCATTTCGGC
801 GGAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 466; ORF 126>:

```
m126.pep (partial)
1   ..HYTKEPIMLT LYGETFPSRL LLGTAAYPTP EILKQSIQTA QPAMITVSLR
51  RAGSGGEAHG QGFWSLQET GVPVLPNTAG QSVQEAHTT AQMAREVFET
```


Homology with a predicted ORF from *N. gonorrhoeae*

m126/g126

		10	20	30	40
m126.pep		HYTKEPIMLTLYGETFP	SRLLLGTAAYPTPEILKQSIQTAQ		
		:	:	:	:
g126		MPSETPKARRRLSDG	IASDNHTKESIMLTLYGETFP	SRLLLGTAAYPTPEILKQSVRTAR	
		10	20	30	40
		50	60	70	80
m126.pep		PAMITVSLRRAGSGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD			
		:	:	:	:
g126		PAMITVSLRRTGCGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD			
		70	80	90	100
		110	120	130	140
m126.pep		WIKLELIGDDDTLQPDVFQLVEAAEILIKDGFKVL	PYCTEDLIACRRLLDAGCQALMPWA		
		:	:	:	:
g126		WIKLELIGDDDTLQPDVFQLVEAAEILIKDGFKVL	PYCTEDLIACRRLLDAGCQALMPWA		
		130	140	150	160
		170	180	190	200
m126.pep		APIGTGLGAVHAYALNVLRLRERLPDTP	LIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSG		
		:	:	:	:
g126		APIGTGLGAVHAYALKILRLRERLPDTP	LIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSG		
		190	200	210	220
		230	240	250	260
m126.pep		DPVNMARAFALAVESGRLAFEAGPVEARDKAQASTPTVGQPFWHS	AEYX		
		:	:	:	:
g126		DPVNMARAFALAVESGRLAFEAGPVEARTKAQASTPTVGQPFWHS	AEYX		
		250	260	270	280

a126.seq

1	TTGTTAATCC	ACTATACAAA	GGAACCCATT	ATGCTCACCC	TGTACAGCGA
51	AACTTTCCCT	TCGCGGTGC	TGCTCGGCAC	AGCCGCTAC	CCGACCCCTG
101	AAATCTCAA	ACAATCCGT	CGAAGCCGCC	GGCCCGCGAT	GATTACCGTC
151	TCGTCGCGC	CGCGGGGATG	CGGCGGCGAG	CGCGACGGTC	AGGGGTTTTG
201	GTCGCTGCTT	CAAGAAACCG	GCGTTCCTCGT	CCTGCCGAAC	ACGGCAGGCT
251	GCCAAAGCGT	GCAGGAAGCG	GTAACGACGG	CGCAATAGC	GCGCGAAGTG
301	TTTGAAACCG	ATTGGATTAA	ACTCGAACTC	ATCGGCGCAG	ACGACACCTT
351	GCAGCCGAT	GTGTTCCAA	TTGTGGAAG	GCGCGAAATC	CTGATTAAAG
401	ACGGCTTCAA	AGTGCTGCCT	TATTGCACCG	AAGACCTGAT	TGCTTGCCGC
451	CGCCTGCTCG	ACGCGGGCTG	TCAGGCGTTG	ATGCCGTGGG	CGGCCCGGAT
501	CGGCACGGGT	TTGGGCGCGG	TTCAACGCCTA	CGCGTTGAAC	GTCTTGCGCG
551	AACGCCTGCC	CGACACGGCT	CTGATTATCG	ACGCGGGCTT	GGGTTTGCCC
601	TCACAGCGCG	CACAAGTGA	GGAATGGGCG	TTTGACGGCG	TGCTTTTGAA
651	TACTGCCGTT	TCCCGCAGCG	GCGATCCGGT	CAATATGGCA	CGCGCCTTCG
701	CACCTCGCGT	CGAATCCGGA	CGGCTGGCAT	TTGAAGCCGG	ACCGGTCGAA
751	GCACGCGACA	AAGCGCAAGC	CAGCACGCCG	ACAGTCGGAC	AACCGTTTTG
801	GCATTCCGCG	GAATATTGA			

This corresponds to the amino acid sequence <SEQ ID 468; ORF 126.a>:

```
a126.pep
  1  LLIHYTKEPI MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV
 51  SLRRAGCGGE AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV
101  FETDWIKLEL IGDDDTLQPD VFQLVEAAEI LIKDGFKVLP YCTEDLIACR
151  RLLDAGCQAL MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP
201  SQAAQVMEWG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE
251  ARDKAQASTP TVGQPFWHS A EY*
```

m126/a126 98.1% identity in 269 aa overlap

```

              10      20      30      40      50
m126.pep      HYTKEPIMLTLYGETFP SRLLLGTAAYPTPEILKQSIQTAQPAMITVSLRRAGSGGE
              |||||
a126           LLIHYTKEPIMLTLYSETFPSRLLLGTAAYPTPEILKQSVRTARPAMITVSLRRAGCGGE
              10      20      30      40      50      60

              60      70      80      90      100     110
m126.pep      AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREVFETDWIKLELIGDDDTLQPD
              |||||
a126           AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREVFETDWIKLELIGDDDTLQPD
              70      80      90      100     110     120

              120     130     140     150     160     170
m126.pep      VFQLVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWAAPIGTGLGAVHAYALN
              |||||
a126           VFQLVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWAAPIGTGLGAVHAYALN
              130     140     150     160     170     180

              180     190     200     210     220     230
m126.pep      VLRERLPDTP LIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSGDPVNMA RAFALAVESG
              |||||
a126           VLRERLPDTP LIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSGDPVNMA RAFALAVESG
              190     200     210     220     230     240

              240     250     260     270
m126.pep      RLAFEAGPVEARDKAQASTPTVGQPFWHS A EYX
              |||||
a126           RLAFEAGPVEARDKAQASTPTVGQPFWHS A EYX
              250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 469>:

```
g126-1.seq
  1  ATGCTCACCC TGTACGGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
 51  GGCCGCGTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACC GCCC
101  GGCCCGCGAT GATTACCGTC TCGCTGCGCC GCACGGGATG CGGCGGCGAG
151  GCGCACGGTC AGGGGTTTGT GTGCTGCTT CAAGAAACCG GCGTTCCCGT
201  CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251  CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATTGGAATC
301  ATCGGCGACG ACGACACCTT GCAGCCGGAC GTGTTCCAAC TCGTCGAAGC
351  GCGCGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401  AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ATGCGGGCTG TCAGGCGTTG
451  ATGCCGTGGG CGGCTCCCAT CGGCACGGGT TTGGGGGCGG TTCACGCC TA
501  TGCCTCAAA ATCCTGCGCG AACGCCTGCC CGACACGCCG CTGATTATCG
551  ACGCGGGCTT GGGTTTGCCT TCCCAAGCGG CACAAGTGAT GGAATGGGGT
601  TTTGACGGCG TATTGTTAAA CACCGCCGTT TCCCGCAGCG GCGACCCCGT
651  CAACATGGCG CGCGCCTTCG CACTCGCGGT CGAATCCGGA CGGCTGCGAT
701  TTGAAGCCGG GCCGGTCGAA GCGCGAACCA AAGCCCAAGC CAGCACGCCG
751  ACAGTCGGAC AACCGTTTGT GCATTGCGCG GAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 470; ORF 126-1.ng>:

```
g126-1.pep
  1  MLTLYGETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRTGCGGE
```

```

51 AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALK ILRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGBPVMNA RAFALAVESG RLAFEAGPVE ARTKAQASTP
251 TVGQPFWWSA EY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 471>:

```

m126-1.seq
1 ATGCTCACCC TATACGGCGA AACTTTCCCC TCGCGGCTGC TGCTCGGCAC
51 GGCTGCCTAC CCGACCCCGG AAATCCTCAA ACAATCCATC CAAACCGCCC
101 AGCCTGCGAT GATTACCGTC TCGCTGCGCC GCGCGGGAAG CCGCGGCGAG
151 GCGCACGGTC AGGGGTTTTG GTCGCTGCTT CAAGAAACCG GCGTTCCCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATTGGAACCTC
301 ATCGGAGATG ACGACACCTT GCAGCCGGAT GTGTTCACG TTGTCGAAGC
351 GCGCGAAATC CTGATTAAAG ACGGCTTCAA AGTGTGCTT TATTGCACCG
401 AAGACCTGAT TGCCCTGCCG CCGCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CCGCCCCGAT CCGCACGGGT TTGGCGCGCG TTCACGCCCTA
501 CCGCTTGAAC GTCCTGCGCG AACGCTGCC CGACACGCGG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCG TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTCGCCGT CGAATCCGGA CCGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCGTTTTG GCATTGGCGG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 5; ORF 126-1>:

```

m126-1.pep
1 MLTLYGETFP SRLLLGTAAY PTPEILKQSI QTAQPAMITV SLRRAGSGGE
51 AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGBPVMNA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWWSA EY*

```

m126-1/g126-1 96.9% identity in 262 aa overlap

	10	20	30	40	50	60
m126-1.pep	MLTLYGETF	PSRLLLGTAAYPT	PEILKQSIQTAQPAMITV	SLRRAGSGGE	AHGQGFWSLL	
g126-1	MLTLYGETF	PSRLLLGTAAYPT	PEILKQSVRTARPAMITV	SLRRTGCGGE	AHGQGFWSLL	

	70	80	90	100	110	120
m126-1.pep	QETGVPVLPNTAGCQSVQEA	VTTAQMAREVFETDWIKLEL	IGDDDTLQPDVFQVLEAAEI			
g126-1	QETGVPVLPNTAGCQSVQEA	VTTAQMAREVFETDWIKLEL	IGDDDTLQPDVFQVLEAAEI			

	130	140	150	160	170	180
m126-1.pep	LIKDGFKVLPYCTEDLIACR	RLLDAGCQALMPWAAPIGTGLGAVHAYALN	VLRERLPDTP			
g126-1	LIKDGFKVLPYCTEDLIACR	RLLDAGCQALMPWAAPIGTGLGAVHAYALK	ILRERLPDTP			

	190	200	210	220	230	240
m126-1.pep	LIIDAGLGLPSQAAQVMEWG	FDGVLLNTAVSRSGBPVMNARAFALAVESG	RLAFEAGPVE			
g126-1	LIIDAGLGLPSQAAQVMEWG	FDGVLLNTAVSRSGBPVMNARAFALAVESG	RLAFEAGPVE			

	250	260
m126-1.pep	ARDKAQASTPTVGQPFWWSAEYX	
g126-1	ARTKAQASTPTVGQPFWWSAEYX	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 473>:

```

a126-1.seq
1 ATGCTCACCC TGTACAGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
51 AGCCGCTTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACCGCCC
101 GGCCCGCGAT GATTACCGTC TCGCTGCGCC GCGCGGGATG CCGCGGCGAG

```

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```

151 GCGCACGGTC AGGGGTTTTG GTCGCTGCTT CAAGAAACCG GCGTTCCCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATGGGATTAA ACTCGAACTC
301 ATCGGCGACG ACGACACCTT GCAGCCGGAT GTGTTCCAAC TTGTCGAAGC
351 GCGCGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCTGCCGC CGCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCCCCGAT CGGCACGGGT TTGGGCGCGG TTCACGCCTA
501 CGCGTTGAAC GTCCTGCGCG AACGCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCC TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCCG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCGTTTTG GCATTCGGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 474; ORF 126-1.a>:

a126-1.pep

```

1  MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE
51  AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQLVAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWWSA EY*

```

a126-1/m126-1 98.1% identity in 262 aa overlap

	10	20	30	40	50	60
a126-1.pep	MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE AHGQGFWSLL					
	: : : : : :					
m126-1	MLTLYGETFP SRLLLGTAAY PTPEILKQSIQTAQPAMITV SLRRAGSGGE AHGQGFWSLL					
	10	20	30	40	50	60
a126-1.pep	70	80	90	100	110	120
	QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDTLQPD VFQLVAAEI					
m126-1	QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDTLQPD VFQLVAAEI					
	70	80	90	100	110	120
a126-1.pep	130	140	150	160	170	180
	LIKDGFKVLP YCTEDLIACR RLLDAGCQAL MPWAAPIGTGLGAVHAYALN VLRERLPDTP					
m126-1	LIKDGFKVLP YCTEDLIACR RLLDAGCQAL MPWAAPIGTGLGAVHAYALN VLRERLPDTP					
	130	140	150	160	170	180
a126-1.pep	190	200	210	220	230	240
	LIIDAGLGLP SQAAQVMEWG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE					
m126-1	LIIDAGLGLP SQAAQVMEWG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE					
	190	200	210	220	230	240
a126-1.pep	250	260				
	ARDKAQASTP TVGQPFWWSA EYX					
m126-1	ARDKAQASTP TVGQPFWWSA EYX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 475>:

g127.seq

```

1  ATGGAAATAT GGAATATGTT GAACACTTGG CCCGATGCCG TCCCAGATACG
51  CGCGGAGGCG GCCGAATCCG TGGCGGCGGT CGCGGCTTTG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAGAC GGCATCCGGA TTTCGGCATC
151 GAAAGCAAGC GCGGTTTTTT GGTGCCAGC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GGCGCAAATT CAAACGCTGG
251 CTTTGTCGAT GTTGCGGTG GCGGCGGCGG TCGTCGTGGC GACAAAAGAA
301 CTGATTATGT GTCGTGCGG CAGTATTTTA aggtctGCCA CCCAGCAATA
351 CTCGGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGTCG
401 ACATCAATCT GTTGAACACG CTGATGATGC AGGTCGGTCC GAACCCCTTG
451 GTCGGACAGC TTGCGGGAAC CACCGTTTCT TTCCCAACA GCCTGTTGTT
501 GAGCCACCCC GTGCGCCGCG ACAATATTTT GGGCGACTAT GTCATCCATA

```

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```

551 CGGTCGAAAT CCCC GTTCCC ATCCATTGG ATT CGGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 TCAGCGGTAT TTGAAAACG TGCAGGCGGA AAAACTGTTT ATCACGCCCG
701 CCGCCAGGCC GCGCGTTACC CGCGTACCGT ACGACGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCCCTC CCCC GTTTCA AAGCGGCTGG AAATCCAACA
801 GCGGTTATG GACGAATTTT TCGCGGTACA ATACCGCCTG TTAAATCATC
851 CCGCCGgctc cgAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 476; ORF 127.ng>:

```

g127.pep
1  MEIWNMLNTW PDAVPIRAEA AESVAAVAAL LLARALLLNI HFRRHPDFGI
51  ESKRRFLVAS RNITLLLVLF SLAFIWSAQI QTLALSMFAV AAADV VATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VGQLAGTTVS FPNSLLLSHP VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVS KRLEIQQAVM DEFLRVQYRL LNHPAGSETL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 477>:

```

m127.seq
1  ATGGAATAT GGAATATGTT GGACACTTGG CTCGGTGCCG TCCCGATACG
51  TCGGAGGCG GTCGAATCCG TGGCGGCGGT TCGGCTTTG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAAAC GGCATCCGGA TTTCGGCATC
151 GAAAGCAAGC GCGGTTT TTT GGTGCGCAGC CGCAATATAA CGTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GCGCGAAATC CAAACGCTGG
251 CTTTGTGCGAT GTTTGCGGTG GCGGCGGCGG TCGTCTGGC GACGAAGGAA
301 CTGATTATGT GTCTGTCGGG CAGTATTTTA AGGTCTGCCA CCCAGCAATA
351 CTCGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAACCT GTTGAACACG CTGATGATGC AGGTCTGGTCC GAACCCCTTG
451 GTCGACAGC TTGCGGGAAC CACCGTTTCT TCCCCAACA GCCTGTTGTT
501 GAGCCACCCC GTGCGCCGCG ACAATATTTT GGGCGACTAT GTCATCCATA
551 CCGTCGAAAT CCCC GTTCCC ATCCATTGG ATT CGGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 CCAACGgAT TTGAAAACG TGCAGGCGGA AAAACTGTTT ATCACGCCCG
701 CCGCCAGACC GCGCGTTACC CGCGTGCCGT ACGATGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCTTC CCCC GTTTCA AAGCGGCTGG AAATCCAACA
801 GCGGTTATG GACGAATTTT TCGCGGTACA ATACCGCCTG TTAAATCACC
851 CCGCCGGCTC CGAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 478; ORF 127>:

```

m127.pep
1  MEIWNMLDTW LGAVPIRAEA VESVAAVAAL LLARALLLNI HFKRHPDFGI
51  ESKRRFLVAS RNITLLLVLF SLAFIWSAQI QTLALSMFAV AAADV VATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VGQLAGTTVS FPNSLLLSHP VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVS KRLEIQQAVM DEFLRVQYRL LNHPAGSETL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 127 shows 97.9% identity over a 290 aa overlap with a predicted ORF (ORF 127.ng) from *N. gonorrhoeae*:

```

m127/g127
      10      20      30      40      50      60
m127.pep  MEIWNMLDTWLGAVPIRAEAVESVAAVAALLLARALLLNIHFKRHPDFGIESKRRFLVAS
          |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
g127      MEIWNMLNTWPDVPIRAEAAESVAAVAALLLARALLLNIHFRRHPDFGIESKRRFLVAS
          |||  |||  |||  |||  |||  |||
      10      20      30      40      50      60

      70      80      90     100     110     120
m127.pep  RNITLLLVLFSLAFIWSAQIOTLALSMFAVAAADV VATKELIMCLSGSILRSATQQYSVG
          |||:|  |||:|  |||:|  |||:|  |||:|  |||:|
g127      RNITLLLVLFSLAFIWSAQIOTLALSMFAVAAADV VATKELIMCLSGSILRSATQQYSVG
          |||:|  |||:|  |||:|  |||:|  |||:|  |||:|

```

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	70	80	90	100	110	120
	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVQLAGTTVSFPNSLLLSHPVRRDNILGDY					
g127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVQLAGTTVSFPNSLLLSHPVRRDNILGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRYLENVQAEKLFITPAARPRVT					
g127	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRYLENVQAEKLFITPAARPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
g127	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 479>:

```

a127.seq
1  ATGGAAATAT  GGAATATGTT  GGACACTTGG  CTCGGTGCCG  TCCCGATACG
51  TGC GGAGGCG  GTCGAATCCG  TGGCGGTGGT  CGCGGCTTTG  CTGCTGGCGC
101 GCGCCCTTCT  GTTGAATATC  CACTTCAAAC  GGCATCCGGA  TTTCGGCATC
151 GAAAGCAAGC  GGC GGTTTTT  GGT TGCCAGC  CGCAATATAA  CGCTGCTTTT
201 GGTGCTGTTT  TCGCTGGCAT  TTATCTGGTC  GGCGCAAATC  CAAACGCTGG
251 CTTTGTCGAT  GTTTGCGGTG  GCGGCGGCGG  TCGTCGTGGC  GACGAAGGAA
301 CTGATTATGT  GTCTGTCGGG  CAGCATTTTA  AGGTCTGCCA  CCCAGCAATA
351 CTCGGTCGGC  GACTATATCG  AAATCAACGG  CCTGCGCGGG  CGCGTGGTCG
401 ACATCAACCT  GTTGAACACG  CTGATGATGC  AGGTCGGTCC  GAACCCCTTG
451 GTCGGACAGC  TTGCGGGAAC  CACCGTTTCT  TTCCCAACA  GCCTGTTGTT
501 GAGCCACCCC  GTGCGCGCGG  ACAATATTTT  GGGCGACTAC  GTCATCCATA
551 CGGTCGAAAT  CCCGGTTCCC  ATCCATTTGG  ATTCGATGA  AGCCGTATGC
601 CGTCTGAAAG  CCGTACTCGA  GCCCTTGTGC  GCGCCCTACA  TCCCGCCCAT
651 CCAACGGCAT  TTGGAACACG  TGCAGGCGGA  AAAACTGTTT  ATCACGCCCG
701 CCGCCAAACC  GCGCGTTACC  CGCGTGCCGT  ACGATGACAA  GGCATACCGC
751 ATCATCGTCC  GCTTCGCCTC  CCCC GTTTCA  AAGCGGCTGG  AAATCCAACA
801 GCGCGTTATG  GACGAATTTT  TCGCGGTACA  ATACCGCCTG  TTAAATTACC
851 CCGCCGGCTC  CGAAACACTT  TAA

```

This corresponds to the amino acid sequence <SEQ ID 480; ORF 127.a>:

```

a127.pep
1  MEIWNMLDTW  LGAVPIRAEA  VESVAVVAAL  LLARALLLNI  HFKRHPDFGI
51  ESKRRFLVAS  RNITLLLVLF  SLAFIWSAQI  QTLALSMFAV  AAAVVVATKE
101 LIMCLSGSIL  RSATQQYSVG  DYIEINGLRG  RVVDINLLNT  LMMQVGNPL
151 VGQLAGTTVS  FPNSLLLSHP  VRRDNILGDY  VIHTVEIPVP  IHLDSDEAVC
201 RLKAVLEPLC  APYIPAIQRH  LENVQAEKLF  ITPAAKPRVT  RVPYDDKAYR
251 IIVRFASPV  KRLEIQQAVM  DEFLRVQYRL  LNYPAGSETL  *

```

m127/a127 98.6% identity in 290 aa overlap

	10	20	30	40	50	60
m127.pep	MEIWNMLDTWLGAVPIRAEAVESVAVVAALLARALLLNIHFKRHPDFGIESKRRFLVAS					
a127	MEIWNMLDTWLGAVPIRAEAVESVAVVAALLARALLLNIHFKRHPDFGIESKRRFLVAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m127.pep	RNITLLLVLFSLAFIWSAQIQTALALSMFAVAAA VVATKELIMCLSGSILRSATQQYSVG					
a127	RNITLLLVLFSLAFIWSAQIQTALALSMFAVAAA VVATKELIMCLSGSILRSATQQYSVG					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGQLAGTTVSFPNSLLLSHPVRRDNILGDY					
a127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGQLAGTTVSFPNSLLLSHPVRRDNILGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
a127	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRHLENVQAEKLFITPAAKPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
a127	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNYPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 481>:

g128.seq

1	atgattgaca	acgCActgct	ccacttgggc	gaagaaccCC	GTTTaatca
51	aatccaaacc	gaagACAtca	AACCCGCCGT	CCAAACCGCC	ATCGCCGAAG
101	CGCGCGGACA	AATCGCCGCC	GTCAAAGCGC	AAACGCACAC	CGGCTGGGCG
151	AACACCGTCG	AGCGTCTGAC	CGGCATCACC	GAACGCGTCG	GCAGGATTTG
201	GGGCGTCGTG	TCCCATCTCA	ACTCCGTCGT	CGACACGCCC	GAACGCGCGC
251	CCGTCTATAA	CGAACTGATG	CCTGAAATCA	CCGTCTTCTT	CACCGAAATC
301	GGACAAGACA	TCGAACTGTA	CAACCGCTTC	AAAACCATCA	AAAAATCCCC
351	CGAATTTGCA	ACGCTTTCCC	CCGCACAAAA	AACCAAGCTC	GATCAGGACC
401	TGCGCGATTT	CGTATTGAGC	GGCGCGGAAC	TGCCGCCCGA	ACGCGAGGCA
451	GAACCTGGCA	AACCTGCAAC	CGAAGGCGCG	CAACTTTCCG	CCAAATTTCT
501	CCAAAACGTC	CTAGACGCGA	CCGACGCGTT	CGGCATTTAC	TTTGACGATG
551	CCGACCCGCT	TGCCGCGCATT	CCCGAAGACG	CGCTCGCCAT	GTTTGCCGCC
601	GCCGCGCAAA	GCGAAGGCAA	AACAGGTTAC	AAAATCGGCT	TGCAGATTCC
651	GCACTACCTT	GCCGTTATCC	AATACGCCGG	CAACCGCGAA	CTGCGCGAAC
701	AAATCTACCG	CGCCTACGTT	ACCCGTGCCA	GCGAACTTTC	AAACGACGGC
751	AAATTCGACA	ACACCGCCAA	CATCGACCGC	ACGCTCGAAA	ACGCATTGAA
801	AACCGccaaa	cTGCTCGGCT	TTAAAAATTA	CGCCGAATTG	TCGCTGGCAA
851	CCAAAATGGC	GGACACGCCC	GAACAGGTTT	TAAACTTCCT	GCACGACCTC
901	GCCCGCCGCG	CCAAACCTTA	CGCCGAAAAA	GACCTCGCCG	AAGTCAAAGC
951	CTTCGCCCCG	GAACACCTCG	GTCTCGCCGA	CCCGCAGCCG	TGGGACTTGA
1001	GCTACGCCGG	CGAAAACTG	CGCGAAGCCA	AATACGCATT	CAGCGAAACC
1051	GAAGTCAAAA	AATACTTCCC	CGTCGGCAAA	GTTCTGGCAG	GCTGTTCGCG
1101	CCAAATCAAA	AAACTCTACG	GCATCGGATT	CGCCGAAAAA	ACCGTTCCCC
1151	TCTGGCACAA	AGACGTGCGC	TATTTTGAAT	TGCAACAAAA	CGGCAAAACC
1201	ATCGGCGGCG	TTTATATGGA	TTTGTACGCA	CGCGAAGGCA	AACGCGGCGG
1251	CGCGTGGATG	AACGActaca	AAGGCCGCCG	CCGCTTTGCC	GACGgcacGC
1301	TGCAACTGCC	CACCGCCTAC	CTCGTCTGCA	ACTTCGCCCC	GCCCGTCGGC
1351	GGCAAAGAAG	CGCGTTTAAG	CCACGACGAA	ATCCTCACCC	TCTTCCACGA
1401	AacCGGCCAC	GGACTGCACC	ACCTGCTTAC	CCAAGTGGAC	GAACGGGGCG
1451	TGTCCGGCAT	CAAcggcgtA	GAATGGGACG	CGGTCGAACT	GCCCAGCCAG
1501	TTATATGAAA	ACTTCGTTTG	GGAATACAAT	GTATTGGCAC	AAATGTCCGC
1551	CCACGAAGAA	AccgGCGAGC	CCCTGCCGAA	AGAACTCTTC	GACAAAAATGC
1601	TcgcCGCCAA	AAACTTCCAG	CGCGGTATGT	TCCTCGTCCG	GCAAAATGGAG
1651	TTCGCCCTCT	TCGATATGAT	GATTTACAGT	GAAAGCGACG	AATGCCGTCT
1701	GAAAAAATGG	CAGCAGGTTT	TAGACAGCGT	GCGCAAAGAA	GTcGCCGTCA
1751	TCCAACCGCC	CGAATACAAC	CGCTTCGCCA	ACAGCTTCGG	CCacatctTC
1801	GCcggcGGCT	ATTCCGCAGG	CTATTACAGC	TACGCATGGG	CCGAAGTCCT
1851	cAGCACCGAT	GCCTACGCCG	CCTTTGAAGA	AAGcGACGac	gtcGCCGCCA
1901	CAGGCAAACG	CTTCTGGCAA	GAAAtccttg	ccgtcggcgg	ctCCCGCAGC
1951	gcgGCGGAAT	CCTTCAAAGC	CTTCCGCCGA	CGCGAACCGA	GCATAGACGC

2001 ACTGCTGCGC CAaagcggT TCGACAACGC gGcttgA

This corresponds to the amino acid sequence <SEQ ID 482; ORF 128.ng>:

```

gl28.pep
  1 MIDNALLHLG EEPRFNQIQT EDIKPAVQTA IAEARGQIAA VKAQHTGTGWA
 51 NTVERLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEI SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDLSYAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDVR YFELQONGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTLLQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGEPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS ESDECRLKNW QQVLDSVRKE VAVIQPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSTD AYAFAEESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR QSGFDNAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 483>:

```

m128.seq (partial)
  1 ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
 51 AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCTGTAC CGGCATCACC GAACGCGTCG GCAGGATTGT
201 GGGCGTGGTG TCGCACCTCA ACTGCGTCGC CGACACGCCG GAACCTCGCG
251 CCGTCTATAA CGAAGTATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 CGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAAA AACCAAACTC AACCAC
  1 TACGCCAGCG AAAAAGTGGC CGAAGCCAAA TACGCGTTCA GCGAAACCGA
 51 wGTCAAAAAA TAyTTCCcyG TCGGCAAwGT ATTAAACGGA CTGTTTCGCCC
101 AAmTCAAAAA ACTmTACGGC ATCGGATTTA CCGAAAAAAC yGTCCCGCTC
151 TGGCACAAG ACGTGCCTA TtkTGAATTG CAACAAAACG GCGAaCCAT
201 AGGCGGCGTT TATATGGATT TGTACGCACG CGAAGGCAAA CGCGGCGGCG
251 CGTGGATGAA CGACTACAAA GGCCGCCGCC GTTTTTTCTG CCGCACGCTG
301 CAayTGCCCA CCGCCTACCT CGTCTGCAAC TTCGCCCCAC CCGTCGGCGG
351 CAGGGAAGCC CGCyTGAGCC ACGACGAAAT CCTCATCCTC TTCCACGAAA
401 CCGGACACGG GCTGCACCAC CTGCTTACCC AAGTGGACGA ACTGGGCGTA
451 TCCGGCATCA ACGGCGTaka ATGGGACGCG GTCGAACTGC CCAGCCAGTT
501 TATGGAAAAT TTCGTTTGGG AATACAATGT CTTGGCACAA mTGTCAGCCC
551 ACGAAGAAAC CGGcgTTCCC yTGCCGAAAG AACTCTTsGA CAAAwTGCTC
601 GCCGCCAAAA ACTTCCAAsG CGGCATGTTC yTsGTCCGGC AAwTGGAGTT
651 CGCCCTCTTT GATATGATGA TTTACAGCGA AGACGACGAA GGCCGTCTGA
701 AAAACTGGCA ACAGGTTTTTA GACAGCGTGC GCAAAAAAGT CGCCGTCATC
751 CAGCCGCCCG AATACAACCG CTTGCGCTTG AGCTTCGGCC ACATCTTCGC
801 AGGCGGCTAT TCCGCAGCTn ATTACAGCTA CGCGTGGGCG GAAGTATTGA
851 GCGCGGACGC ATACGCCGCC TTTGAAGAAA GCGACGATGT CGCCGCCACA
901 GGCAAACGCT TTTGGCAGGA AATCCTCGCC GTCGGGGnAT CGCGCAGCGG
951 nGCAGAATCC TTCAAAGCCT TCCGCGGCCG CGAACCGAGC ATAGACGCAC
1001 TCTTGCGCCA CAGCGGTTTC GACAACGCGG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 484; ORF 128>:

```

m128.pep (partial)
  1 MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGTGWA
 51 NTVEPLTGIT ERVGRIWGVV SHLNCVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NH
//
  1 YASEKLREAK YAFSETXVKK YFPVGXVLNG LFAQXKKLYG IGFTEKTVPV
 51 WHKDVRYXEL QQNGEXIGGV YMDLYAREGK RGGAWMNDYK GRRRFS DGTL
101 QLPTAYLVCN FAPPVGGREA RLSDHEILIL FHETGHGLHH LLTQVDELGV
151 SGINGVXWDA VELPSQFMEN FVWEYNVLAQ XSAHEETGVP LPKELXDKXL
201 AAKNFQXGMF XVRQXEFALF DMMIYSEDDE GRLKNWQQVL DSVRKKVAVI
251 QPEYNNRFAL SFGHIFAGGY SAAXYSYAWA EVLSADAYAA FEESDDVAAT

```


365

301 GKRFWQEILA VGXSRSGAES FKAFRGREPS IDALLRHSGF DNAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng) from *N. gonorrhoeae*:

m128/g128

	10	20	30	40	50	60
g128.pep	MIDNALLHLGEEPRFNQIQTEDIKPAVQTAIAEARGQIAAVKAQTHGTWANTVERLTGIT					
	: :					
m128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQTHGTWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g128.pep	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
	:					
m128	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130	140	150	160	170	180
g128.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	:					
m128	TLSPAQKTKLNH					
	130					
	//					
			340	350	360	
g128.pep	YAGEKLREAKYAFSETEVKKYFPVGKVLG					
	:					
m128	YASEKLREAKYAFSETXVKKYFPVGXVLNG					
			10	20	30	
	370	380	390	400	410	420
g128.pep	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWMNDYK					
	:					
m128	LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
	430	440	450	460	470	480
g128.pep	GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVDELGV					
	:					
m128	GRRRFSGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVDELGV					
	100	110	120	130	140	150
	490	500	510	520	530	540
g128.pep	SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQGMF					
m128	SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQXGMF					
	160	170	180	190	200	210
	550	560	570	580	590	600
g128.pep	LVRQMEFALFDMMIYSESDCRLKNWQQVLDVSRKEVAVIQPPEYNRFANSFGHIFAGGY					
	:					
m128	XVRQXEFALFDMMIYSEDDEGRCLKNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIFAGGY					
	220	230	240	250	260	270
	610	620	630	640	650	660
g128.pep	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRGREPS					
	:					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSAGAESFKAFRGREPS					
	280	290	300	310	320	330

366

	670	679
g128.pep	IDALLRQSGFDNAA	X
	: :	
m128	IDALLRHSFGDNAV	X
	340	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 485>:

```

a128.seq
1   ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCCTGAC CGGCATCACC GAACGCGTCTG GCAGGATTTG
201 GGGCGTGTTG TCGCACCTCA ACTCCGTAC CGACACGCCG GAACTCGCGG
251 CCGCCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAACCTC AACCACGATC
401 TGCGCGATTT CGTCTCAGC GCGCGGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAAC CGAAGGCGCG CAACTTTCCG CCAAATTTCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTATCC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTGACAC ACACGCCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTATTAAACG GACTGTTTCG
1101 CCAAATCAAA AAATCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACCGGCGCG
1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGTTTTTCA GACGGCAGCG
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTACCCC GCCCGTCGGC
1351 GGCAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCAGACAC GGCTGACAC ACCTGCTTAC CCAAGTCGAC GAATGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAAT GCCCAGTCAG
1501 TTTATGGAAT ATTTCGTTT GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAATTTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTGCGCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 TAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCCGTCTG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 486; ORF 128.a>:

```

a128.pep
1   MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51  NTVEPLTGIT ERVGRIWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEI SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME

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367

551 FALFDMMIYS EDDEGR LKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
 601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRWFQ EILAVGGSRS
 651 AAESFKAFRG REPSIDALLR HSGFDNAA*

m128/a128 66.0% identity in 677 aa overlap

m128.pep	10	20	30	40	50	60
	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT					
a128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT					
	10	20	30	40	50	60
m128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
a128	ERVGRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
m128.pep	130					
	TLSPAQKTKLNH-----					
a128	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
m128.pep	-----					
a128	FDDAAPLAGIPEDALAMFAAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLRQIYRAYV					
	190	200	210	220	230	240
m128.pep	-----					
a128	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL					
	250	260	270	280	290	300
m128.pep	-----					140
						150
						YASEKLREAKYAFSETXVKKYFPVGX
a128	ARRAKPYAEKDLAEVKAFARESGLGLADLPWDLGYAGEKLREAKYAFSETEVKKYFPVGK					
	310	320	330	340	350	360
m128.pep	160	170	180	190	200	210
	VLNGLFAQXKKLYGIGFTEKTPVWVKDVRVYXELQONGEXIGGVYMDLYAREGKRGGAWM					
a128	VLNGLFAQIKKLYGIGFTEKTPVWVKDVRVYFELQONGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
m128.pep	220	230	240	250	260	270
	NDYKGRRRFSDGTLQLPTAYLVCNFPVGGREARLSHDEILILFHETGHGLHLLTQVD					
a128	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTTFHETGHGLHLLTQVD					
	430	440	450	460	470	480
m128.pep	280	290	300	310	320	330
	ELGVSGINGVXWDAAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQ					
a128	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540
m128.pep	340	350	360	370	380	390
	XGMFXVRQXEFALFDMMIYSEDDEGR LKNWQQVLDSVRKKVAVIQPPEYNRFALSFGHIF					
a128	RGMFLVRQMEFALFDMMIYSEDDEGR LKNWQQVLDSVRKEVAVVRPPEYNRFANSFGHIF					
	550	560	570	580	590	600

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          400      410      420      430      440      450
m128.pep  AGGYSAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRGAESFKAFRG
          |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRAAESFKAFRG
          610      620      630      640      650      660

          460      470
m128.pep  REPSIDALLRHSGFDNAVX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      REPSIDALLRHSGFDNAAX
          670

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The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 487>:

g128-1.seq (partial)

```

1  ATGATTGACA ACGCACTGCT CCACTTGGGC GAAGAACCCC GTTTTAATCA
51  AATCAAAACC GAAGACATCA AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCG GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAAGTGTG CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTGCA ACGCTTTCCC CGGCACAAAA AACCAAGCTC GATCACGACC
401 TGCGCGATTG CGTATTGAGC GGCGCGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAA CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCCGG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAAGTTT AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACC GCCCAA CTGCTCGGCT TTAATAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACGCCG GAACAGGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCGCCCGC GAACACCTCG GTCTCGCCGA CCCGACGCCG TGGGACTTGA
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTTCTGGCAG GCCTGTTCGC
1101 CCAAATCAAA AACTCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCAAAACC
1201 ATCGGCGGCG TTTATATGGA TTGTACGCA CGCGAAGGCA AACGCGCGCG
1251 CGCGTGGATG AACGACTACA AAGGCCGCGC CCGCTTTGCC GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTGCTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACCC TCTTCCACGA
1401 AACC GGCAC GGACTGCACC ACCTGCTTAC CCAAGTGAC GAACTGGGCG
1451 TGTCCGCAT CAACGGCGTA AAA

```

This corresponds to the amino acid sequence <SEQ ID 488; ORF 128-1.ng>:

g128-1.pep (partial)

```

1  MIDNALLHLG EEPRFNQIKT EDIKPAVQTA IAEARGQIAA VKAQHTGWA
51  NTVERLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDLSYAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDVR YFELQNGK
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTQLQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLLTQVD ELGVSGINGV K

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 489>:

m128-1.seq

```

1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTG AACCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG

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201 GGGCGTGGTG TCGCACCTCA ACTCCGTCGC CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAA AACCAACTC AACCACGATC
401 TGCGCGATTT CGTCTCAGC GCGCGGAAC TGCCGCCGA ACAGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGC CAACTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGT CCGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGAC CGCTCGCCAT GTTTGCGGCC
601 GCCGCGCAA GCGAAAGCAA AACAGGCTAC AAAATCGGCT TGCAGATTCC
651 ACACTACCTC GCCGTCTCC AATACGCCGA CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAACTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACCTCGCAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAATA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACGCCC GAACAAGTTT TAAACTTCTT GCACGACCTC
901 GCCCGCGCG CCAAACCCTA CGCCGAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTGA ACCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCAG CGAAAAATG CGCGAAGCCA AATACGCGT CAGCGAAACC
1051 GAAGTCGAAA AATACTTCCC CGTCGGCAA GTATTAAAC GACTGTTCGC
1101 CCAAATCAAA AAATCTACG GCATCGGATT TACCGAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 GAGCTGGATG AACGACTACA AAGGCCGCG CCGTTTTCA GACGGACGCG
1301 TGCAACTGCC CACCGCTAC CTGCTGCA ACTTCGCCCC ACCCGTCGGC
1351 GGCAGGGAAG CCCGCCTGAG CCACGACGAA ATCCTCATCC TCTTCCACGA
1401 AACCAGACAC GGGCTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGAC CGTTCGAACT GCCAGCCAG
1501 TTTATGAAA ATTTCTGTTT GGAATACAAT GTCTTGGCAC AAATGTCAGC
1551 CCACGAAGAA ACCGGCGTTC CCTTGCCGAA AGAACTCTC GACAAAATGC
1601 TCGCCGCCAA AAATTTCAA CGCGCATGT TCCTCGTCCG GCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGAC AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAAA GTCCCGTCA
1751 TCCAGCCGCC CGAATACAAC CGCTCGCCT TGAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCGCGAG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTGAAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAACG CTTTGGCAG GAAATCCTCG CCGTCGGCG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCCGCGC CGCGAACCGA GCATAGACGC
2001 ACTCTTGGC CACAGCGGTT TCGACAACGC GGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 490; ORF 128-1>:

m128-1.pep.

```

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWGA
51 NTVEPLTGIT ERVGRIVGVV SHLSNVADTP ELRAVYNELM PEITVFFTEI
101 QQDIELYNRF KTIKNSPEFD TLSPAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSESKTGY KIGLQIPHYL AVIQYADNRE LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLALALQTA LGLFKNYAEL SLATKMAADP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLNLADLQP WDLGYASEKL REAKYAFSET
351 EVKKYFPVGK VNLGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFAPPVG
451 GREARLSHDE ILILFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRLKNW QQVLDSVRKK VAVIQPPEYN RFALSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRWFQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAV*

```

m128-1/g128-1 94.5% identity in 491 aa overlap

```

          10      20      30      40      50      60
g128-1.pep MIDNALLHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m128-1      MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAA IKAQHTGWANTVEPLTGIT
          10      20      30      40      50      60

          70      80      90      100     110     120
g128-1.pep ERVGRIVGVVSHLSNVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m128-1      ERVGRIVGVVSHLSNVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          70      80      90      100     110     120

```

370

	130	140	150	160	170	180
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAE	AKLQTEGAQLSAKFSQNVLDATDAFGIY				
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
	190	200	210	220	230	240
g128-1.pep	FDDAAPLAGIPEDALAMFAAAAQSEGKTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYV					
m128-1	FDDAAPLAGIPEDALAMFAAAAQSESKTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV					
	190	200	210	220	230	240
	250	260	270	280	290	300
g128-1.pep	TRASELSNDGKFDNTANIDRTLLENALKTAKLLGFKNYAELSLATKMADTPEQVLNHLHDL					
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNHLHDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
g128-1.pep	ARRAKPYAEKDLAEVKAFAREHLGLADPQPWDL	SYAGEKLREAKYAFSETEVKKYFPVGK				
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLPWDLGYASEKLREAKYAFSETEVKKYFPVGK					
	310	320	330	340	350	360
	370	380	390	400	410	420
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQQNGKTIGGVYMDLYAREGKRGGAWM					
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD					
	430	440	450	460	470	480
	490					
g128-1.pep	ELGVSGINGVK					
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 491>:

a128-1.seq

1	ATGACTGACA	ACGCACTGCT	CCATTTGGGC	GAAGAACCCC	GTTTTGATCA
51	AATCAAAACC	GAAGACATCA	AACCCGCCCT	GCAAACGCCC	ATTGCCGAAG
101	CGCGCGAACA	AATCGCGGCC	ATCAAAGCCC	AAACGCACAC	CGGCTGGGCA
151	AACACTGTGC	AACCCCTGAC	CGGCATCACC	GAACGCGTCG	GCAGGATTTG
201	GGGCGTGGTG	TCGCACCTCA	ACTCCGTCAC	CGACACGCCC	GAAGTGC
251	CCGCCTACAA	TGAATTAATG	CCCGAAATTA	CCGTCTTCTT	CACCGAAATC
301	GGACAAGACA	TCGAGCTGTA	CAACCGCTTC	AAAACCATCA	AAAACTCCCC
351	CGAGTTCGAC	ACCCTCTCCC	ACGCGCAAAA	AACCAAACTC	AACCACGATC
401	TGCGCGATTT	CGTCCTCAGC	GGCGCGGAAC	TGCCGCCCCG	ACAGCAGGCA
451	GAATTGGCAA	AACTGCAAAC	CGAAGGCGCG	CAACTTCCG	CCAAATCTC
501	CCAAAACGTC	CTAGACGCGA	CCGACGCGTT	CGGCATTAC	TTTGACGATG
551	CCGCACCGCT	TGCCGCGATT	CCCGAAGACG	CGCTCGCCAT	GTTTGCCGCT
601	GCCGCGCAAA	GCGAAGGCAA	AACAGGCTAC	AAAATCGGTT	TGCAGATTCC
651	GCACTACCTC	GCCGTCATCC	AATACGCGCA	CAACCGCAAA	CTGCGCGAAC
701	AAATCTACCG	CGCCTACGTT	ACCCGCGCCA	GCGAGCTTTC	AGACGACGGC
751	AAATTCGACA	ACACCGCCAA	CATCGACCGC	ACGCTCGAAA	ACGCCCTGCA
801	AACCGCCAAA	CTGCTCGGCT	TCAAAACTA	CGCCGAATTG	TCGCTGGCAA
851	CCAAAATGGC	GGACACCCCC	GAACAAGTTT	TAAACTTCCT	GCACGACCTC
901	GCCCGCCGCG	GCAAACCCCTA	CGCCGAAAAA	GACCTCGCCG	AAGTCAAAGC
951	CTTCGCCCCG	GAAAGCCTCG	GCCTCGCGCA	TTTGCAACCG	TGGGACTTGG
1001	GCTACGCCGG	CGAAAACTG	CGCGAAGCCA	AATACGCATT	CAGCGAAACC
1051	GAAATCAAAA	AATACTTCCC	CGTCGGCAAA	GTATTAAACG	GACTGTTCGC
1101	CCAAATCAAA	AAACTCTACG	GCATCGGATT	TACCGAAAAA	ACCGTCCCCG
1151	TCTGGCACAA	AGACGTGCGC	TATTTTGAAT	TGCAACAAAA	CGGCGAAACC
1201	ATAGGCGGCG	TTTATATGGA	TTTGTACGCA	CGCGAAGGCA	AACGCGGCGG

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1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAT ATTTCTGTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AACTTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCCGCGGA CGGAACCGA GCATAGACGC
2001 ACTCTTGC GC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 492; ORF 128-1.a>:

a128-1.pep

```

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGTWA
51 NTVEPLTGIT ERVGRIWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVEPLSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRLEKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRWFQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAA*

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m128-1/a128-1 97.8% identity in 677 aa overlap

```

          10      20      30      40      50      60
a128-1.pep MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGTWANTVEPLTGIT
          |||
m128-1     MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGTWANTVEPLTGIT
          10      20      30      40      50      60

          70      80      90      100     110     120
a128-1.pep ERVGRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          |||
m128-1     ERVGRIWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          70      80      90      100     110     120

          130     140     150     160     170     180
a128-1.pep TLSHAQKTKLNHDLRDFVLGSAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
          |||
m128-1     TLSPAQKTKLNHDLRDFVLGSAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
          130     140     150     160     170     180

          190     200     210     220     230     240
a128-1.pep FDDAAPLAGI PEDALAMFAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
          |||
m128-1     FDDAAPLAGI PEDALAMFAAAQSEKGTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV
          190     200     210     220     230     240

          250     260     270     280     290     300
a128-1.pep TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
          |||
m128-1     TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
          250     260     270     280     290     300

          310     320     330     340     350     360
a128-1.pep ARRAKPYAEKDLAEVKAFARESLGLADLQPWDLGYAGEKLREAKYAFSETEVKKYFPVGK
          |||

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m128-1      ARRAKPYAEKDLAEVKAFARESLNLADLPWDLGYASEKLREAKYAFSETEVKKYFPVGK
              310      320      330      340      350      360

a128-1.pep  VLNGLFAQIKKLYGIGFTEKTPVWVKDVRVFELQQNGETIGGVYMDLYAREGKRGGAWM
              370      380      390      400      410      420
|||||
m128-1      VLNGLFAQIKKLYGIGFTEKTPVWVKDVRVFELQQNGETIGGVYMDLYAREGKRGGAWM
              370      380      390      400      410      420

a128-1.pep  NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
              430      440      450      460      470      480
|||||
m128-1      NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
              430      440      450      460      470      480

a128-1.pep  ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
              490      500      510      520      530      540
|||||
m128-1      ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
              490      500      510      520      530      540

a128-1.pep  RGMFLVRQMEFALFDMMIYSEDDEGRKLNWQQVLDVSRKEVAVVRPPEYNRFANSFGHIF
              550      560      570      580      590      600
|||||
m128-1      RGMFLVRQMEFALFDMMIYSEDDEGRKLNWQQVLDVSRKVKAVIQPPEYNRFALSFGHIF
              550      560      570      580      590      600

a128-1.pep  AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
              610      620      630      640      650      660
|||||
m128-1      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
              610      620      630      640      650      660

a128-1.pep  REPSIDALLRHSGFDNAAX
              670      679
|||||
m128-1      REPSIDALLRHSGFDNAVX
              670
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a128-1/ P44573

```
sp|P44573|OPDA_HAEIN OLIGOPEPTIDASE A >gi|1075082|pir||C64055 oligopeptidase A (prlC) homolog
- Haemophilus influenzae (strain Rd KW20)
>gi|1573174 (U32706) oligopeptidase A (prlC) [Haemophilus influenzae Rd] Length = 681
Score = 591 bits (1507), Expect = e-168
Identities = 309/677 (45%), Positives = 415/677 (60%), Gaps = 4/677 (0%)
```

```
Query: 4 NALLHLGEEPRFDQIKTEDIKPALQTXXXXXXXXXXXXXXXXXHTGWANTVEPLTGITERV 63
          N LL++ P F QIK E I+PA++ H W N + PLT +R+
Sbjct: 5 NPLLNIIQGLPPFSQIKPEHIRPAVEKLIQDCRNTIEQVLKQPHFTWENFILPLTETNDRL 64

Query: 64 GRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFDTLS 123
          R W VSHLNSV ++ ELR AY +P ++ + T +GQ LYN + +KNS EF S
Sbjct: 65 NRAWSPVSHLNSVKNSTELREAYQTCLPLLSEYSTWVGQHKGLYNAYLALKNSAEFADYS 124

Query: 124 HAQKTKLNHDLRDFVLSGAELPPEQQABLAKLQTEGAQLSAKFSQNVLDATDAFGIYFDD 183
          AQK + + LRDF LSG L E+Q ++ ++L+++FS NVLDAT + ++
Sbjct: 125 IAQKKAIEENSLRDFELSGIGLSEKQQRYSGEIVARLSELNSQFSNNVLDATMGWEKLIEN 184

Query: 184 AAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLEQIYRAYVTRA 243
          A LAG+PE AL +A+S+G GY+ L+IP YL V+ Y +NR LRE++YRAY TRA
Sbjct: 185 EAELAGLPESALQAAQQAESKGLKGYRFTLEIPSYLPVMTYCENRALREEMYRAYATRA 244

Query: 244 SELSDD-GKFDNTANIDRTLLENALQTAKLLGPKNYAELSLATKMATDPEQVLNFLHDLAR 302
          SE + GK+DN+ ++ L ++ AKLLGF Y ELSLATKMA+ P+QVL+FL LA
Sbjct: 245 SEQGPNAGKWDNSKVMEEILTLRVELAKLLGFNTYTELSLATKMAENPQQVLDFLDHLAE 304

Query: 303 RAKPYAEKDLAEVKAFARESLGLADLPWDLGYAGEKLREAKYAFSETEVKKYFPVGKVL 362
          RAKP EK+L E+K + + G+ +L PWD+G+ EK ++ YA ++ E++ YFP +V+
Sbjct: 305 RAKPQGEKELQELKGYCEKEFGVTLELPWDIGFYSEKQKQHLVAINDEELRPYPFENRVI 364
```


Query: 363 NGLFAQIKKLYGIGFTE-KTVPVWHKDVRYFEL-QQNGETIGGVYMDLYAREGKRGGAWM 420
 +GLF IK+++ I E K V WHKDVR+F+L +N + G Y+DLYARE KRGGAWM
 Sbjct: 365 SGLFELIKRIFNIRAVRKGVDTWKDVRFDLIDENDQLRGSFYLDLYAREHKRGGAWM 424

Query: 421 NDYKGRRRRSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEIXXXXXXXXXXXXXXXXXQVD 480
 +D GR+R DG+++ P AYL CNF P+G K A +H+E+ Q+D
 Sbjct: 425 DDCIGRKRKLDGSIETFPVAYLTCNFNAPIGNKPAFTHNEVTTLFHEFGHGIHMLTQID 484

Query: 481 ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ 540
 V+GINGV WDAVELPSQFMEN+ WE LA +S H ETG PLPKE ++L AKNFQ
 Sbjct: 485 VSDVAGINGVPWDAVELPSQFMENWCWEEELAFISGHYETGEPLPKEKLTQLLKAKNFQ 544

Query: 541 RGMFLVRQMEFALFDMMIYSEDDEGRKKNWQQVLDSVRKEVAVVRPEYNRFANSFGHIF 600
 MF++RQ+EF +FD ++ D + L SV+ +VAV++ ++ R +SF HIF
 Sbjct: 545 AAMFILRQLEFGIFDFRLHHTFDAEKTNQILDTLKSVKSQVAVIKGVDWARAPHFSFHHIF 604

Query: 601 XXXXXXXXXXXXXWAEVLSADAYAAPFEESDDV-AATGKRFWQEILAVGGSRAAESPKAFR 659
 WAEVLSADAY+ FEE TGK F EIL GGS E FK FR
 Sbjct: 605 AGGYAAGYYSYLWAEVLSADAYSRFEEGIFNPITGKSFLDEILTRGSEEPMEFLFKRFR 664

Query: 660 GREPSIDALLRHSGFDN 676
 GREP +DALLRH G N
 Sbjct: 665 GREPQLDALLRHKGIMN 681

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 493>:

g129.seq
 1 ATGCTTTTCAC CTCCTCGGCG TAAACGGCG GCACATCAAT CAAGCCGTCT
 51 TTCATTTGCG TGCGGAAAAA ATGCGGCGTG TTGCCGTGAT CAAAATCAAT
 101 ATCGTGCAGC ATCCAGCCCA AATCGCGGTT TGCCTCGCTT TCCGATAACG
 151 CCGACGGCGG CAGCGGTTCA CCCTTATCCG CGCTTTCGCC ATTTGCCCTT
 201 TCAGGCTGCG GGCATAGGGG CGGAACAGGC GGCGGTGCGA TCCTGTTTCA
 251 TCCGGACAAA CGCGTTGGCA GTCGGAAT CCGCCCGGCC GTGTCAAATA
 301 ATGCGTTACT TTGGCCGGGT CTGTCTCTTT GTAAGCGGCG GTCTTTTTTT
 351 GCGCGCCATC CGCATCTGTT TGGGCGCATG GCAAACGGCG GCTGCCGTAC
 401 AATCAAATG TTTGGCGATT TCATGCAGAC AGGCATCCGG ATGCCGCCCG
 451 ACATATCGAG CCGGTTTTTG CCTATCCGAT TTGGCGGCAT TTAGCCGGGT
 501 AACTTGA

This corresponds to the amino acid sequence <SEQ ID 494; ORF 129.ng>:

g129.pep
 1 MLSPPRRKTA AHQSSRLSFA CGKNAACCRD QNQYRAASSP NRGLPRFPIT
 51 PTAAAVHPYP RFRHLPPQAA GIGAEQAAVE SCFIRTNALA VGKSGRPCQI
 101 MRYFGRVLSF VSGGLFLRAI RICLGAWQTA AAVQSKCLAI SCRQASGCRP
 151 TYRAGFCLSD LAAFRPVT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 495>:

m129.seq (partial)
 1 ..TATCTGCGCT TCACTATTT GCCCTTTCAG GCTGCGGGCA TAGGGACGGA
 51 ACAGGTAGCG GTCAAATCCT GTTTCATCCA AATAAACACG TTGGTAGTCG
 101 GAAAATTTCG CCGGCTGTGT CAAATAATGC GTTACTTTGG CCGGGTCTTG
 151 TTCTTTGTAA GTGGTGGTCT TTTTTCGCG GTTATCCCCA TCTGTTTGAG
 201 TGCATAGCAA ATGGTGGCTG CCGTACAATC AAAATGTTTG GCGATTTTCAT
 251 GCAGATAGGC ATCCGGGTGT TGCCCAACAT ATTGAGCCGG TTTTTCGCTA
 301 TCCGATTTGA CGGCATTTAG ACCGGTAACT TGA

This corresponds to the amino acid sequence <SEQ ID 496; ORF 129>:

m129.pep (partial)
 1 ..YLRPHYLPFQ AAGIGTEQVA VKSCFIQINT LVVGKFGRLC QIMRYFGRVL
 51 FVSGGLFLR VIPICLSAXQ MVAAVQSKCL AISCRXASGC CPTYXAGFCL
 101 SDLTAFRPVT *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 129 shows 79.1% identity over a 110 aa overlap with a predicted ORF (ORF 129.ng) from *N. gonorrhoeae*:

m129/g129

```

                                10      20      30
m129.pep                      YLRFHYLPFQAAGIGTEQVAVKSCFIQINT
                                | | | : | | | | | | | : | | | : | | | : | :
g129      RDQNQYRAASSPNRGLPRFPITPTAAAVHPYPRFRHLPFQAAGIGAEQAAVESCIRTNA
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m129.pep      LVVGKFGRLCQIMRYFGRVLFVSGGLFLRVIPICLSAXQMVAAVQSKCLAISCRXASGC
                | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g129      LAVGKSGRPCQIMRYFGRVLSFVSGGLFLRAIRICLGAWQTAAAVQSKCLAISCRQASGC
                90      100     110     120     130     140

                                100     110
m129.pep      CPTYXAGFCLSDLTAFRPVTX
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g129      RPTYRAGFCLSDLAAFRPVTX
                150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 497>:

```

a129.seq (partial)
1  TATCTGCGCT TTCACTATTT GCCCTTTTCAG GCTGCGGGCA TAGGGACGGA
51 ACAGGTAGCG GTCAAATCCT GTTTCATCCA AATAAACACG TTGGTAGTCG
101 GAAAATTCGG CCAGCTGTGT CAAATAATGC GTTACTTTGG CCGGGTCTTG
151 TTCTTTGTAA GTGGTGGTCT TTTTTCGCGC GTTATCCCCA TCTGTTTGAG
201 TGCATAGCAA ATGGTGGCTG CCGTACAATC AAAATGTTTG GCGATTTTAT
251 GCAGATAGGC ATCCTGGTGT TGCCCAACAT ATTGAGCCGG TTTTTCGCTA
301 TCCGATTGA CGGCATTTAG ACCGGTAACT TGA

```

This corresponds to the amino acid sequence <SEQ ID 498; ORF 129.a>:

```

a129.pep (partial)
1  YLRFHYLPFQ AAGIGTEQVA VKSCFIQINT LVVGKFGQLC QIMRYFGRVL
51 FVSGGLFLR VIPICLSA*Q MVAAVQSKCL AISCR*ASWC CPTY*AGFCL
101 SDLTAFRPVT *

```

m129/a129 98.2% identity in 110 aa overlap

```

                                10      20      30      40      50      60
m129.pep      YLRFHYLPFQAAGIGTEQVAVKSCFIQINTLVVGKFGRLCQIMRYFGRVLFVSGGLFLR
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a129      YLRFHYLPFQAAGIGTEQVAVKSCFIQINTLVVGKFGQLCQIMRYFGRVLFVSGGLFLR
                10      20      30      40      50      60

                                70      80      90      100     110
m129.pep      VIPICLSAXQMVAAVQSKCLAISCRXASGCCPTYXAGFCLSDLTAFRPVTX
                | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a129      VIPICLSAXQMVAAVQSKCLAISCRXASWCCPTYXAGFCLSDLTAFRPVTX
                70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 499>:

```

g130.seq
1  ATGAAACAAC TCCGCGACAA CAAAGCCCAA GGCTCTGCAC TGTTTACCCCT
51 TGTGAGCGGT ATCGTTATTG TTATTGCAGT CCTTTATTTC CTGATTAAGC
101 TGGCGGGCAG TGGATCGTTC GGCGATGTCG ATGCCACTAC GGAAGCGGCA
151 ACGCAGACCC GCATCCAGCC TGTCGACAAA TTGACGATGG GTGACGGCAT
201 CCCCCTCGGC GAACGCCAAG GCGAACAGAT TTTCCGGCAA ATCTGTATCC

```

```

251 AATGCCACGC GCGGACAGC AATGTGCCGA ACGCTCCGAA ACTGGAACAC
301 AACGGCGACT GGGCGCCGCG TATCGCGCAA GGCTTCGATA CCTTGTTCCTA
351 ACACGCGCTG AACGGCTTTA ACGCCATGCC TGCCAAAGGC GGTGCGGCAG
401 ACCTGACCGA TCAGGAAGTC AAACGGGCGA TTACCTACAT GGCGAATAAA
451 AGCGGCGGTT CTTTCCCGAA TCCTGATGAG GCTGCGCCTG CCGACAATGC
501 CGCTTCAGGA ACAGCTTCTG CTCCTGCCGA TAGTGACAGT CCGGCAGAAG
551 CGAAGGCAGA AGACAAGGGT GCGGCAGCCC CTGCGGTCGG CGTTGACGGT
601 AAAAAAGTCT TCGAAGCAAC CTGTCAGGTG TGCCACGGCG GTTCGATTCC
651 CGGTATTCCC GGCATAGGCA AAAAAGACGA TTGGGCACCG CGTATCAAAA
701 AAGGCAAAGA AACCTGCAC AAACATGCCC TTGAAGGCTT TAACGCGATG
751 CCGGCCAAAG GCGGCAATGC AGGTTTGAGC GATGACGAAG TCAAAGCGGC
801 TGTGACTAT ATGGCAAACC AATCCGGTGC AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 500; ORF 130.ng>:

```

g130.pep
1 MKQLRDNKAQ GSALFTLVSG IVIVIAVLVF LIKLAGSGSF GDVDATTEAA
51 TQTRIQPVGQ LTMGDGIPVG ERQGEQIFGK ICIQCHAADS NVPNAPKLEH
101 NGDWAPRIAQ GFDTLFQHAL NGFNAMPAKG GAADLTDOEL KRAITYMANK
151 SGGSPNPDE AAPADNAASG TASAPADSAA PAEAKAEDKG AAPAVGVGDG
201 KKVFEATCQV CHGGSIPGIP GIGKKDDWAP RIKKGKETLH KHALEGFNAM
251 PAKGGNAGLS DDEVKAAVDY MANQSGAKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 501>:

```

m130.seq (partial)
1 ..GGCGAACAGA TTTTCGGCAA AATCTGTATC CAATGCCACG CCGCGGACAG
51 CAATGTGCCG AACGCTCCGA AACTGGAACA CAACGGCGAT TrGGCACCGC
101 GTATCGgCAA GGCTTCGATA CCTTGTTCCTA ACACGCGCTG AACGGCTTTA
151 ACGCCATGCC TGCAAAGGC GGTGCGGCAG ACCTGACCGA TCAGGAAGTCTT
201 AAACGGGCGA TTACTTACAT GGCGAACAAA AGCGGCGGTT CTTTCCCGAA
251 TCCTGATGAG GCTGCGCCTG CCGACAATGC CGCTTCAGGA ACAGCTTCTG
301 CTCCTGCCGA TAGTGACAGT CCGGCAGAAG CGAAGGCAGA AGACAAGGGT
351 GCGGCACcCCC TGCGGTGCGC GTTGACGGTA AAAAAGTCTT CGAAGCAACC
401 TGTGAGGTGT GCCACGGCGG TTCGATTCCC GGTATTCCCG GCATAGGCAA
451 AAAAGACGAT TGGGCACCGC GTATCAAAAA AGGCAAAGAA ACCTTGACAA
501 AACACGCCCT TGAAGGCTTT AACGCGATGC CTGCCAAAG CGgCAATGCA
551 GGTTTGAGCG ATGACGAAGT CAAAGCGGCT GTTGACTATA TGGCAAACCA
601 ATCCGGTGCA AAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 502; ORF 130>:

```

m130.pep (partial)
1 ..GEQIFGKICI QCHAADSNVP NAPKLEHNGD XAPRIQFDT LFQHALNGFN
51 AMPAKGGAAD LTDQELKRAI TYMANKSGGS FPNPDEAAPA DNAASGTASA
101 PADSAAAPAEA KAEDKGAAPA VGVDGKKVFE ATCQVCHGGS IPGIPGIGKK
151 DDWAPRIKKG KETLHKHALE GFNAMPAXG NAGLSDDEVK AAVDYMANQS
201 GAKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 130 shows 98.1% identity over a 206 aa overlap with a predicted ORF (ORF 130.ng) from *N. gonorrhoeae*:

m130/g130

```

m130.pep
10 20 30
GEQIFGKICIQCHAADSNVPNAPKLEHNGD
|||||
g130
50 60 70 80 90 100
DATTEAATQTRIQPVGQLTMGDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD

40 50 60 70 80 89
XAPRI-QGFDTLFQHALNGFNAMPAKGGGAADLTQELKRAITYMANKSGGSFPNPDEAAP
|||||
g130
110 120 130 140 150 160
WAPRIAQGFDTLFQHALNGFNAMPAKGGGAADLTQELKRAITYMANKSGGSFPNPDEAAP

```

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	90	100	110	120	130	140
m130.pep	ADNAASGTASAPADSAAPAEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG					
g130	ADNAASGTASAPADSAAPAEAKAEDKGAAAPAVGVDGKKVFEATCQVCHGGSIPGIPGIG					
	170	180	190	200	210	220
	150	160	170	180	190	200
m130.pep	KKDDWAPRIKKGKETLHKHALEGFNAMPAXGNAGLSDEVKAADVDMANQSGAKFX					
g130	KKDDWAPRIKKGKETLHKHALEGFNAMPAXGGNAGLSDEVKAADVDMANQSGAKFX					
	230	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 503>:

```

a130.seq
1  ATGAAACAAC TCCGCGACAA CAAAGCCCAA GGCTCTGCAC TGTTTACCCCT
51  TGTGAGCGGT ATCGTTATTG TTATTGCAGT CCTTTATTTC CTGATTAAGC
101 TGGCGGGCAG CGGCTCGTTC GGCATGTCG ATGCCACTAC GGAAGCAGCA
151 ACGCAGACCC GTATCCAGCC TGTCGGACAA TTGACGATGG GCGACGGCAT
201 CCCCGTCGGC GAACGCCAAG GCGAACAGAT TTTCCGCAAA ATCTGTATCC
251 AATGCCACGC GCGGCACAGC AATGTGCCGA ACGCTCCGAA ACTGGAACAC
301 AACGGCGATT GGGCGCCGCG TATCGCGCAA GGCTTCGATA CCTTGTTCCA
351 ACACGCGCTG AACGGCTTTA ACGCCATGCC TGCCAAAGGC GGTGCGGTAG
401 ACCTGACCGA TCAGGAACCTC AAACGGGCGA TTACTTACAT GCGCAACAAA
451 AGCGGCGGTT CTTTCCCGAA TCCTGATGAG GCTGCGCCTG CCGACAATGC
501 CGCTTCAGGA ACAGCTTCTG CTCTGCGCGA TAGTGCAGCT CCGGCAGAAG
551 CGAAGGCAGA AGACAAGGGT GCGGCAGCCC CTGCGGTCGG CGTTGACGGT
601 AAAAAAGTCT TCGAAGCAAC CTGTCAAGTG TGCCACGGCG GTTCGATTCC
651 CCGTATTCCC GGCATAGGCA AAAAAGACGA TTGGGCACCG CGTATCAAAA
701 AAGGCAAAGA AACCTTGCAC AAACACGCCC TTGAAGGCTT TAACGCGATG
751 CTGCCAAAG GCGCAATGC AGGTTTGAGC GATGACGAAG TCAAAGCGGC
801 TGTTGACTAT ATGGCAAACC AATCCGGTGC AAAATTCTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 504; ORF 130.a>:

```

a130.pep
1  MKQLRDNKAQ GSALFTLVSG IVIVIAVLVF LIKLAGSGSF GDVDATTEAA
51  TQTRIQPVGQ LTMGDGIPVG ERQGEQIFGK ICIQCHAADS NVPNAPKLEH
101 NGDWAPRIAQ GFDTLFQHAL NGFNAMPAKG GAVDLTDQEL KRAITYMANK
151 SGGSFNPDE AAPADNAASG TASAPADSAA PAEAKAEDKG AAPAVGVDG
201 KKVFEATCQV CHGGSIPGIP GIGKKDDWAP RIKKGKETLH KHALEGFNAM
251 PAKGGNAGLS DDEVKAADV DMANQSGAKF*
  
```

m130/a130 97.6% identity in 206 aa overlap

				10	20	30
m130.pep				GEQIFGKICIQCHAADS NVPNAPKLEHNGD		
a130	DATTEAATQTRIQPVGQLTMDGIPVGERQGEQIFGKICIQCHAADS NVPNAPKLEHNGD					
	50	60	70	80	90	100
	40	50	60	70	80	89
m130.pep	XAPRI-QGFDTLFQHALNGFNAMPAKGGAADLTDQELKRAITYMANKSGGSFNPDEAAP					
a130	WAPRIAQGFDTLFQHALNGFNAMPAKGGAADLTDQELKRAITYMANKSGGSFNPDEAAP					
	110	120	130	140	150	160
	90	100	110	120	130	140
m130.pep	ADNAASGTASAPADSAAPAEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG					
a130	ADNAASGTASAPADSAAPAEAKAEDKGAAAPAVGVDGKKVFEATCQVCHGGSIPGIPGIG					
	170	180	190	200	210	220
	150	160	170	180	190	200
m130.pep	KKDDWAPRIKKGKETLHKHALEGFNAMPAXGNAGLSDEVKAADVDMANQSGAKFX					

|||||
a130 KKDDWAPRIKKGKETLHKHALEGFNAMPAGGNAGLSDDEVKAAVDYMANQSGAKFX
230 240 250 260 270 280

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 505>:

g132.seq
1 ATGGAAGCCT TCAAAACCCT AATTTGGATT ATTAATATTA TTTCCGCTTT
51 GGCCGTCATC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACCTT CCGATCGGGA AGCGGCAGCG CGCAAGGCGT ATTCGGCTCT
151 GCCGGCAACG CCAACTTcct CAgccGCTCG AccGccGTTG CAGCAACAtt
201 tttcttTGca acctgcAtgg gctatggTgt atattcacac CCACACGACA
251 AAACACGGTT TGGACTTcag caacataCGA CAGACTCAGC AagcACCCAA
301 ACCcgtAAGC AATACCGAAC CTTCTGCCCC TGTTCTCAG CAGCAGAAAT
351 AACagtTTTT CAAATgccga caTGgtga

This corresponds to the amino acid sequence <SEQ ID 506; ORF 132.ng>:

g132.pep
1 MEAFKTLIWI INIISALAVI VLVLLQHGKG ADAGATFGSG SGSAQGVFGS
51 AGNANFLSRS TAVAATFFFA TCMGYGVYSH PHDKTRFGLQ QHTTDSASTQ
101 TRKQYRTFCP CSSAAEITVF QMPTW*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 507>:

m132.seq (partial)
1 ATGGAACCCT TCAAAACCTT AATTTGGATT GTTAATTTAA TTTCCGCTTT
51 GGCCGTCTTC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACTTT CGGA...

This corresponds to the amino acid sequence <SEQ ID 508; ORF 132>:

m132.pep (partial)
1 MEAFKTLIWI VNLISALAVF VLVLLQHGKG ADAGATFG...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 132 shows 89.5% identity over a 38 aa overlap with a predicted ORF (ORF 132.ng) from *N. gonorrhoeae*:

m132/g132

	10	20	30	
m132.pep	MEPFKTLIWI VNLISALAVF VLVLLQHGKG ADAGATFG			
	: : :			
g132	MEAFKTLIWI INIISALAVI VLVLLQHGKG ADAGATFGSGSGSAQGVFGSAGNANFLSRS			
	10	20	30	40 50 60

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 509>:

a132.seq
1 ATGGAAGCCT TCAAAACCCT AATTTGGATT GTTAATATAA TTTCCGCTTT
51 GGCCGTCATC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACTTT CCGATCGGGA AGCGGCAGCG CGCAAGGCGT ATTCGGCTCT
151 GCCGGCAACG CTAACCTTCT CAGCCGCTCG ACCGCGGTTG CAGCAACATT
201 TTTCTTTGCA ACCTGCATGg GCTATGGTGT ATATTCACAC CCACACGACA
251 AAACACGGTT TGGACTTCAG CAACGTACAA CAAACTCAGC AAGCACCCAA
301 ACCCGTAAGC AATACCGAAC CTTCTGCCCC TGTTCTCAG CAGCAGAAAT
351 AACAGTTTTT CAAATGCCGA CATGGTGA

This corresponds to the amino acid sequence <SEQ ID 510; ORF 132.a>:

a132.pep
1 MEAFKTLIWI VNIISALAVI VLVLLQHGKG ADAGATFGSG SGSAQGVFGS
51 AGNANFLSRS TAVAATFFFA TCMGYGVYSH PHDKTRFGLQ QRTTNSASTQ
101 TRKQYRTFCP CSSAAEITVF QMPTW*

m132/a132 92.1% identity in 38 aa overlap

378

	10	20	30	
m132.pep	MEPFKTLIWIIVNLISALAVFVLVLLQHGKGADAGATFG			
	: :			
a132	MEAFKTLIWIIVNIISALAVIVLVLLQHGKGADAGATFGSGSGSAQGVFGSAGNANFLSRS			
	10	20	30	40 50 60

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 511>:

g134.seq

1	ATGTCCCAAG	AAATCCTCGA	CCAAGTGCGC	CGCCGCCGCA	CGTTTGCCAT
51	CATCTCCAC	CCCATGCGG	GTAAACCAC	GCTGACCGAA	AAACTGCTGC
101	TGTTTCGGG	CGCGATTCAA	AGCGCAGGCA	CGGTGAAAGG	TAAGAAAACC
151	GGCAAATTCG	CCACCTCCGA	CTGGATGGAC	ATCGAGAAGC	AGCGCGGCAT
201	TTCCGTGGCA	TCAAGCGTGA	TGCAGTTCGA	CTACAAAGAC	CACACCGTCA
251	ACCTCTTGA	CACGCCGGA	CACCAAGACT	TCTCCGAAGA	CACCTACCGC
301	GTTTAAACCG	CAGTGGACAG	CGCCTTGATG	GTCATCGACG	CGGCAAAAGG
351	CGTGAAGCG	CAAACCATCA	AACCTTGAA	CGTCTGCCGC	CTGCGCGATA
401	CGCCGATTGT	TACCTTCATG	AACAAATACG	ACCGCGAAGT	GCGCGATTCT
451	TTGGAACCTCT	TGGACGAAGT	GGAAGACATC	CTGCAAAATC	GCTGCGCGCC
501	CGTTACCTGG	CCGATCGGTA	TGGGCAAAAA	CTTCAAGGGC	GTGTACCACA
551	TCCTGAACGA	CGAAATCTAT	CTCTTTGAAG	CGGGCGGCGA	ACGCCTGCCG
601	CACGAGTTCG	ACATCATCAA	AGGCATAAAC	AATCCCGAAT	TGGAACAACG
651	CTTCCGTTG	GAAATCCAGC	AGTTGCGCGA	CGAAATCGAA	TTGGTGCAGG
701	CGGCTTCCAA	CGAATTTAAT	CTCGacgaAT	TTCTCGccgG	CGAACTCACG
751	CCAGTGTTCT	TCGGCTCTGC	GATTAACAAC	TTCGGCATTG	AGGAAATCCT
801	CAATTCATTG	ATTGACTGGG	CACCCGCACC	GAAACCGCGC	GACGCGACCA
851	TGCGCATGGT	CGGGCCGGAC	GAGCCGAAAT	TTTCCGGATT	TATCTTTAAA
901	ATCCAAGCCA	ATATGGACCC	GAAACACCGC	GACCGTATCG	CCTTCTTGCG
951	CGTCTGCTCC	GGTAAATTCG	AGCGCGGCAT	GAAGATGAAA	CACCTGCGTA
1001	TCAACCGCGA	AATCGCCGCC	TCCAGCGTAG	TAACCTTCAT	GTCGCACGAC
1051	CGCGAACTGG	CGGAAGAAGC	CTACGCCGGC	GACATCATCG	GCATCCCGAA
1101	CCACGGCAAC	ATCCAAATCG	GCGACAGCTT	CTCCGAAGGC	GAACAACCTG
1151	CGTTTACCGG	CATCCCATTC	TTCGCGCCCG	AACTGTTCCG	CAGCGTCCGC
1201	ATCAAAAACC	CGCTGAAAAT	CAAACAACCTG	CAAAAAGGTT	TGCAACAACCT
1251	CGGCGAAGAA	GGTGCGGTTT	AAGTATTCAA	ACCGATGAGC	GGCGCGGATT
1301	TGATTTTGGG	TGCGGTCCGC	GTGTTGCAGT	TTGAAGTCGT	AACCTCACGC
1351	CTCGCCAACG	AATACGGCGT	GGAAGCCGTG	TTCGACAGCG	CATCCATCTG
1401	GTCGGCGCGC	TGGGTATCGT	GCGACGACAA	GAAAAAACTG	GCGGAATTTG
1451	AAAAAGCCAA	CGCAGGCAAC	CTCGCCATCG	ACGCAAGGCG	CAACCTCGCC
1501	TACCTCGCCC	CCAACCGCGT	GAATTTGGGG	TTGACGCAAG	AACGCTGGCC
1551	GGACATCGTG	TTCCACGAAA	CGCGCGAACA	TTCGGTCAAA	CTCTAA

This corresponds to the amino acid sequence <SEQ ID 512; ORF 134.ng>:

g134.pep

1	MSQEILDQVR	RRRTFAIISH	PDAGKTLTE	KLLLFSGAIQ	SAGTVKGKKT
51	GKFATSDWMD	IEKQRGISVA	SSVMQFDYKD	HTVNLLDTPG	HQDFSEDYR
101	VLTAVDSALM	VIDAAKGVEA	QTIKLLNVCR	LRDTPIVTFM	NKYDREVRDS
151	LELLDEVEDI	LQIRCAPVTW	PIGMGKNFKG	VYHILNDEIY	LFEAGGERLP
201	HEFDIIKGIN	NPELEQRFPL	EIQQLRDEIE	LVQAASNEFN	LDEFILAGELT
251	PVFFGSAINN	FGIQEILNSL	IDWAPAPKPR	DATMRMVGPD	EPKFSGFIFK
301	IQANMDPKHR	DRIAPLRVCS	GKFERGMKMK	HLRINREIAA	SSVVTFMSSHD
351	RELAEAYAG	DIIGIPNHGN	IQIGDSFSEG	EQLAFTGIPF	FAPELFRSVR
401	IKNPLKIKQL	QKGLQQLGEE	GAVQVFKPMS	GADLILGAVG	VLQFEVVTSR
451	LANEYGVAV	FDSASIWSAR	WVSCDDKKKL	AEFEKANAGN	LAIDAGGNLA
501	YLAPNRVNLG	LTQERWPDIV	FHETREHSVK	L*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 513>:

m134.seq

1	ATGTCCCAAG	AAATCCTCGA	CCAAGTGCGC	CGCCGCCGCA	CGTTTGCCAT
51	CATCTCCAC	CCTGACGCAG	GTAAACCAC	GTTGACTGAA	AAACTCTTGC
101	TGTTTCGGG	CGCGATTGAG	AGCGCGGGTA	CGGTAAAAGG	CAAGAAAACC
151	GGCAAATTCG	CCACTTCCGA	CTGGATGGAA	ATCGAGAAGC	AGCGCGGCAT

```

201 TTCCGTGGCA TCAAGTGTGA TGCAGTTCGA TTACAAAGAC CACACCGTCA
251 ACCTCTTGGA CACGCCGGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTAACCG CCGTGGACAG CGCATTAAATG GTCATCGACG CGGCAAAAGG
351 CGTGGGAAGCG CAAACCATCA AGCTCTTAAA CGTCTGCCGC CTGCGCGATA
401 CACCGATTGT TACGTTTATG AACAAATACG ACCGCGAAGT GCGCGATTCC
451 CTGGAAC TTT TGGACGAAGT GGAAAACATT TAAAAATCC GCTGCGCGCC
501 CGTTACCTGG CCGATCGGTA TGGGCAAAAA CTTCAAGGGC GTGTACCACA
551 TCCTGAACGA TGAAATTTAT CTCTTTGAAG CTGGCGGCGA ACGCCTGCCG
601 CACGAGTTCG ACATCATCAA AGGCATCGAT AATCCTGAAT TGGAACAACG
651 CTTTCCGTTG GAAATCCAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701 CGGCTTCCAA CGAGTTTAAAT CTCGACGAAT TCCTCGCCGG CGAACTCACG
751 CCCGTATTCT TCGGCTCTGC GATTAACAAC TTCGGTATTC AGGAAATCCT
801 CAATTCATTG ATTGACTGGG CGCCC GCGCC GAAACCGCGC GACGCGACCG
851 TACGTATGGT CGAGCCGGAC GAGCCGAAGT TTTCCGGATT TATCTTCAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATTG CCTTCTTGGC
951 CGTCTGCTCC GGCAAATTCG AGCGCGGCAT GAAGATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTGG TTACCTTCAT GTGCGACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGGC GACATTATCG GCATCCCGAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAAC TGG
1151 CGTTCACCGG CATCCCATTC TTCGCACCCG AACTGTTCCG CAGCGTACGC
1201 ATCAAAAACC CGCTGAAAAT CAAACAAC T GCAAAAGGCT TGCAACAGCT
1251 CGGCGAAGAA GGCGCGGTGC AGGTGTTCAA ACCGATGAGC GGCGCGGATT
1301 TGATTTTGGG CGCGGTGCGC GTGTTGCAGT TTGAAGTCGT TACCTCGCGC
1351 CTCGCCAACG AATACGGCGT AGAAGCCGTG TTCGACAGCG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAACTG GCTGAATTTG
1451 AAAAAGCCAA CGCGGGCAAC CTCGCCATCG ACGCAGGCGG CAACCTCGCC
1501 TACCTCGCCC CCAACGCGCT GAATTTGGGA CTCACGCAAG AACGTTGGCC
1551 GGACATCGTG TTCCACGAAA CACGCGAACA TTCGGTCAAA CTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 514; ORF 134>:

m134.pep

```

1 MSQEILDQVR RRRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
51 GKFATSDWME IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRDPITVTFM NKYDREVRDS
151 LELLDEVENI LKIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIKID NPELEQRFPL EIQQRLDEIE LVQAASNEFN LDEFLEGELT
251 PVFFGSAINN FGIQEILNSL IDWAPAPKPR DATVRMVEPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELVEEAYAG DIIGIPNHGN IQIGDSFSEG EQLAFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451 LANEYGVEAV FDSASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 134 shows 98.7% identity over a 531 aa overlap with a predicted ORF (ORF 134.ng) from *N. gonorrhoeae*:

m134/g134

```

          10      20      30      40      50      60
m134.pep  MSQEILDQVRRRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWME
          |||||
g134      MSQEILDQVRRRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWMD
          10      20      30      40      50      60

          70      80      90     100     110     120
m134.pep  IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDSALMVIDAAKGVEA
          |||||
g134      IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDSALMVIDAAKGVEA
          70      80      90     100     110     120

          130     140     150     160     170     180

```

380

m134 . pep	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLLDEVENILKIRCAPVTWPIGMGKNFKG
g134	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLLDEVEDILQIRCAPVTWPIGMGKNFKG
	130 140 150 160 170 180
m134 . pep	VYHILNDEIYLF EAGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN
g134	VYHILNDEIYLF EAGGERLPHEFDIIKGINNPELEQRFPLEIQQLRDEIELVQAASNEFN
	190 200 210 220 230 240
m134 . pep	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATVRMVEPDEPKFSGFIFK
g134	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATMRMVGPDPEPKFSGFIFK
	250 260 270 280 290 300
m134 . pep	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFM SHDRELVEEAYAG
g134	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFM SHDRELAEEAYAG
	310 320 330 340 350 360
m134 . pep	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE
g134	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE
	370 380 390 400 410 420
m134 . pep	GAVQVFKPMSGADLILGAVGV LQFEVVTSRLANEYGV EAVFDSASIWSARVWSCDDKKKL
g134	GAVQVFKPMSGADLILGAVGV LQFEVVTSRLANEYGV EAVFDSASIWSARVWSCDDKKKL
	430 440 450 460 470 480
m134 . pep	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
g134	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
	490 500 510 520 530

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 515>:

```

a134 . seq
1  ATGTCCCAAG AAATCCTCGA CCAAGTGCGC CGCCGCCGCA CGTTTGCCAT
51 CATCTCCAC CCTGACGCAG GTAAAACAC GTTGACTGAA AAACCTTGC
101 TGTTTTCAGG TGCATTCAA AGCGCGGGTA CGGTAAAAGG CAAGAAAACC
151 GGCAAATTCG CCACCTCCGA CTGGATGGAC ATCGAGAAGC AGCGCGGCAT
201 TTCCGTGGCA TCAAGCGTGA TGCAGTTCGA CTATAAGAC CACACCGTCA
251 ACCTTTTGGA CACGCCGGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTGACCG CCGTCGATAG TGCCTTGATG GTCATCGACG CGGCAAAAGG
351 CGTGGAAGCG CAAACCATCA AACTCTTGAA CGTCTGCCGC CTGCGCAATA
401 CGCCGATTGT TACGTTTCATG AACAAATACG ACCGCGAAGT GCGCGATTCC
451 CTGGAATTGC TGGACGAAGT GGAAAACATC CTGCAAAATCC GCTGCGCGCC
501 CGTAACCTGG CCGATCGGCA TGGGCAAAAA CTTCAAAGGC GTGTACCACA
551 TCCTGAACGA CGAAATCTAT CTCTTTGAAG CGGGCGGCGA ACGCTTGCCG
601 CACGAGTTCG ACATCATCAA AGGCATCGAT AATCCCGAAT TGGAAACAACG
651 CTTTCCGTTA GAAATACAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701 CGGCTTCCAA CGAGTTCAAT CTCGACGAAT TCCTCGCCGG CGAATCACG
751 CCCGATTCT TCGGCTCTGC GATTAACAAC TTCGGTATTC AGGAAATCCT
801 CAATTCATTG ATTGAATGGG CGCCCGCGCC GAAACCACGC GATGCGACCG
851 TGCGTATGGT CGAGCCGAC GAGCCGAAGT TTTCCGGATT TATCTTCAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATTG CCTTCTTGCG

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951 CGTCTGCTCC GGCAAATTCG AGCGCGGCAT GAAATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTGG TAACCTTCAT GTCCCACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGGC GACATTATCG GTATCCCAAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACTGA
1151 CGTTTACCGG CATCCCATTG TTCGCGCCCG AACTGTTCCG CAGCGTTCGC
1201 ATCAAAAACC CGCTGAAAAT CAAGCAACTG CAAAAAGGTT TGCAACAGCT
1251 TGGCGAAGAA GGTGCGGTGC AGGTGTTCAA ACCAATGAGC GCGCGGATT
1301 TGATTTTGGG CGCGGTCGGC GTGTTGCAGT TTGAAGTCGT TACCTCGCGC
1351 CTTGCCAACG AATACGGCGT GGAAGCCGTG TTCGACAACG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAAGT GCGGAATTTG
1451 AAAAAGCCAA CGCGGGCAAC CTCGCCATCG ACGCGGGCGG CAACCTCGCC
1501 TACCTCGCCC CTAACCGCGT GAATCTGGGA CTCACGCAAG AACGCTGGCC
1551 GGACATCGTG TTCCACGAAA CGCGCGAGCA TTCGGTCAAA CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 516; ORF 134.a>:

```

a134.pep
1 MSQEILDQVR RRRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
51 GKFATSDWMD IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRNTPIVTFM NKYDREVRDS
151 LELLDEVENI LQIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIGKID NPELEQRFPL EIQLLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFFGSAINN FGIQEILNSL IEWAPAPKPR DATVRMVEPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELVEEAYAG DIIGIPNHGN IQIGDSFSEG EQLTFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451 LANEYGVEAV FDNASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

m134/a134 98.9% identity in 531 aa overlap

```

m134.pep      10      20      30      40      50      60
MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWME
|||||:
a134          10      20      30      40      50      60
MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWMD

m134.pep      70      80      90      100     110     120
IEKQRGISVASSVMQFDYKDHTVNLLDTPGHHQDFSEDYRVLTAVDSALMVIDAAGVEA
|||||:
a134          70      80      90      100     110     120
IEKQRGISVASSVMQFDYKDHTVNLLDTPGHHQDFSEDYRVLTAVDSALMVIDAAGVEA

m134.pep     130     140     150     160     170     180
QTIKLLNVCRRLRDTPIVTFMKNKYDREVRDSLELLDEVENILKIRCAPVTWPPIGMGKNFKG
|||||:
a134         130     140     150     160     170     180
QTIKLLNVCRRLRNTPIVTFMKNKYDREVRDSLELLDEVENILQIRCAPVTWPPIGMGKNFKG

m134.pep     190     200     210     220     230     240
VYHILNDEIYLFEEAGGERLPHEFDIIGKIDNPELEQRFPLEIQQLRDEIELVQAASNEFN
|||||:
a134         190     200     210     220     230     240
VYHILNDEIYLFEEAGGERLPHEFDIIGKIDNPELEQRFPLEIQQLRDEIELVQAASNEFN

m134.pep     250     260     270     280     290     300
LDEFLAGELTPVFFGSAINNFGIQEIILNSLIDWAPAPKPRDATVRMVEPDEPKFSGFIFK
|||||:
a134         250     260     270     280     290     300
LDEFLAGELTPVFFGSAINNFGIQEIILNSLIEWAPAPKPRDATVRMVEPDEPKFSGFIFK

m134.pep     310     320     330     340     350     360
IQANMDPKHRDRIAFRLRVCSGKFERGMKMKHLRINREIAASSSVVTFMSHDRELVEEAYAG
|||||:
a134         310     320     330     340     350     360
IQANMDPKHRDRIAFRLRVCSGKFERGMKMKHLRINREIAASSSVVTFMSHDRELVEEAYAG

```

382

	370	380	390	400	410	420
m134.pep	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
a134	DIIGIPNHGNIQIGDSFSEGEQLTFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m134.pep	GAVQVFKPMSGADLILGAVGVLFQFEVVTSRLANEYGVFAVFDNASIWSARVWSCDDKKKL					
a134	GAVQVFKPMSGADLILGAVGVLFQFEVVTSRLANEYGVFAVFDNASIWSARVWSCDDKKKL					
	430	440	450	460	470	480
	490	500	510	520	530	
m134.pep	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
a134	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 517>:

g135.seq

```

1 ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCG
51 TTCGGAcgGC AGCCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCTG CAGGGTTTCGG CGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CGGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GTGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCGATTCCC ATCATCAATG
401 AAAACGACAC GGTTTCGGTT GAGGAGTTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTTCGGC AAACGGCACG GGCGGTATGC TGACCAAAAT
651 CAAAGCGGCA ACCATCGCCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701 CCTCACTCAA ACCCGATTCA TTGGCCGAAG CCGCCGAACA TCAGGCGGAC
751 GGCTCGTTTT TCGTcccCcg tgCCAAAGGT TTGCGGACAC AGAAGCAATG
801 GctggCGTTC TATTcggaaa gcggGGgcag cgttTAtgtg gacgaaagtg
851 cggaacacgc tTgtccgaa caagggaag cctgCTGA

```

This corresponds to the amino acid sequence <SEQ ID 518; ORF 135.ng>:

g135.pep

```

1 MKYKRIVFKV GTSSITRSDG SLSRGIQTI TRQLAALHHA GHELVLVSSG
51 AVAAGFGALG FKRPVKIAD KQASAAVQGG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRRAIP IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGNPNS NPDAVRLDKI EHNHEI IEM
201 AGGSGSANGT GGMLTKIKAA TIAAESGVPV YICSSLKPDS LAEAAEHQAD
251 GSFFVPRAKG LRTQKQWLAF YSESGSVYV DESAEHALSE QGKAC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 519>:

m135.seq

```

1 ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51 TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCTGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCGG CAGGGTTTCGG TGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CGGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCGCAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTTCGGTT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT

```

```

501  GACCGACATA GACGGTCTTT ACACGGGCAA CCCGAACAGC AATCCCAGTG
551  CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601  GCGGGCGGCT CGGGTTCGGC AAACGGCACG GCGGGTATGC TGACCAAAAT
651  CAAAGCGGCA ACCATCGCCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701  CCTCGCTCAA ACCCGATGCA CTTGCCGAAG CTGCCGAACA TCAGGCGGAC
751  GGCTCGTTTT TCGTCCCCCG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801  GCTGGCGTTC TATTCCGAAA GCCGGGGCAG CGTTTATGTG GACGAAGGTG
851  CGGAACACGC TTTGTCCGAA CAGGGGAAAA GCCTGCTGAT GTCGGGCATT
901  GCCGGAATCG AAGGGCATT TCCCGTATG GACACCGTAA CCGTGACAG
951  CAAGGCAACC AAACAGCCCC TGGGCAAAGG GCGCGTCCTG TTCGGCTCTG
1001 CCGCCGCCGA AGACCTGCTC AAATCGCGTA AGGCGAAAGG CGTGTCATC
1051 CATCGGACG ACTGGATTTC CATCACGCCC GAAATACGCC TGCTTCTGAC
1101 CGAATTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 520; ORF 135>:

```

m135.pep
1  MKYKRIVFKV GTSSITHSDG SLRSGKIQTI TCQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRVAP IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGPNPS NPDAVRLDKI EHINHEIEM
201 AGGSGSANGT GGMLTKIKAA TIAESGVVP YICSSLKPDA LAEAAEHQAD
251 GSFFVPRAKG LRTQKQWLAF YSESRGSVYV DEGAEHALSE QGKSLLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAAEDLL KSRKAKGVFI
351 HRDDWISITP EIRLLLLTEF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 135 shows 97.6% identity over a 294 aa overlap with a predicted ORF (ORF 135.ng) from *N. gonorrhoeae*:

m135/g135

	10	20	30	40	50	60
m135.pep	MKYKRIVFKVGTSSITHSDGSLRSGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG					
g135	MKYKRIVFKVGTSSITRSDGSLRSGKIQTITRQLAALHHAGHELVLVSSGAVAAGFGALG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m135.pep	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLSRADFADKRRYQNAGGAL					
g135	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLSRADFADKRRYQNAGGAL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m135.pep	SVLLQRRVAPIINENDTVSVEELKIGDNDTL SAQVAAMIQADLLVLLTDIDGLYTGPNPS					
g135	SVLLQRRAPIINENDTVSVEELKIGDNDTL SAQVAAMIQADLLVLLTDIDGLYTGPNPS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m135.pep	NPDAVR LD KIEHINHEIEMAGGSGSANGTGGMLTKIKAATIAESGV VP YICSSLK PD A					
g135	NPDAVR LD KIEHINHEIEMAGGSGSANGTGGMLTKIKAATIAESGV VP YICSSLK PD S					
	190	200	210	220	230	240
	250	260	270	280	290	300
m135.pep	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSESRGSVYVDEGAEH AL SEQGKSLLMSGI					
g135	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSESGSVYVDESAEH AL SEQGKACX					
	250	260	270	280	290	
	310	320	330	340	350	360

384

m135.pep AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFSGAAAEDLLKSRKAKGVFIHRDDWISITP

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 521>:

```

a135.seq
1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCGG CAGGGTTCGG TCGCTGCGG TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CCGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGGTT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCCAGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTCCGGC AAACGGCACA GCGGGTATGC TGAATAAAAT
651 CAAAGCGGCG ACGATTGCGA CCGAGTCCGG CGTACCGGTC TATATCTGTT
701 CCTCGCTCAA ACCCGATGCA CTTGCCGAAG CGGCAGATAA TCAGGCGGAC
751 GGCTCGTTTT TCGTCCCCCG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801 LTTGGCGTTC TATTCGAAA GCAGGGGCGG CGTTTATGTG GACGAAGGTG
851 CGGAACACGC TTTGTCCGAA CAGGGAAAAA GCCTGCTGAT GTCGGGCATT
901 GCCGGAATCG AAGGGCATTT TTCCCGTATG GACACCGTAA CCGTGTACAG
951 CAAGGCAACC AAACAGCCTT TGGGCAAAGG GCGAGTCCTG TTCGGCTCTG
1001 CCGCCGCCGA AGACCTGCTC AAATTGCGTA AGGCGAAAGG CGTGTTCATC
1051 CATCGGGACG ACTGGATTTC CATCACGCC GAAATACGCC TGCTTCTGAC
1101 CGAATTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 522; ORF 135.a>:

```

a135.pep
1  MKYKRIVFKV GTSSITHSDG SLRSGKIQTI TRQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRAPV IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGNPNS NPDAVRLDKI EHINHEIIEI
201 AGGSGSANGT GGMLTKIKAA TIATESGVPV YICSSLKPDA LAEAAADNQAD
251 GSFFVPRAKG LRTQKQWLAF YSESRGGVYV DEGAEHALSE QGKSLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAAEDLL KLRKAKGVFI
351 HRDDWISITP EIRLLLTEF*

```

m135/a135 98.4% identity in 369 aa overlap

	10	20	30	40	50	60
m135.pep	MKYKRIVFKVGTSSITHSDGSLRSGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG					
a135	MKYKRIVFKVGTSSITHSDGSLRSGKIQTITRQLAALHHAGHELVLVSSGAVAAGFGALG					
	10	20	30	40	50	60
m135.pep	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
a135	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
	70	80	90	100	110	120
m135.pep	SVLLQRRAPVIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTNPNS					
a135	SVLLQRRAPVIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTNPNS					
	130	140	150	160	170	180
m135.pep	NPDAVRLDKIEHINHEIEMAGGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPDA					
a135	NPDAVRLDKIEHINHEIEMAGGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPDA					
	190	200	210	220	230	240

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	250	260	270	280	290	300
m135.pep	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSES	SRGSVYVDEGAEHALSEQ	GKSLMSGI			
	:					
a135	LAEAADNQADGSFFVPRAKGLRTQKQWLAFYSES	SRGGVYVDEGAEHALSEQ	GKSLMSGI			
	250	260	270	280	290	300
	310	320	330	340	350	360
m135.pep	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLF	GSAAAEDLLKSRKAKGVFIHRDDWISITP				
a135	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLF	GSAAAEDLLKLRKAKGVFIHRDDWISITP				
	310	320	330	340	350	360
	370					
m135.pep	EIRLLLTEFX					
a135	EIRLLLTEFX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 523>:

```

g136.seq
1  ATGGAAATCC GGTTCAGAC AGCATTTTTA CGTTTGGTTC AGatgaAAAC
51  AACGCTtca aTTCtaccg caACACGCCT TGTATTCCT GccgCTGCCG
101 CACGACAGG GATCGTTCCT GCCGgtTTTT TCCCTTCCC TCGGACGGT
151 TTGCGGTTT TGTATGACCG CCTGCCAGTA GCGGTAGATG Tctgccagcg
201 cgTAAGGCag tTCGGAcgca agttccgccca gctcgccctc ggTGAATTGC
251 AGgcgataa cgccgtttTC CTCTTCGTcG taaatgccgc ccactgccat
301 cacgGGGTAA AACAGCTCTT CAAACGCTTC ATCATCGGCG GCTTCAAACC
351 AATCGGTCGG CACAATGTCC AAACCGTAAA GATAGGCGTT GCACCAAGTG
401 TAAAAATCGC TGCCGCCCTC GCCGTCTCG TAGAGCCACA AATCGGGCAG
451 CTTTtATCC GACATCGCGG CGGTTGTTTC CATCGCCATT GCCAAAACCA
501 GCCGTTCGAT TTCGGAACGT TCGGCGGCGG TAAATTGCGA TTCGTGCCCC
551 AACACTTCGG GCAGCCAGTC GAGCGGTGCC AATTtGTCCG GCCCGCTCAA
601 CAGCGCCGTC ATAAACCTT GAACCTCGTC GCAACGCATC GTGTTGCCTT
651 GTTCGCTTTT GGCATCCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 524; ORF 136.ng>:

```

g136.pep
1  MEIRFQTAF LRLVQMKTNAS ILTATRLVFP AAAARTGIVP AGFFPFPADG
51  LRFVDDR L P V AVDVCQRVRQ FGRKFRQLAF GELQADNAV L FV V N A A H C H
101 HGVKQLFKRF I IGGFKPIGR HNVQTVKIGV APSVKIAAAL AVVVEPQIGQ
151 LFIHRGGCF HRHCQNQPF D FGTFGGGKLR FVAQHFGQPV ERCQFVRPAQ
201 QRRHKT L N L V A T H R V A L F A F G I Q *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 525>:

```

m136.seq
1  ATGGAAACAA ACGCTTCAAT TCTTACCGCA ACACGCCTTG TATTTTCTGC
51  CGCTGCCGCA CGGACAGGGA TCGTTCCTGC CTGTTTTTTC GCCTTCCCTG
101 CGGACGGTTT GCGGTTTGTT GATGACTGCC TGCCAGTAGC GGTAGATATC
151 CGCCAATGCA TAAGGCAACT CGGATTCCAG TTCCGCCAGC TCGCCTTCTG
201 TGAATTGCAG ACGGATAGCG CCGTTTTCTT CTTCGTCGTA AATACCGCCC
251 AATGCCATGA TGGGATAAAA CAACTCTTCA AACGCTTCAT CATCGACGGC
301 TTCAAACCAA TCGGTCGGCA CAATATCCAA ACCGTAAAGA TAAGCATTCG
351 ACCATGTGTA AAAATCGCTG CCGCCGTCTT CGTTTTATA CAGCCACAAA
401 TCGGGCAGTT TTTTATCCGA CATCGCGGCG GTTGTTTCCA TCGCCATTGC
451 CAAAACCAGC CGTTCGATT TCGGAACGTT GCGGCGGTA AATTGCGATT
501 CGTCGCCCAA CACTTCGGGC AGCCAGTCGA GCGGTGTCAA TTTGTCCGGC
551 CCGCTCAACA GCGCCGTCAT AAAACCTTGA ACCTCGTCGC AACGCATCGT
601 GTTGCCCTGT TCGCTTTTGG CATCCAACAA TTCGCTCAAC CGCCGTTTGG
651 ATGCTTCGGT AAATTTTCGG GAATCCATCA TTTTCCTTTT CAAATGGGTT
701 TTGCGCCCTA TTATCGCCGC AATGCCGTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 526; ORF 136>:

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```

m136.pep
1  METNASILTA  TRLVFSAAAA  RTGIVPACFF  AFPADGLRFV  DDCLPVAVDI
51  RQCIRQLGFQ  FRQLAFCELO  TDSAVFLFVV  NTAQCHDGIK  QLFKRFIIDG
101 FKPIGRHNIQ  TVKISIAPCV  KIAAAVFVFI  QPQIGQFFIR  HRGGCFHRHC
151 QNQPFDGTF  GGGKLRFVAQ  HFGQPVERCQ  FVRPAQQRH  KTLNLVATHR
201 VALFAFGIQQ  FAQPPFGCFG  KFSGIHHFPF  QMGFAPYYRR  NAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 136 shows 85.6% identity over a 209 aa overlap with a predicted ORF (ORF 136.ng) from *N. gonorrhoeae*:

m136/g136

```

                                10      20      30      40
m136.pep      METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRFVDDCLPV
                |:||||||||||||| | | | | | | | | | | | | | | | |
g136           MEIRFQTAFRLRLVQMKTNASILTATRLVFPAAAARTGIVPAGFFPFPADGLRFVDDRLPV
                10      20      30      40      50      60

                                50      60      70      80      90      100
m136.pep      AVDIRQCIRQLGFQFRQLAFCELOTD SAVFLFVVNTAQCHDGIKQLFKRFIIDGFKPIGR
                ||:| | :||:| :||||| ||:|:||||| ||:| | :||||| | | | | |
g136           AVDVCQVRVQFGRKFRQLAFGELQADNAVFLFVVNAAHCHHGKQLFKRFIIGGFKPIGR
                70      80      90      100     110     120

                                110     120     130     140     150     160
m136.pep      HNIQTVKISIAPCVKIAAAVFVFIQPQIGQFFIRHRGGCFHRHCQNQPFDGTFGGGKLR
                ||:|||||:| | | | | : | :| | | | | | | | | | | | | | | |
g136           HNVQTVKIGVAPSVKIAAALAVVVEPQIGQLFIRHRGGCFHRHCQNQPFDGTFGGGKLR
                130     140     150     160     170     180

                                170     180     190     200     210     220
m136.pep      FVAQHFGQPVERCQFVRPAQQRHKTNLNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIH
                ||| | | | | | | | | | | | | | | | | | | | | | | |
g136           FVAQHFGQPVERCQFVRPAQQRHKTNLNLVATHRVALFAFGIQX
                190     200     210     220

                                230     240
m136.pep      HFPPQMGFAPYYRRNAVX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 527>:

```

a136.seq
1  ATGGAAACAA  ACGCTTCAAT  TCTTACCGCA  ACACGCCTTG  TATTTTCTGC
51  CGCTGCCGCA  CGGACAGGGA  TCGTTCCGTC  CTGTTTTCCT  GCCTTCCTG
101 CGGACGGTTT  GCGGCTTGTT  GATGACCGCC  TGCCAGTAGC  GGTAGATATC
151 CGCCAATGCA  TAAGGCAACT  CGGATTCCAG  TTCCGCCAGC  TCGCCTTCTG
201 TGAATTGCAG  ACGGATAGTG  CCGTTGTCTT  CTTCGTCGTA  AATACCGCCC
251 AATGCCATGA  TGGGATAAAA  CAACTCTTCA  AACGCTTCAT  CATCGACGGC
301 TTCAAACCAA  TCGGTCGGCA  CAATATCCAA  ACCGTAAAGA  TAAGCATTGC
351 ACCATGTGTA  AAAATCGCTG  CCGCCGTCTT  CGTTTTCATA  CAGCCACAAA
401 TCGGGCAGTT  TTTTATCCGA  CATCGCGGCG  GTTGTTCCTA  TCGCCATTGC
451 CAAAACCAGC  CGTTCGATTT  CGGAACGTC  GCGCGCGGTA  AATTGCGATT
501 CGTCGCCCAA  CACTTCGGGC  AGCCAGTCGA  GCGGTGTCAA  TTTGTCCGGC
551 CCGCTCAACA  GCGCCGTCAT  AAAACCTTGA  ACCTCGTCGC  AACGCATCGT
601 GTTGCCCTGT  TCGCTTTTGG  CATCCAACAA  TTCGCTCAAC  CGCCGTTTGG
651 ATGCTTCGGT  AAATTTTCGG  GAATCCATCA  TTTTCCTTTT  CCAATGGGTT
701 TTGCGCCCTA  TTATAGTGGA  TTAAATTAA  ATCAGGACAA  GGCGACGAAG
751 CCGCAGACAG  TACAAATAGT  ACGGCAAGGC  GAGGCAACGC  CGTACTGGTT
801 TAAATTTAAT  CCACTATATC  GCCGCAATGC  CGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 528; ORF 136.a>:

a136.pep

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```

1  METNASILTA  TRLVFSAAAA  RTGIVPACFF  AFPADGLRLV  DDRLPVAVDI
51  RQCIRQLGFQ  FRQLAFCELO  TDSAVVLFVV  NTAQCHDGIK  QLFKRFIIDG
101 FKPIGRHNIQ  TVKISIAPCV  KIAAAVFVEI  QPQIGQFFIR  HRGGCFHRHC
151 QNQPFDFGTF  GGGKLRFVAQ  HFGQPVERCQ  FVRPAQQRH  KTLNLVATHR
201 VALFAFGIQQ  FAQPPFGCFG  KFSGIHHFPP  PMGFAPYYSG  LNLNQDKATK
251 PQTQIVRQG  EATPYWFKFN  PLYRRNAV*

```

m136/a136 98.3% identity in 238 aa overlap

	10	20	30	40	50	60
m136.pep	METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRFVDDCLPVAVDIRQCIRQLGFQ					
a136	METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRLVDDRLLPVAVDIRQCIRQLGFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m136.pep	FRQLAFCELOTDASAVVLFVVNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV					
a136	FRQLAFCELOTDASAVVLFVVNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m136.pep	KIAAAVFVFIQPIQIGQFFIRHRGGCFHRHCQNQPFDFGTFGGGKLRFVAQHFGQPVERCQ					
a136	KIAAAVFVFIQPIQIGQFFIRHRGGCFHRHCQNQPFDFGTFGGGKLRFVAQHFGQPVERCQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m136.pep	FVRPAQQRHKTNLNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFPPMGFAPYYRR					
a136	FVRPAQQRHKTNLNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFPPMGFAPYYSG					
	190	200	210	220	230	240
m136.pep	NAVX					
a136	LNLNQDKATKPQTQIVRQGEATPYWFKFNPLYRRNAVX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 529>:

g137.seq

```

1  ATGATTATCC  ATCACcaaTT  CGATCCCGTC  CTCATCAGTA  TCGGCCCGCT
51  TGCCGTCCGC  TGGTATGCCT  TAAGCTACAT  CCTCGGATTT  ATTCTTTTTA
101 CCTTTCTCGG  CAGAAGGCGC  ATCGCGCAAG  GCTTGTCCGT  TTTTACCAAA
151 GAATCGCTCG  ACGACTTCCT  GACATGGGGC  ATTTTGGGCG  TGATTTTGGG
201 CGGACGCTTG  GGCTATGTCC  TGTTTTACAA  ATTCTCCGAC  TACCTCGCCC
251 ATCCGCTTGA  TATTTTCAAG  GTATGGGAAG  GCGGAATGTC  GTTCCACGGC
301 GGCTTTTGG  GTGTAGTTAT  TGCCATATGG  TTGTTCAGCC  GCAAGCACGG
351 CATCGGCTTC  CTCAAAGTGA  TGGACACGGT  CGCGCCGCTC  GTTCCGCTGG
401 GTCTCGCTTC  GGGACGTATC  GGCAACTTTA  TCAACGGCGA  ACTTTGGGGA
451 CGCATTACCG  ACATTAACGC  ATTTTGGGCA  ATGGGCTTCC  CGCAAGCGCA
501 TTACGAAGAT  GCCGAAGCCG  CCGCGCACAA  TCCGCTTGG  GCAGAATGGC
551 TGCAACAATA  CGGTATGCTG  CCGCGTCATC  CCTCGCAGCT  TTATCAGTTT
601 GCCCTTGAAG  GCATCTGCCT  GTTCGCCGTC  GTTTGGCTGT  TTTCCAAAAA
651 ACCGCGCCCG  ACCGGGCAGA  CTGCCGCGCT  TTTTCTCGGC  GGCTACGGCG
701 TGTTCGCTT  TATTGCCGAA  TTTGCCGCGC  AACCCGACGA  CTATCTCGGG
751 CTGCTGACCT  TGGGGCTGTC  GATGGGGCAA  TGGTTGAGCG  TCCCGATGAT
801 TGTTTTGGGT  ATCGTCGGCT  TTGTCCGGTT  CGGCATGAAA  AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 530; ORF 137.ng>:

g137.pep

```

1  MIIHHQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTGW ILGVILGGRL GYVLFYKFSD YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIW LFSRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINDELWG
151 RITDINAFWA MGFPQAHYED AEAAAHNPLW AEWLQOYGML PRHPSQLYQF
201 ALEGICLFAV VWLFSKKPRP TGQTAALFLG GYGVFRFIAE FARQPDDYLG
251 LTLGLSMGQ WLSVPMIVLG IVGFVRFGMK KQH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 531>:

```

m137.seq
1  ATGATTACCC ATCCCCAATT CGATCCCGTC CTTATCAGTA TCGGCCCCGCT
51  TGCCGTCCGC TGGTATGCCC TAAGCTACAT CCTCGGATTT ATCTTTTSTA
101 CCTTCTCGG CAGAAGCGC ATCGCGCAAG GCTTGTCCTG TTTTACCAA
151 GAATCGCTCG ACGACTTCCT GACATGGGGC ATTTTGGGCG TAATTTGGG
201 CGGGCGTTTG GGTACGTCC TGTTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG GCGGAATGTC GTTCCACGGC
301 GGCTTTTTTG GTGTAGTTAT TGCCATACGG TTGTTCGGCC GCAAACACGG
351 CATCGGCTTC CTCAAACTGA TGGATACGGT CGCACCGCTC GTTCCGCTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTCA TCAACGGCGA ACTTTGGGGA
451 CGCGTTACCG ACATCAACGC ATTTTGGGCA ATGGGCTTCC CGCAGGCGCG
501 TTACGAAGAT GCCGAAGCCG CCGCGCACAA TCCGCTTTGG GCAGAATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGCAGCT TTATCAGTTT
601 GCACTTGAAG GCATCTGCCT GTTACCGGTC ATTTGGCTGT TCTCTAAAAA
651 ACAGCGGTCG ACCGGACAAG TCGCCTCGCT CTCCTCGGC GGCTACGGCA
701 TATTCGCTT CATTGCCGAA TTCGCACGCC AACCCGACGA CTATCTCGGG
751 CTGCTGACCT TGGGCTGTC GATGGGGCAA TGGTTGAGCG TCCCGATGAT
801 TGTTTTGGGT ATCGTCGGCT TTGTCCGGTT CGGCATGAAA AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 532; ORF 137>:

```

m137.pep
1  MITHPQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTGW ILGVILGGRL GYVLFYKFSD YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIR LFSRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINDELWG
151 RVTDINAFWA MGFPQARYED AEAAAHNPLW AEWLQOYGML PRHPSQLYQF
201 ALEGICLFTV IWLFSKKQRS TGQVASLFLG GYGI FRFIAE FARQPDDYLG
251 LTLGLSMGQ WLSVPMIVLG IVGFVRFGMK KQH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 137 shows 95.4% identity over a 283 aa overlap with a predicted ORF (ORF 137.ng) from *N. gonorrhoeae*:

m137/g137

	10	20	30	40	50	60
m137.pep	MITHPQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW					
g137	MIIHHQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW					
	10	20	30	40	50	60
m137.pep	ILGVILGGRLGYVLFYKFSDYLAHPLDIFKVWEGGMSFHGGFLGVVIAIRLFSRKHGIGF					
g137	ILGVILGGRLGYVLFYKFSDYLAHPLDIFKVWEGGMSFHGGFLGVVIAIWLFSRKHGIGF					
	70	80	90	100	110	120
m137.pep	LKLMDTVAPLVPLGLASGRIGNFINDELWGRVTDINAFWAMGFPQARYEDAEAAAHNPLW					
g137	LKLMDTVAPLVPLGLASGRIGNFINDELWGRITDINAFWAMGFPQAHYEDAEAAAHNPLW					
	130	140	150	160	170	180
m137.pep	AEWLQOYGMLPRHPSQLYQFALEGICLFTVIWLFSKKQRSTGQVASLFLGGYGI FRFIAE					
g137	AEWLQOYGMLPRHPSQLYQFALEGICLFTVIWLFSKKQRSTGQVASLFLGGYGI FRFIAE					
	190	200	210	220	230	240
m137.pep	AEWLQOYGMLPRHPSQLYQFALEGICLFTVIWLFSKKQRSTGQVASLFLGGYGI FRFIAE					
g137	AEWLQOYGMLPRHPSQLYQFALEGICLFTVIWLFSKKQRSTGQVASLFLGGYGI FRFIAE					

389

```

g137      |||||:|:|||||:|:|||||:|:|||||
          AEWLQQYGMLPRHPSQLYQFALEGICLFAVVWLFSSKKPRPTGQTAALFLGGYGVFRFIAE
          190      200      210      220      230      240

          250      260      270      280
m137.pep  FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFMGKKQH
          |||||:|:|||||:|:|||||:|:|||||
g137      FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFMGKKQH
          250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 533>:

```

a137.seq
1  ATGATTACCC ATCCCAATT CGACCCCGTC CTTATCAGTA TCGGCCCGCT
51  TGCCGTCGCC TGGTATGCC TAAGCTACAT CCTCGGATTT ATTCTTTTTA
101 CCTTCTCGG CAGAAGCGC ATCGCGCAAG GCTTGTCCGT TTTACCAA
151 GAATCGCTCG ACGACTTCCT GACATGGGCG ATTTTGGGCG TAATTTTGGG
201 CGGGCGTTTG GGTACGTCC TGTTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG GCGGAATGTC GTCCACGGC
301 GGCTTTTTTG GTGTAGTTAT TGCCATATGG TTGTTCCGTC GCAAACACGG
351 CATCGGCTTC CTCAAACCTGA TGGACACGGT CGCACCGCTC GTTCCACTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTCA TCAACGGCGA ACTTTGGGGA
451 CGCGTTACCG ACATCAACGC ATTTTGGGCA ATGGGCTTCC CGCAGGCGCG
501 TTACGAAGAC CTCGAAGCCG CCGCGCACAA TCCGCTTTGG GCAGAATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGCAGCT TTATCAGTTT
601 GCACTTGAAG GCATCTGCCT GTTCGCCGTC GTTTGGCTGT TCTCTAAAAA
651 ACAGCGGCCG ACCGGACAAG TCGCCTCACT CTTCCTCGGC GGCTACGGCA
701 TATTCCGCTT CATTGCCGAA TTTGCACGCC AACCCGACGA CTATCTCGGG
751 CTGCTGACCT TGGGGCTGTC GATGGGGCAA TGTTGAGCG TCCCGATGAT
801 TGTTTTGGGT ATCGTCGGCT TTGTCCGGTT CGGCATGAAA AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 534; ORF 137.a>:

```

a137.pep
1  MITHPQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTGW ILGVILGGRL GYVLFYKFSD YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIW LFGRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINDELWG
151 RVTDINAFWA MGFPQARYED LEAAAHNPLW AEWLQQYGML PRHPSQLYQF
201 ALEGICLFAV VWLFSSKKQRP TGQVASLFLG GYGIFRFIAE FARQPDDYL
251 LLTLGLSMGQ WLSVPMIVLG IVGFVRFMGK KQH*

```

m137/a137 98.2% identity in 283 aa overlap

```

m137.pep      10      20      30      40      50      60
MITHPQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW
|||||
a137          10      20      30      40      50      60
MITHPQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW
|||||

m137.pep      70      80      90      100     110     120
ILGVILGGRLGYVLFYKFSDYLAHPLDIFKVWEGGMSFHGGFLGVVIAIRLFGRKHGIGF
|||||
a137          70      80      90      100     110     120
ILGVILGGRLGYVLFYKFSDYLAHPLDIFKVWEGGMSFHGGFLGVVIAIWLFGGRKHGIGF
|||||

m137.pep     130      140      150      160      170      180
LKLMDTVAPLVPLGLASGRIGNFINDELWGRVTDINAFWAMGFPQARYEDAEAAAHNPLW
|||||
a137         130      140      150      160      170      180
LKLMDTVAPLVPLGLASGRIGNFINDELWGRVTDINAFWAMGFPQARYEDLEAAAHNPLW
|||||

m137.pep     190      200      210      220      230      240
AEWLQQYGMLPRHPSQLYQFALEGICLFTVIWLFSSKKQORSTGQVASLFLGGYGYFRFIAE
|||||:|:|||||
a137         190      200      210      220      230      240
AEWLQQYGMLPRHPSQLYQFALEGICLFAVVWLFSSKKQORPTGQVASLFLGGYGYFRFIAE
|||||:|:|||||

```

390

	190	200	210	220	230	240
	250	260	270	280		
m137.pep	FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQH	X				
a137	FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQH	X				
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 535>:

g138.seq

```

1   ATGGAGTTTG AAAACATTAT TTCCGCCGCGc gaCAAGGCGC GTATCCTTGC
51  CGAAGCACTG CCTTACAtcc gccgGTTTTC CGGTTCCGTC GCCGTCATCA
101 AGTATGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGA AAAAGTC GGCAAAAAGG
251 GCGAATTTGT CCAAGGAATG CGCGTTACCG ACAAAAGAGAC GATGGATATT
301 GTCGAAATGG TATTGGGCGG GCACGTCAAC AAGGAAATCG TGTCGATGAT
351 TAACACATAT GGAGGGCACG CGGTCGGCGT GAGCGGGCGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGGTCGATA CGCCCGAACA GAATAGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGCGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGGT GGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAAtatcgc
651 cgGTGTGATG GACAAAACGG GCAATCTGCT GACCAAACCTC acgCCGAAAC
701 GGATTGATGG GCTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCcgccgtc aACGGTGTGA AAGCCACGCA
801 CATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGGTAT CGGGTCGATG ATTTTAGGCA GAGGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 536; ORF 138.ng>:

g138.pep

```

1   MEFENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
51  RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVDKETMDI
101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LVDTPQNSV
151 DIGQVGTVES IDTGLVKGLI ERGCI PVVAP VGVGEKGEAF NINADLVAGK
201 LAEELNAEKL LMMTNIAQVM DKTGNLLTKL TPKRIDGLIA DGTLYGGMLP
251 KIASAVEAAV NGVKATHIID GRLPNALLLE IFTDAGIGSM ILGRGEDA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 537>:

m138.seq

```

1   ATGGAGTCTG AAAACATTAT TTCCGCCGCC GACAAGGCGC GTATCCTTGC
51  CGAAGCGCTG CCTTACATCC GCCGGTTTTC CGGTTCCGTC GCCGTCATCA
101 AATACGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGA AAAAGTC GGCAAAAAGG
251 GTGAGTTTGT CCAAGGAATG CGCGTTACCG ACAAAAGAGG C GATGGATATT
301 GTCGAAATGG TGTTGGGCGG GCATGTCAAT AAAGAAATCG TGTCGATGAT
351 TAACACATAT GGCGGACACG CGGTCGGCGT AAGCGGACGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGATCGATA CGCCCGAACA GAATGGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGTGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGGT AGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAATATCGC
651 CGGTGTGATG GACAAAACGG GCAATCTGCT GACCAAACCTC ACGCCGAAAC
701 GGATTGATGA ACTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCCGCCGTC AACGGTGTGA AAGCCACGCA
801 TATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGGTAT CGGTTTCGAT ATTTTGGGCG GTGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 538; ORF 138>:

m138.pep

```

1   MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA

```

```

51  RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKAMDI
101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV
151 DIGQVGTVES IDTGLVKGLI ERGCI PVVAP VGVGEKGEAF NINADLVAGK
201 LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDELIA DGTLYGGMLP
251 KIASAVEAAV NGVKATHIID GRLPNALLLE IFTDAGIGSM ILGGGEDA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 138 shows 98.0% identity over a 298 aa overlap with a predicted ORF (ORF 138.ng) from *N. gonorrhoeae*:

m138/g138

	10	20	30	40	50	60
m138.pep	MESENII SAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVLLKLVG					
g138	MEFENII SAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVLLKLVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m138.pep	IHPVIVHGGGPQINAMLEKV GKKGEFVQGM RVTDKAMDI VEMVLGGHVNKEIVSMINTY					
g138	IHPVIVHGGGPQINAMLEKV GKKGEFVQGM RVTDKETMDI VEMVLGGHVNKEIVSMINTY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m138.pep	GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV DIGQVGTVES IDTGLVKGLIERGCI PVVAP					
g138	GGHAVGVSGR DDHFIKAKKL LVDTP EQNSVDIGQVGTVES IDTGLVKGLIERGCI PVVAP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m138.pep	VGVGEKGEAF NINADLVAGK LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDELIA					
g138	VGVGEKGEAF NINADLVAGK LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDGLIA					
	190	200	210	220	230	240
	250	260	270	280	290	299
m138.pep	DGTLYGGMLPKIASAVEAAV NGVKATHIID GRLPNALLLE IFTDAGIGSM ILGGGEDAX					
g138	DGTLYGGMLPKIASAVEAAV NGVKATHIID GRLPNALLLE IFTDAGIGSM ILGRGEDAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 539>:

a138.seq

```

1  ATGGAGTCTG AAAACATTAT TTCCGCCGCC GACAAGGCGC GTATCCTTGC
51  CGAAGCGCTG CCTTACATCC GCCGTTTTC CGGTTCGGTC GCCGTCATCA
101 AATACGCGCG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GTGAGTTTGT CCAAGGAATG CGCGTTACCG ACAAAGAGGC GATGGATATT
301 GTCGAAATGG TGTTGGGCGG GCATGTCAAT AAAGAAATCG TGTCGATGAT
351 TAACACATAT GGCGGACACG CGGTCGGCGT AAGCGGACGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGATCGATA CGCCGAACA GAATGGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGTGGCT GCATTCCCGT CGTCGCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGT AGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAATATCGC
651 CCGTGTGATG GACAAAACG GCAATCTGCT GACCAAACG ACGCCGAAAC
701 GGATTGATGA ACTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCCGCCGTC AACGGCGTGA AAGCCACGCA
801 TATCATCGAC GGCAGGGTGC CCAACGCGCT TTTGCTGGA ATCTTTACCG
851 ATGCCGGTAT CGGTTCGATG ATTTTGGGCG GTGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 540; ORF 138.a>:

```
a138.pep
  1  MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
 51  RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKAEMDI
101  VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV
151  DIGQVGTVES IDTGLVKGLI ERGCIPVVAP VGVGEKGEAF NINADLVAGK
201  LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDELIA DGTLYGGMLP
251  KIASAVEAAV NGVKATHIID GRVNPALLLE IFTDAGIGSM ILGGGEDA*
```

m138/a138 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m138.pep	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
a138	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m138.pep	IHPVIVHGGGPQINAMLEKVGKKGEFVQGM RVTDKAEMDIVEMVLGGHVNKEIVSMINTY					
a138	IHPVIVHGGGPQINAMLEKVGKKGEFVQGM RVTDKAEMDIVEMVLGGHVNKEIVSMINTY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m138.pep	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCIPVVAP					
a138	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCIPVVAP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m138.pep	VGVGEKGEAFNINADLVAGKLAEEELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
a138	VGVGEKGEAFNINADLVAGKLAEEELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
	190	200	210	220	230	240
	250	260	270	280	290	299
m138.pep	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRLPNALLLEIFTDAGIGSMILGGGEDAX					
a138	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRVNPALLLEIFTDAGIGSMILGGGEDAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 541>:

```
g139.seq
  1  ATGCGAACCA CCTCAACCTT CCCTACAAAA ACTTTCAAAC CGGCTGCCAT
 51  GGC GTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAggc ggcggcggag
101  gcGGCACTTC TGCTCCCGAC TTTAATGCAG GCGGCACCGG TATCGGCAGC
151  AACAGCAGGG CAACGATAGC GGAATCAGCA GCAGTATCTT ACGCCGGTAT
201  AAAAAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTCCGGATG
251  ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAAAGCCCC CCGAATCTGC
301  ATACCGGAGA CTTTTCAAAC CCAAATGACC AATATTAAGA ATATGATCAA
351  CCTCAAACCT GCAATTGAAG CAGGCTATAC AGGACGCGGG GTAGAGGTAG
401  GTATCGTCGA TACAGGCGAA TCCGTCGGCA GCATATCCTT TCCCGAACTG
451  TATGGCAGAA AAGAACACGG CTATAACGAA AATTACAAAA ACAAAATTACA
501  AAAACTATAC GCGGTATATG CGGAAGGAAG CGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 542; ORF 138.ng>:

```
g139.pep
  1  MRTTSTFPTK TFKPAAMALA VATTLSACLG GGGGTSAPD FNAGGTGIGS
 51  NSRATIAESA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKIKAPRIC
101  IPETFQTQMT NIKNMINLKP AIEAGYTGRG VEVGIVDTGE SVGSISFPPEL
151  YGRKEHGYNE NYKNKLQKLY GVYAEGSA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 543>:

```
m139.seq
1   ATGCGAACGA CCCCAACCTT CCCTACAAAA ACTTTCAAAC CGACTGCCAT
51  GCGGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAGGC GGCGGCGGAG
101 GCGGCACTTC TGCGCCCGAC TTCAATGCAG GCGGTACCGG TATCGGCAGC
151 AACAGCAGAG CAACAACAGC GAAATCAGCA GCAGTATCTT ACGCCGGTAT
201 CAAGAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTCTGGGATG
251 ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAATGCCCC CCCCCGAATC
301 TGCATACCGG AGACTTTCCA AACCCTAAATG ACGCATtACA AGAATTTGAT
351 CAACCTCAAA CCTGCAATTG AAGCAGGCTA TACAGGACGC GGGGTAGAGG
401 TAGGTATCGT CGACACAGGC GAATCCGTCG GCAGCATATC CTTTCCCGAA
451 CTGTATGGCA GAAAAGAACA CGGCTATAAC GAAAATTACG AAAAATAATA
501 CGGCGTATAT GCGGAAGGAA GCGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 544; ORF 138>:

```
m139.pep
1   MRTTPTFPTK TFKPTAMALA VATTLSACLG GGGGGTSAPD FNAGGTGIGS
51  NSRATTAKSA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPRI
101 CIPETFQTM THYKNLINLK PAIEAGYTGR GVEVGIVDTG ESVGSISFPE
151 LYGRKEHGYN ENYEKLYGVY AEGSA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 138 shows 92.2% identity over a 179 aa overlap with a predicted ORF (ORF 138.ng) from *N. gonorrhoeae*:

```
m139/g139

      10      20      30      40      50      60
m139.pep  MRTTPTFPTKTFKPTAMALAVATTLSACLGGGGGGTSAPDFNAGGTGIGSNSRATTAKSA
g139      MRTTSTFPTKTFKPAAMALAVATTLSACLGGGGGGTSAPDFNAGGTGIGSNSRATIAESA
      10      20      30      40      50      60

      70      80      90     100     110     120
m139.pep  AVSYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKINAPPRICIPETFQTMTHYKNLINLK
g139      AVSYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKIKAP-RICIPETFQTMNIKMINLNK
      70      80      90     100     110

      130     140     150     160     170
m139.pep  PAIEAGYTGRGVEVGIVDTGESVGSISFPPELYGRKEHGYNENY----EKLYGVYAEGSAX
g139      PAIEAGYTGRGVEVGIVDTGESVGSISFPPELYGRKEHGYNENYKNKLQKLYGVYAEGSAX
      120     130     140     150     160     170
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 545>:

```
a139.seq
1   ATGCGAACGA CCCCAACCTT CCCTACAAAA ACTTTCAAAC CGGCTGCCAT
51  GCGGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAGGC GGCGGCGGAG
101 GCGGCACTTC TGCGCCCGAC TTCAATGCAG GCGGCACCGG TATCGGCAGC
151 AACAGCAGGG CAACAACAGC GAAATCAGCA GCAATATCTT ACGCCGGTAT
201 CAAGAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTCTGGGATG
251 ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAATGCCCC CCCCCGAATC
301 TGCATACCGG AGACTTTACA AACCCTAAATG ACGCAT. ACA AGAATTTGAT
351 CAACCTCAAA CCTGCAATTG AAGCAGGCTA TACAGGACGC GGGGTAGAGG
401 TAGGTATCGT CGACACAGGC GAATCCGTCG GCAGCATATC CTTTCCCGAA
451 CTGTATGGCA GAAAAGAACA CGGCTATAAC GAAAATTAC. AAAAATAATA
501 CGGCGTATAT GCGGAAGGAA GCGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 546; ORF 139.a>:

```
a139.pep
1   MRTTPTFPTK TFKPAAMALA VATTLSACLG GGGGGTSAPD FNAGGTGIGS
```

394

51 NSRATTAKSA AISYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPRI
 101 CIPETLQTOM THXKNLINLK PAIEAGYTGR GVEVGIVDTG ES VGSI SFPE
 151 LYGRKEHGYN ENYXKLYGVY AEGSA*

m139/a139 97.1% identity in 175 aa overlap

	10	20	30	40	50	60
m139.pep	MRTTPTFPKTFKPTAMALAVAT	TL	SACLG	GGGGG	TSAPDFNAGGTGIGSNSRATTAKSA	
a139	MRTTPTFPKTFKPAAMALAVAT	TL	SACLG	GGGGG	TSAPDFNAGGTGIGSNSRATTAKSA	
	10	20	30	40	50	60
	70	80	90	100	110	120
m139.pep	AVSYAGIKNEMCKDRSMLCAGR	DDVAVTDR	DAKINAPPRICIPET	FQTM	THYKNLINLK	
a139	AISYAGIKNEMCKDRSMLCAGR	DDVAVTDR	DAKINAPPRICIPET	LQTM	THXKNLINLK	
	70	80	90	100	110	120
	130	140	150	160	170	
m139.pep	PAIEAGYTGRGVEVGIVDTG	ESVGSISFPELYGRKEHGYN	ENYXKLYGVYAEGSAX			
a139	PAIEAGYTGRGVEVGIVDTG	ESVGSISFPELYGRKEHGYN	ENYXKLYGVYAEGSAX			
	130	140	150	160	170	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 547>:

g140.seq

1	Atgtcggcac	gCGGCAAGGG	GGCAGgctat	ctcAACAGTA	CCGGACGACa
51	TGTTCCCTTC	CTGAGTGCCG	CCAAAATCGG	GCAGGATTAT	TCTTTCTTCA
101	AAAATATCAA	AACCGACGGC	GGTCTGCTGG	CTTCCCTCGA	CAGCGTCGAA
151	AAAACAGCGG	GCAGTGAAGG	CGACACGCCG	TCCTATTATG	TCCGTCGCGG
201	CAATGCGGCA	CGGACTGCTT	CGGCAGCGGC	ACATTCCGCG	CCCGCCGGTC
251	TGAAACACGC	CGTAGAACAG	GGCGGCAGCA	ATCTGGA AAA	CCTGATGGTC
301	GAGCTGGATG	CCTCCGAATC	ATCCGCAACA	CCCAGACCGG	TTGAAACTGC
351	GGTCGCCGAC	CGCACAGATA	TGCCGGGCAT	CCGCCTACGG	CGCACA ACTT
401	TCCGCACAGC	GGCAGCCGTA	CAGCATGCGA	ATACCGCCGA	CGCGGTACGc
451	aTCTTcaaCA	GTCTCGCCGC	TAccgTCTAt	GccgACAGTG	CCGCCGCCCA
501	TGccgATATG	CAGGGACGCC	GCCTGAAAGC	CGTATCGGAC	GGGTTGGACC
551	ACAACGGTAC	GGGTCTGCGC	GTCATCGCGC	AAACCCAACA	GGACGGTGGA
601	ACGTGGGAAC	AGGGCGGTGT	CGAAGGCAAA	ATGCGCGGCA	GTACCCAAAC
651	TATCGGCATT	GCCGCGAAAA	CCGCGCAAAA	TACGACAGCA	GCCGCCACAC
701	TGGGCATAGG	ACGCAGCACA	TGGAGCGAAA	ACAGTGCAAA	TGCAAAAACC
751	GACAGCATTa	GTCTGTTTGC	AGGCATACGG	CACGATGTGG	GCGATATCGG
801	CTATCTCAAA	GGCCTGTTCT	CctaCGGACG	CTACAAAAAC	AGCATCAGCC
851	GCAGCACC GG	TGCGGATGAA	TATGCGGAAG	GCAGCGTCAA	CGGCACGCTG
901	ATGCAGCTGG	GCGCACTGGG	TGGTGTCAAC	GTTCCGTTTG	CCGCAACGGG
951	AGATTTGACG	GTTGAAGGCG	GTCGCGCCA	CGACCTGCTC	AAACAGGATG
1001	CATTTCGCCG	AAAAGGCagt	GCTTTGGGCT	GGAGCGGCAA	CAGCCTCACT
1051	GAAGGCACAC	TGGTCGGACT	CGCGGGTCTG	AAACTGTCGC	AACCCTTGAG
1101	CGATAAAGCC	GTCTGTCTTG	CGACGGCGGG	CGTGAACGC	GACCTGAACG
1151	GACGCGACTA	CGCGGTAACG	GGCGGCTTTA	CCGCGCGGCG	TGCAGCAACC
1201	GGCAAGACGG	GTGCACGCAA	TATGCCGCAC	ACCCGCCGGG	TTGCCGGTCT
1251	GGGGGTGGAT	GTCGAATTCTG	GCAACGGCTG	GAACGGCTTG	GCACGTTACA
1301	GCTACACCGG	TTCCAAACAG	TACGGCAACC	ACAGCGGACA	AATCGGCGTA
1351	GGCTACCGGT	TCTGA			

This corresponds to the amino acid sequence <SEQ ID 548; ORF 140.ng>:

g140.pep

1	MSARGKGAGY	LNSTGRHVPF	LSAAKIGQDY	SFFKNIKTDG	GLLASLDSVE
51	KTAGSEGDTP	SYVVRRGNA	RTASAAAHSA	PAGLKHAVEQ	GGSNLENLMV
101	ELDASESSAT	PETVETAVAD	RTDMPGIRLR	RTTFR TAAAV	QHANTADGVR
151	IFNSLAATVY	ADSAAAHADM	QGRRLKAVSD	GLDHNGTGLR	VIAQTQDGG
201	TWEQGGVEGK	MRGSTQTIGI	AAKTGENTTA	AATLGIGRST	WSENSANA KT

m140.seq

1	ATGTCGGCAC	GCGGCAAGGG	GGCAGGCTAT	CTCAACAGTA	CCGGACGACG
51	TGTTCCCTTC	CTGAGTGCCG	CCAAAATCGG	GCAGGATTAT	TCTTTCTTCA
101	CAAACATCGA	AACCGACGGC	GGCCTGCTGG	CTTCCCTCGA	CAGCGTCGAA
151	AAAACAGCGG	GCAGTGAAGG	CGACACGCTG	TCCTATTATG	TCCGTCGCGG
201	CAATGCGGCA	CGGACTGCTT	CGGCAGCGGC	ACATTCCGCG	CCCGCCGGTG
251	TGAAACACGC	CGTAGAACAG	GGCGGCAGCA	ATCTGGAAAA	CCTGATGGTC
301	GAACTGGATG	CCTCCGAATC	ATCCGCACA	CCCGAGACGG	TTGAAACTGC
351	GGCAGCCGAC	CGCACAGATA	TGCCGGGCAT	CCGCCCTTAC	GGCGCAACTT
401	TCCGCGCAGC	GGCAGCCGTA	CAGCATGCGA	ATGCCGCCGA	CGGTGTACGC
451	ATCTTCAACA	GTCTCGCCGC	TACCGTCTAT	GCCGACAGTA	CCGCCGCCCA
501	TGCCGATATG	CAGGGACGCC	GCCTGAAAGC	CGTATCGGAC	GGGTGGGACC
551	ACAACGGCAC	GGGTCTGCGC	GTCATCGCGC	AAACCCAACA	GGACGGTGGA
601	ACGTGGGAAC	AGGGCGGTGT	TGAAGCCAAA	ATGCGCGGCA	GTACCCAACAC
651	CGTGGCAATT	CCCGCGAAAA	CCGGCGAAAA	TACGACAGCA	CCCGCCACAC
701	TGGGCATGGG	ACGCAGCACA	TGGAGCGAAA	ACAGTGCAAA	TGCAAAAAACC
751	GACAGCATTA	GTCTGTTTGC	AGGCATACGG	CACGATGCGG	GCGATATCGG
801	CTATCTCAAA	GGCCTGTTCT	CCTACGGACG	CTACAAAAAC	AGCATCAGCC
851	GCAGCACCGG	TGCGGACGAA	CATGCGGAAG	GCAGCGTCAA	CGGCACGCTG
901	ATGCAGCTGG	GCGCACTGGG	CGGTGTCAAC	GTTCCGTTTG	CCGCAACGGG
951	AGATTTGACG	GTCGGAAGCG	GTCCTGCCTA	CGACCTGCTC	AAACAGGATG
1001	CATTGCGCGA	AAAAGCGAGT	CGTTTGCGTA	GAGACGGCAA	GACGCTFACT
1051	GAAGGCACGC	TGGTCGGACT	CGCGGGTCTG	AAGCTGTGCG	AACCCCTTGAG
1101	CGATAAAGCC	GTCTGTGTTG	CAACGGCGGG	CGTGGAACGC	GACCTGAACG
1151	GACGCGACTA	CACGGTAAACG	GGCGGCTTTA	CCGGCGCGAC	TGCAGCAACC
1201	GGCAAGACCG	GGGCACGCAA	TATGCCGCAC	ACCCGTCTGG	TTGCCGGCCT
1251	GGGCGCGGAT	GTCCAAATTCG	GCAACGGCTG	GAACGGCTTG	GCACGTTACA
1301	GCTACGGCCG	TTCCAAACAG	TACGGCAACC	ACAGCGGACG	AGTCGGCGTA
1351	GGCTACCGGT	TCTGA			

m140.pep

1	MSARGKGAGY	LNSTGRRVPF	LSAAKIGQDY	SFFTNIETDG	GLLASLDSVE
51	KTAGSEGDTL	SYYYRRGNAA	RTASAAAHSA	PAGLKHAVEQ	GGSNLENLMV
101	ELDASESSAT	PETVETAAAD	RTDMPGIRPY	GATFRAAAAV	QHANAADGVR
151	IFNSLAATVY	ADSTAAHADM	QGRRLKAVSD	GLDHNGTGLR	VIAQTQDDGG
201	TWEQGGVEGK	MRGSTQTVGI	AAKTGENTTA	AATLGMGRST	WSENSANAKT
251	DSISLFAGIR	HDAGDIGYLK	GLFSYGRYKN	SISRSTGADE	HAEGSVNGTL
301	MQLGALGGVN	VPFAATGDLT	VEGGLRYDLL	KQDAFAEKGS	ALGWSGNSLT
351	EGTLVGLLAGL	KLSQPLSDKA	VLFATAGVER	DLNGRDYTVT	GGFTGATAAT
401	GKGTGARNMPH	TRLVAGLGAD	VEFGNGWNGL	ARYSYAGSKQ	YGNHSGRGGV
451	GYRF*				

Homology with a predicted ORF from *N.gonorrhoeae*

m140/g140

```

      10      20      30      40      50      60
m140.pep  MSARGKGAGYLNSTGRRVPFLSAAKIGQDYSFFTNIETDGLLASLDSVEKTAGSEGDTL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g140      MSARGKGAGYLNSTGRHVPFLSAAKIGQDYSFFKNIKTDGLLASLDSVEKTAGSEGDTP
          10      20      30      40      50      60
          70      80      90     100     110     120

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m140.pep	SYVVRGNAARTASAAAH SAPAGLK HAVEQGGSNLENLMVELDASESSATPETVETAAAD
g140	SYVVRGNAARTASAAAH SAPAGLK HAVEQGGSNLENLMVELDASESSATPETVETAVAD
	70 80 90 100 110 120
m140.pep	130 140 150 160 170 180
	RTDMPGIRPYGATFRAAAVQHANAADGVRI FNSLAATVYADSTAAHADMQGRRLKAVSD
g140	RTDMPGIRLRRTTFR TAAAVQHANTADGVRI FNSLAATVYADSAAAHADMQGRRLKAVSD
	130 140 150 160 170 180
m140.pep	190 200 210 220 230 240
	GLDHNGTGLRVIAQTQDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGRST
g140	GLDHNGTGLRVIAQTQDGGTWEQGGVEGKMRGSTQTIGIAAKTGENTTAAATLGIGRST
	190 200 210 220 230 240
m140.pep	250 260 270 280 290 300
	WSENSANAKTDSISL FAGIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL
g140	WSENSANAKTDSISL FAGIRHDVGDIGYLKGLFSYGRYKNSISRSTGADEYAEGSVNGTL
	250 260 270 280 290 300
m140.pep	310 320 330 340 350 360
	MQLGALGGVNPFAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSLTEGTLVGLAGL
g140	MQLGALGGVNPFAATGDLTVEGGLRHDLLKQDAFAEKGSALGWSGNSLTEGTLVGLAGL
	310 320 330 340 350 360
m140.pep	370 380 390 400 410 420
	KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD
g140	KLSQPLSDKAVLSATAGVERDLNGRDYAVTGGFTGAAAATGKTGARNMPHTRRVAGLGVD
	370 380 390 400 410 420
m140.pep	430 440 450
	VEFGNGWNLARYSYAGSKQYGNHSGRVGVG YRFX
g140	VEFGNGWNLARYSYTGSKQYGNHSGQIGVG YRFX
	430 440 450

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 551>:

```

a140.seq
1  ATGTCGGCAG GCGGTAAGGG GGCAGGCTAT CTCAACCGTA CCGGACAACG
51  TGTTCCTTTC CTGAGTGCCG CCAAAATCGG GCGGGATTAT TCTTCTTCA
101 CAAACATCGA AACCGACGGC GGTCTGCTGG CTTCCTCGA CAGCGTCGAA
151 AAAACAGCGG GTAGTGAAGG CGACACGCTG TCCTATTATG TCCGTCCGG
201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCCGCCGGTC
251 TGAACACAGC CGTAGAACAG GGCGGCAGCA ATCTGGAAAA CCTGATGGTC
301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC
351 GGCCGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCTAC GGCGCAACTT
401 TCCGCGCAGC GGCAGCCGTA CAGCATGCGA ATGCCGCCGA CGGTGTACGC
451 ATCTTCAACA ATCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCCGCCCA
501 TGCCGATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGTTTGGACC
551 ACAACGCTAC GGGTCTGCGC GTCATCGCGC AAACCCAACA GGACGGTGGA
601 ACGTGGGAAC AGGGCGGTGT TGAAGGCAAA ATGCGCGGCA GTACCCAAAC
651 CGTCGGCATT GCCGCGAAAA CCGGCGAAAA TACGACAGCA GCCGCCACAC
701 TGGGCATGGG ACACAGCACA TGGAGCGAAA ACAGTGCAAA TGAACAAAAC
751 GACAGCATTG GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG
801 CTATCTCAAA GGCCTGTTCT CCTACGGACG CTACAAAAAC AGCATCAGCC
851 GCAGCACCGG TGCGGACGAA CATGCGGAAG GCAGCGTCAA CGGCACGCTG
901 ATGCAGCTGG GCGCACTGGG CCGTGTCAAC GTTCCGTTTG CCGCAACGGG

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```

951 AGATTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AAACAGGATG
1001 CATTCGCCGA AAAAGGCAGT GCTTTGGGCT GGAGCGGCAA CAGCATCACT
1051 GAAGGCACAC TGGTCGGACT CGCGGGTCTG AAGCTGTCGC AACCTTGAG
1101 CGATAAAGCC GTCCTGTTTG CAACGGCGGG CGTGAACGC GACCTGAACG
1151 GACGCGACTA CACGGTAACG GCGGGCTTTA CCGCGCGGAC TGCAGCAACC
1201 GGCAAGACGG GGGCACGCAA TATGCCGCAC ACCCGCTGG TTGCCGGTCT
1251 GGGCGCGGAT GTCGAATTCTG GCAACGGCTG GAACGGCTTG GCACGTTACA
1301 GCTACGCCGG TTCCAAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA
1351 GGCTACCGGT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 552; ORF 140.a>:

```

a140.pep
1 MSAGGKGAGY LNRTGQRVFP LSAAKIGRDY SFFTNIETDG GLLASLDSVE
51 KTAGSEGDTL SYVRRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
101 ELDAESSAT PETVETAAAD RTDMPGIRPY GATFRAAAV QHANAADGVR
151 IFNNLAATVY ADSTAAHADM QGRRLKAVSD GLDHNATGLR VIAQTQDGG
201 TWEQGVVEGK MRGSTQTVGI AAKTGENTTA AATLGMGHST WSENSANAKT
251 DSISLFAGIR HDAGDIGYLK GLFSYGRYKN SISRSTGADE HAEGSVNGTL
301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL KQDAFAEKGS ALGWSGNSIT
351 EGTTLVGLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGTGATAAT
401 GKTGARNMPH TRLVAGLGAD VEFNGWNGL ARYSYAGSKQ YGNHSGRVGV
451 GYRF*

```

m140/a140 98.2% identity in 454 aa overlap

m140.pep	10	20	30	40	50	60
	MSARGKGAGYLNSTGRRVPFLSAAKIGQDYSFFTNIETDGGLLASLDSVEKTAGSEGDTL					
a140	MSAGGKGAGYLNRTGQRVFPFLSAAKIGRDYSFFTNIETDGGLLASLDSVEKTAGSEGDTL					
	10	20	30	40	50	60
m140.pep	70	80	90	100	110	120
	SYVRRGNAAARTASAAHSAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD					
a140	SYVRRGNAAARTASAAHSAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD					
	70	80	90	100	110	120
m140.pep	130	140	150	160	170	180
	RTDMPGIRPYGATFRAAAVQHANAADGVRIFNLSLAATVYADSTAAHADMQGRRLKAVSD					
a140	RTDMPGIRPYGATFRAAAVQHANAADGVRIFNLAATVYADSTAAHADMQGRRLKAVSD					
	130	140	150	160	170	180
m140.pep	190	200	210	220	230	240
	GLDHNATGLRVIAQTQDGGTWEQGVVEGKMRGSTQTVGIAAKTGENTTAAATLGMGRST					
a140	GLDHNATGLRVIAQTQDGGTWEQGVVEGKMRGSTQTVGIAAKTGENTTAAATLGMGHST					
	190	200	210	220	230	240
m140.pep	250	260	270	280	290	300
	WSENSANAKTDSISLFAGIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL					
a140	WSENSANAKTDSISLFAGIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL					
	250	260	270	280	290	300
m140.pep	310	320	330	340	350	360
	MQLGALGGVNVFPAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSLTEGTLVGLAGL					
a140	MQLGALGGVNVFPAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSITEGTLVGLAGL					
	310	320	330	340	350	360
m140.pep	370	380	390	400	410	420
	KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD					
a140	KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD					

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	370	380	390	400	410	420
	430	440	450			
m140.pep	VEFGNGWNGGLARYSYAGSKQYGNHSGRVGVGYRFX					
a140	VEFGNGWNGGLARYSYAGSKQYGNHSGRVGVGYRFX					
	430	440	450			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 553>:

```

gl41.seq
1  atgagcttca aAAccgATGC CGAAACCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAGCTG
151 CCGCAAAAC AAGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GGC GGCGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TGCGCGAGCC TTCTTTGGGT
301 CCGGTGTTTC GCGTGAAGG CGGCGCGGCA GCGCGCGGCT ACGCGCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGCGAC TTCCACGCCA
401 TCGGTGCGGC GAATAACCTC CTCGCCGCCA TGCTCGACAA CCATATCTAC
451 CAAGGTAACG AGTTGAACAT CGACCCCAA CGCGTGCTGT GCGGCGCGT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGTATGGGCA
551 AGCCTGTtga cggCGTGATG CGtcccGACG GCTTCGACAT CACCGTCGCC
601 TCCGAAGTGa tggcgGTATT CTGCCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTtTt gGCAATATTC TCGTCGCCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTGAAAG GCACACGGCG CGATGGCGGC ATTGCTAAAA
751 GATGCGATTA AGCCCAATTT GGTGCAAACC ATCGAAGGCA CTCCGGCCTT
801 TGTACACGGC GGCCCGTTCG CCAACATCGC CCACGGCTGC AACTCCGTTA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG TGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCAGT CGTCGTGGCG ACTGTCCGCG
1001 CCCTGAAATA CAACGGCGGC GTGGAACGCG CCAACCTTGG TGAAGAAAC
1051 CTCGAAGCCT TGGCAAAAGG TTTGCCCAAC CTGTTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTCGGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCTT GACCGAAGTG TGGGGCAAAG GCGGCGCGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA TGCCATCGAC AACCAACCTA
1301 ATAACCTCGG TTTTCGCCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCCAAAAAGT GTACGGCGCG GAAGATGTCG ATTTCAGCGC
1401 GGAAGCGTCT GCCGAAATCG CCTCGCTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATATT CATTGAGCGA CAACGCCAAA
1501 CTCTTGGGCT GCCCGAAGG CTTCCGCATC GCCGTACGCG GTATCACTGT
1551 TTCCGCCGGC GCGGGCTTCA TCGTTGCGTT GTGCGGCAAT ATGATGAAAA
1601 TGCCGGGCTT GCCGAAAGTT CCGGCTGCCG AGAAAATCGA TGTGGACGAA
1651 CACGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 554; ORF 141.ng>:

```

gl41.pep
1  MSFKTDAETA QSSTMRPIGE IAAKLGLNVD NIEPYGHYKA KINPAEAFKL
51  PQKQGRILIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFGVKGGA GGGYAQVLPM EDINLHFTGD PHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNIID GMGKPDVGV RPDGFDITVA
201 SEVMAVFCLA KDISDLKERF GNILVAYAKD GSPVYAKDLK AHGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LEALAKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDSDAE LAMIEKACAE
401 HGVEVSLTEV WGKGGAGGAD LARKVVNAID NQPNNFGFAY DVELGIKDKI
451 RAIQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TQYSLSDNAK
501 LLGCPEGFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAEKIDVDE
551 HGVIHGLF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 555>:

m141.seq

```

1  ATGAGCTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTTGGTCT GAATGCCGAC AACATTGAGC
101 CTTACGGTCA TTACAAGGCG AAAATCAATC CTGCCGAAGC GTTCAAACCTG
151 CCGCAAAAAC AGGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GGCGGGCGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCGTTGC
251 GCCACATCGG CAAAGATGCC GTGATTGCCC TGC GCGAACC TTCTCTGGGG
301 CCGGTGTTTC GCGTGAAAGG CGGCGCGGCA GCGGCGGCT ATGCCCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAATCTG CTTGCCGCGA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAA CGCGTGCTGT GGCGGCGCGT
501 GGTCGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGTA
551 AACCGGTTGA CGGCGTGATG CGTCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTTTG GGCAACATCC TTGTGCGCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAACC ATCGAAGGCA CGCCGCGCTT
801 CGTACACGGC GGCCCGTTTC CCAACATCGC CCACGGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCGAAGCA
901 GGCTTCGCGC CGGACTTGGG CGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCTGT TGTCGTGGCG ACTGTCCGCG
1001 CGTTGAAATA TAACGGCGGC GTGGAACGCG CCAACCTCGG CGAAGAAAAT
1051 TTAGACGCTT TGGA AAAAGG TTTGCCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTCCGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCGACGCG CGATGCCGAG TTGGCGATGA TTGAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAACCTCGG TTTGCGCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCCAAAAGT GTACGGCGCG GAAGATGTTG ATTTACGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTCACTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAAGCG CAACGCCAAA
1501 CTGTTGGGCT GCCCGAAGA CTTCCGCATC GCCGTGCGCG GCATCACCCT
1551 TTCCGACGGC GCAGGTTTCA TCGTCGCCCT GTGCGCAAC ATGATGAAAA
1601 TGCCCGGCTT GCCCAAAGTT CCGGCTGCCG AGAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 556; ORF 141>:

m141.pep

```

1  MSFKTDAEIA QSSTMRPIGE IAAKLGLNAD NIEPYGHIKA KINPAEAFKL
51  PQKQGRILIV TAINPTPAGE GKTTVTIGLA DALRHIGKDA VIALREPSLG
101 PVFGVKGGAA GGGYAQVLPD EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNDPK RVLWRRVVDN NDRQLRNIID GMGKPVGDV RPDGFDITVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRVSDADAE LAMIEKACAE
401 HGVEVSLTEV WGKGAGGAD LARKVVNAIE SQTNNFGFAY DVELGIKDKI
451 RAIQKVYGA EDVDFSABAS AEIASLEKLG LDKMPICMAK TQYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDA
551 EGVHGLF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 141 shows 97.5% identity over a 558 aa overlap with a predicted ORF (ORF 141.ng) from *N. gonorrhoeae*:

m141/g141

```

              10      20      30      40      50      60
m141.pep  MSFKTDAEIAQSSTMRPIGEIAAKLGLNADNIEPYGHIKAKINPAEAFKL PQKQGRILIV
          ||||| ||||| ||||| ||||| ||||| |||||
g141      MSFKTDAETAQSSTMRPIGEIAAKLGLNVDNIEPYGHIKAKINPAEAFKL PQKQGRILIV
              10      20      30      40      50      60

```

400

m141.pep	70	80	90	100	110	120
	TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPVFGVKGAAGGGYAQVLP					
g141	TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPVFGVKGAAGGGYAQVLP					
	70	80	90	100	110	120
m141.pep	130	140	150	160	170	180
	EDINLHFTGDFHAIGAANNLLAAMLNDNHIYQGNELNIDPKRVLWRRVVDMDRQLRNIID					
g141	EDINLHFTGDFHAIGAANNLLAAMLNDNHIYQGNELNIDPKRVLWRRVVDMDRQLRNIID					
	130	140	150	160	170	180
m141.pep	190	200	210	220	230	240
	GMGKPVGDGVMRPDGFDTVASEVMAVFCIAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
g141	GMGKPVGDGVMRPDGFDTVASEVMAVFCIAKDISDLKERFGNILVAYAKDGSPVYAKDLK					
	190	200	210	220	230	240
m141.pep	250	260	270	280	290	300
	ANGAMAALLKDAIKPNLVQTIETPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
g141	AHGAMAALLKDAIKPNLVQTIETPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
m141.pep	310	320	330	340	350	360
	GFGADLGAEKFCDIKCRLAGLKPDAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
g141	GFGADLGAEKFCDIKCRLAGLKPDAVVVATVRALKYNGGVERANLGEENLEALAKGLPN					
	310	320	330	340	350	360
m141.pep	370	380	390	400	410	420
	LLKHISNLKNVFGLPVVVALNRFVSDADAELAMIEKACAEHGVEVSLTEVWGKGGAGGAD					
g141	LLKHISNLKNVFGLPVVVALNRFVSDSDAELAMIEKACAEHGVEVSLTEVWGKGGAGGAD					
	370	380	390	400	410	420
m141.pep	430	440	450	460	470	480
	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAIQKVYGAEDVDFSAEASAEIASLEKLG					
g141	LARKVVNAIDNQPNNGFAYDVELGIKDKIRAIQKVYGAEDVDFSAEASAEIASLEKLG					
	430	440	450	460	470	480
m141.pep	490	500	510	520	530	540
	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
g141	LDKMPICMAKTQYSLSDNAKLLGCPGEGFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	490	500	510	520	530	540
m141.pep	550	559				
	PAAEKIDVDAEGVIHGLFX					
g141	PAAEKIDVDEHGVHGLFX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 557>:

```

a141.seq
1  ATGAGTTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAACCTG
151 CCGCAAAAAC AGGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC

```

```

201 GCGGGGCGAA GGTAAAACCA CCGTAACCAT CGGTTTGGCG GACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TGCGCGAGCC TTCTTTGGGT
301 CCGGTGTTTCG GCGTGAAAGG CGGCGCGGCA GCGGCGCGCT ATGCCCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAATCTG CTTGCCGCGA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAAA CGCGTGCTGT GCGGCGCGCT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGCA
551 AGCCTGTTGA CGGCGTGATG CGTCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTTTG GGCAACATCC TTGTGCGCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAACC ATCGAAGGCA CGCCCGCCTT
801 CGTACACGGC GGCCCGTTTCG CCAACATCGC CCACGGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCAGAGCA
901 GGCTTCGGCG CGGACTTGCG CGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCTGT TGTCGTGGCG ACTGTCGCG
1001 CGTTGAAATA TAACGGCGGC GTGGAACGCG CCAACCTCGG CGAAGAAAAT
1051 TTAGACGCTT TGGAAAAAGG TTGCCCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTGCGAC TGCCCGTCGT CGTTGCGCTC AACCCTTCG
1151 TGTCCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAACTTCGG TTTCGCCTAC GATGTCGAGT TGGGCATCAA AGACAAATC
1351 CGTGCGATTG CCCAAAAAGT GTACGGCGCG GAAGATGTTG ATTTACGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTCACTGGA AAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCCCGAAGA CTTCCGCATC GCCGTGCGCG GCATCACCGT
1551 TTCCGCAGGC GCAGGTTTCA TCGTCGCCCT GTGCGCAAC ATGATGAAAA
1601 TGCCCGGCCT GCCCAAAGTT CCGGCTGCCG AGAAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 558; ORF 141.a>:

```

a141.pep
1 MSFKTDAEIA QSSTMRPIGE IAAKLGLNVD NIEPYGHYKA KINPAEAFKL
51 PQKQGRILIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFVGKGGAA GGGYAQVLP EDINLHFTGD FHAIGAANNL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNIID GMGKPV DGVM RPDGFDTVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDSDAE LAMIEKACAE
401 HGEVSLTEV WKGAGGAGD LARKVVNAIE SQTNNFGFAY DVELGKDKI
451 RAIQKVYGA EDVDFSASES AEIASLEKLG LDKMPICMAK TOYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAEEKIDVDA
551 EGVHGLF*

```

m141/a141 99.5% identity in 558 aa overlap

```

m141.pep      10      20      30      40      50      60
MSFKTDAEIAQSSTMRPIGEIAAKLGLNADNIEPYGHYKAKINPAEAFKL
|||||:|||||
a141          10      20      30      40      50      60
MSFKTDAEIAQSSTMRPIGEIAAKLGLNVDNIEPYGHYKAKINPAEAFKL
|||||:|||||

m141.pep      70      80      90     100     110     120
TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPFVFGKGAAGGGYAQVLP
|||||:|||||
a141          70      80      90     100     110     120
TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPFVFGKGAAGGGYAQVLP
|||||:|||||

m141.pep     130     140     150     160     170     180
EDINLHFTGDFHAIGAANNLLAAMLNDHIYQGNELNIDPKRVLWRRVVDNDRQLRNIID
|||||:|||||
a141         130     140     150     160     170     180
EDINLHFTGDFHAIGAANNLLAAMLNDHIYQGNELNIDPKRVLWRRVVDNDRQLRNIID
|||||:|||||

```

402

m141.pep	190	200	210	220	230	240
	GMGKPV DGV MRPDGFDITVASEVMAVFCLAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
a141	GMGKPV DGV MRPDGFDITVASEVMAVFCLAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
	190	200	210	220	230	240
m141.pep	250	260	270	280	290	300
	ANGAMAALLKDAIKPNLVQTI EGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
a141	ANGAMAALLKDAIKPNLVQTI EGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
m141.pep	310	320	330	340	350	360
	GFGADLGA EKFC DIKCR LAGLKPDA AVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
a141	GFGADLGA EKFC DIKCR LAGLKPDA AVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
	310	320	330	340	350	360
m141.pep	370	380	390	400	410	420
	LLKHISNLKNVFGLPVVVALNRFVSDADAELAMIEKACAEHGVESL TEVWVGKGGAGGAD					
a141	LLKHISNLKNVFGLPVVVALNRFVSDADAELAMIEKACAEHGVESL TEVWVGKGGAGGAD					
	370	380	390	400	410	420
m141.pep	430	440	450	460	470	480
	LARKVVNAIESQTNNFGFAYDVELGIKDKIRATAQKVYGAEDVDFS AEASAEIASLEKLG					
a141	LARKVVNAIESQTNNFGFAYDVELGIKDKIRATAQKVYGAEDVDFS AEASAEIASLEKLG					
	430	440	450	460	470	480
m141.pep	490	500	510	520	530	540
	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
a141	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	490	500	510	520	530	540
m141.pep	550	559				
	PAAEKIDVDAEGVIHGLFX					
a141	PAAEKIDVDAEGVIHGLFX					
	550					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 559>:

```

g142.seq
1   ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCGTGC AGGTGCGCCA
51  ACGCGCCTTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAAATATGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTT
151 GGCAACATCC TGATGTTTCGT CCGCCAGCAT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATcggaATG AttcgCGCAC TCCGGTTTAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCGGT AACCGGCGCA ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCAC
351 AGGATGCCAT CGCATCACGG AACGAAGTTT GAAAAGTTTT CTGCAAATCC
401 GCCATTTTTT CCCTTTAAAC CGTCCCCTAT ATAAGAATGC TGCACACAAG
451 GCATCCCCC ATGTGCAGCA GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 560; ORF 142.ng>:

```

g142.pep
1   MRADFMFADN MPVQVRQRAF YFKLSRFAAM PNMVGKPLFG RQAGQPGKMF
51  GNILMFVRQH IDAEAAVFRQ DRNDSRTPVY AQHHGRRLVG NRRNRRCNA
101 VTPCRTVCRD DMNACRTGCH RITERSLKSF LQIRHFSPLN RPLYKNAAHK
151 ASPHVQQF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 561>:

```
m142.seq
  1 ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCGTGC AGGTGCGCCA
 51 ACGCGCCCTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAGATGTGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTC
151 GGCAACATCC TGATGTTCGT CCGCCAGCGT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATCGGAATG ATTCGCGCAC TCCGGTTGAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCGGT AACCGGCGCG ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCGC
351 AAGATGCCAT CGCATCACGG AACGAAGTTT GAAAATTTTT CTGCAAATCC
401 GCCATTTTTC CCCTTTAAAC TGTCCCCTAT ATAAGAATGC TGCACACAAG
451 GCATCCCCcC ATGTGCAGCA GTTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 562; ORF 142>:

```
m142.pep
  1 MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF
 51 GNILMFVRQR IDAEAAVFRQ DRNDSRTVPD AQHHGRRLLV NRRDRRHCHNA
101 VTPCRTVCRD DMNACRARCH RITERSLKIF LQIRHFSPLN CPLYKNAAHK
151 ASPHVQQF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 142 shows 93.7% identity over a 158 aa overlap with a predicted ORF (ORF 142.ng) from *N. gonorrhoeae*:

```
m142/g142

      10      20      30      40      50      60
m142.pep MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMFGNILMFVRQR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g142      MRADFMFADNMPVQVRQAFYFKLSRFAAMPNMVGKPLFGRQAGQPGKMFGNILMFVRQH
          10      20      30      40      50      60

      70      80      90      100     110     120
m142.pep IDAEAAVFRQDRNDSRTVPDAQHHGRRLLVGNRRDRRHCHNAVTPCRTVCRDDMNACRARCH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g142      IDAEAAVFRQDRNDSRTVPVYQHHGRRLLVGNRRNRHCHNAVTPCRTVCRDDMNACRTGCH
          70      80      90      100     110     120

      130     140     150     159
m142.pep RITERSLKIFLQIRHFSPLNCPPLYKNAAHKASPHVQQFX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g142      RITERSLKSFQIRHFSPLNRPLYKNAAHKASPHVQQFX
          130     140     150
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 563>:

```
a142.seq
  1 ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCGTGC AGGTGCGCCA
 51 ACGCGCCCTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAGATGTGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTC
151 GGCAACATCC TGATGTTCGT CCGCCAGCGT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATCGGAATG ATTCGCGCAC TCCGGTTGAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCCGT AACCGGCGCA ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCGC
351 AGGATGCCAT CGCATCACGG AACGAAGTTT GAAAAGTTTT CTGCAAATCC
401 GCCATTTTTC CCCTTTAAAC TGTCCCCTAT ATAAGAATGC TGCACACAAG
451 GCACCCCCCA TGTGCAGCAG TTCTGATTCA AAAAGCCGTC GGTCCGACAT
501 TTCCGCGCGT TACGGCGTAT TACGAGTTCA ACGCATCCTC GATTTTGCA
551 AGTTCTGCCA ACAGGTCTTT AAGCAGCAGC ATTTTCTCGC GGCCAGCAC
601 TTCCTCGATA GCGTCGTAAC GCTCGTCCAC TTCTTCGCCG ATTTCCTCAT
651 ACAGCTTCTC GCCCTCGGCA GTCAGCTTCA GAAAAACACG TCGTTGGTCG
701 TTGGAAGGTT TCAGGCGGAC AACCAAACCC GCTTTTCAA GGCGGGTCAG
751 GATACCGGTC AGGCTGGGGC GCAAAATGCA CGCCTGATTG GCCAAATCTT
```

```

801 GAAAGTCCAG CGTGCCGTTT TCCGCCAAAA GACGGATAAT CCGCCATTGC
851 TGATCGGTAA TATTCGCCTG ATTCAGAATA GGCCTGAATT GGGTCATCAG
901 GGCTTCCCTT GCCTGTATCA GACCGATATT GATAGACGCA TGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 564; ORF 142.a>:

```

a142.pep
  1  MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF
 51  GNILMFVRQR IDAEAAVFRQ DRNDSRTPVD AQHHGRRLLVR NRRNRRHCNA
101  VTPCRTVCRD DMNACRTGCH RITERSLKSF LQIRHFSPLN CPLYKNAAHK
151  APPMCSSSDS KSRRSDISAR YGVLRVQRIL DFGKFCQQVF KQQHFLAAQH
201  FLDSVVTLVH FFADFLIQLL ALGSQLOKNT SLVVGRFQAD NQTRFFKAGQ
251  DTGQAGAQNA RLIRQILKVQ RAVFRQKTDN PPLLIGNIRL IQNRPFLGHQ
301  GFPCLYQTDI DRRMF*

```

m142/a142 96.1% identity in 153 aa overlap

```

              10      20      30      40      50      60
m142.pep      MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMFNGNILMFVRQR
              |||||
a142           MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMFNGNILMFVRQR
              10      20      30      40      50      60

              70      80      90      100     110     120
m142.pep      IDAEAAVFRQDRNDSRTPVDAQHHGRRLLVGNRRDRRHCHNAVTPCRTVCRDDMNACRARCH
              |||||
a142           IDAEAAVFRQDRNDSRTPVDAQHHGRRLLVNRNRRRHCHNAVTPCRTVCRDDMNACRTGCH
              70      80      90      100     110     120

              130     140     150     159
m142.pep      RITERSLKI FLQIRHFSPLN CPLYKNAAHKASPHVQQFX
              |||||
a142           RITERSLKSF LQIRHFSPLN CPLYKNAAHKAPPMCSSSDSKSRRSDISARYGVLRVQRIL
              130     140     150     160     170     180

a142           DFGKFCQQVFKQQHFLAAQHFLDSVVTLVHFFADFLIQLLLALGSQLOKNTSLVVGRFQAD
              190     200     210     220     230     240

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 565>:

```

g143.seq
  1  ATGTTGAGCT TCGGCTATCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAAG
 51  CTCGCAGATG AGCCGCATTT TTCAAACGCT AGGCGCAGAC CCGCACAATT
101  TGGGCTGGTT TTTCATCCTG CCGCCGCTGG CGGGGATGCT GGTCAGCCG
151  ATAGTGgGCT ACTACTCAGA CCGCACTTGG AAGCCGCGCT TGGGCGGCCG
201  CCGCCTGCCG TATCTGCTTT ACGGCACGCT GATTGCGGTC ATCGTGATGA
251  TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCCTGGCG
301  GCCTTGTCGT TCGGCGCGCT GATGATTGCG CTGTTGGACG TGTCGTCGAA
351  TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGATATG GTC AACGAGG
401  AGCAGAAAAG CTACGCCTAC GGGATTCAA GTTCTTAGC GAATACGGAC
451  GCGGTTGTGG CAGCGATTCT GCCGTTTGTG TTcgcgata TCGGTTTGGC
501  GAACACTGCC GAGAAAGGCG TTGTGCCACA AACCCTGGTC GTAGCATTCT
551  ATGTGGGTGC GCGGTTACTG ATTATTACCA GTGCGTTCAC AATCTCCAAA
601  GTCAAAGAAT ACGACCCGGA AACCTACGCC CGTTACCACG GCATCGATGT
651  CGCCGCGAAT CAGGAAAAAG CCAACTGGTT CGAACTCTTA AAAACCGCGC
701  CTAAAGTGTT TTGGACGGTT ACTCCGGTAC AGTTTCTCTG TCGGTTTCGC
751  TTCCGGTATA TGTGGACTTA CTCGGCAGGC GCGATTGCAG AAAACGCTCTG
801  GCACACTACC GATGCGTCTT CCGTAGGCCA TCAGGAGGCG GGCAACCGGT
851  ACGGCGTTTT GGCGCGGGTG TAGTCGGTTG CGGCGGTGAT TTGTTCTGTTT
901  ATTCTGGCAA AAGTACCGAA TAAATACCAT AAGGCGGGTT ATTTCCGGCTG
951  TTTGGCTTTG GGCGCGCTCG GTTCTTCTC TATCTTCTC ATCTACAATC
1001 AATACGCACT CATCCTGTCT TATATCTTAA TCGGCATCGC TTGGCGGGC
1051 ATTATCACTT ATCCGCTGAC GATTGTGGCC AACGCTTTGT CGGGCAAAACA
1101 CATGGATACT TATTGGGCC TGTttaacg ctcgtCTGT ATGCcgcaaa
1151 tcgTcgctTC GctgttgAGT TTCGTGCTTT TCCCGATGCT GGGCGGCCAT

```


1201 CAGGCAACCA TGTTCTTGGT TGCAGGCGCA GTCTTGCTGC TGGGAGCCTT
 1251 CTCAGTCTGT CTGATTAAAG AGATCCACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 566; ORF 143.ng>:

g143.pep
 1 MLSFYGLGVQ TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP
 51 IVGYSDRTW KPRLGGRRLP YLLYGTLIAV IVMILMPNSG SFGFGYASLA
 101 ALSFALMIA LLDVSSNMAM QPFKMMVGDM VNEEQKSYAY GIQSFLANTD
 151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL IITSAFTISK
 201 VKEYDPETYA RYHGIDVAAN QEKANWFELL KTAPKVFMTV TPVQFFCWFA
 251 FRYMWYSAG AIAENVWHTT DASSVGHQEA GNRYGVLAHV *SVAVICSF
 301 ILAKVPNKYH KAGYFGCLAL GALGFFSIFV IYNQYALILS YILIGIAWAG
 351 IITYPLTIVA NALSGKHMDT YLGLFNGSVC MPQIVASLLS FVLFPMLGGH
 401 QATMFLVAGA VLLLGAFSVC LIKEIHGGV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 567>:

m143.seq
 1 ATGCTCAGTT TCGGCTTTCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAG
 51 CTCGCAAATG AGCCGCATTT TTCAAACGCT AGGCGCAGAC CCGCACAAAT
 101 TGGGCTGGTT TTTCAATCCTG CCGCCGCTGG CGGGGATGCT GGTGCAGCCG
 151 ATTGTCGGCC ATTACTCCGA CCGCACTTGG AAGCCGCGTT TGGGCGGCCG
 201 CCGTCTGCCG TATCTGCTTT ATGGCACGCT GATTGCGGTT ATTGTGATGA
 251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG
 301 GCTTTGTCTG TCGGCGCGCT GATGATTGCG CTGTTAGACG TGTCGTCAA
 351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGACATG GTCAACGAGG
 401 AGCAGAAAGG CTACGCCTAC GGGATTCAA GTTTCTTAGC AAATACGGGC
 451 GCGTCTGTGG CCGCGATTCT GCCGTTTGTG TTTGCGTATA TCGGTTTGGC
 501 GAACACCGCC GAGAAAGGCG TTGTGCCGCA GACCGTGGTC GTGGCGTTTT
 551 ATGTGGGTGC GCGTGTGCTG GTGATTACCA GCGCGTTCAC GATTTTCAA
 601 GTGAAGGAAT ACGATCCGGA AACCTACGCC CGTTACCACG GCATCGATGT
 651 CGCCGCGAAT CAGGAAAAAG CCAACTGGAT CGAACTCTTG AAAACCGCGC
 701 CTAAGGCGTT TTGGACGGTT ACTTTGGTGC AATTCTTCTG CTGGTTCCGC
 751 TTCCAATATA TGTGGACTTA CTCGGCAGGC GCGATTGCGG AAAACGCTCTG
 801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACTGGT
 851 ACGGCGTTTT GCGCGCGGTG CAGTCGGTTG CGGCGGTGAT TTGTTCTGTT
 901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGGCGGGTT ATTTCCGCTG
 951 TTTGGCTTTG GCGCGCTCG GCTTTTTCTC CGTTTTCTTC ATCGGCAACC
 1001 AATACGCGCT GGTGTTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC
 1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CGGGCAAGCA
 1101 TATGGGCACT TACTTGGGCT TGTTTAACGG CTCTATCTGT ATGCCTCAA
 1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG
 1201 CAGGCCACTA TGTTCTTGGT AGGGGGCGTC GTCCTGCTGC TGGGCGCGTT
 1251 TTCCGTGTTC CTGATTAAAG AAACACACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 568; ORF 143>:

m143.pep
 1 MLSFYGLGVQ TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP
 51 IVGHYSDRTW KPRLGGRRLP YLLYGTLIAV IVMILMPNSG SFGFGYASLA
 101 ALSFALMIA LLDVSSNMAM QPFKMMVGDM VNEEQKGYAY GIQSFLANTG
 151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSAFTIFK
 201 VKEYDPETYA RYHGIDVAAN QEKANWIELL KTAPKAFMTV TLVQFFCWFA
 251 FQYMWYSAG AIAENVWHTT DASSVGYQEA GNWYGVLAHV QSVAVICSF
 301 VLAQVPNKYH KAGYFGCLAL GALGFFSVFF IGNQYALVLS YTLIGIAWAG
 351 IITYPLTIVT NALSGKHMT YLGLFNGSIC MPQIVASLLS FVLFPMLGGH
 401 QATMFLVGGV VLLLGAFSVF LIKETHGGV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m143 / g143 93.9% identity in 429 aa overlap

10 20 30 40 50 60

406

m143.pep	MLSFGFLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSVRTW
g143	MLSFGYLGVTQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGYSDRTW
	10 20 30 40 50 60
m143.pep	70 80 90 100 110 120
	KPRLGGRRLLPYLLYGTLLIAVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
g143	KPRLGGRRLLPYLLYGTLLIAVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
	70 80 90 100 110 120
m143.pep	130 140 150 160 170 180
	QPFKMMVGDVNEEQGYAYGIQSFLANTGAVVAAILPFVFAYIGLANTAEGKVVPQTVV
g143	QPFKMMVGDVNEEQKSYAYGIQSFLANTDAVVAAILPFVFAYIGLANTAEGKVVPQTVV
	130 140 150 160 170 180
m143.pep	190 200 210 220 230 240
	VAFYVGAALLVITSFTIFKVKEYDPETYARYHGIDVAANQEKANWIELLKTA PKAFWTV
g143	VAFYVGAALLIITSFTISKVKEYDPETYARYHGIDVAANQEKANWFELLLKTA PKVFWTV
	190 200 210 220 230 240
m143.pep	250 260 270 280 290 300
	TLVQFFCWFAFYQYMWYSAGAIAENVWHTTDASSVGYQEAGNWWGVLA AVQSVAVICSF
g143	TPVQFFCWFAFRYMWYSAGAIAENVWHTTDASSVGHQEAGNRYGVLA AVXSVAVICSF
	250 260 270 280 290 300
m143.pep	310 320 330 340 350 360
	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT
g143	ILAKVPNKYHKAGYFGCLALGALGFFSIFFIYQYALILSYTLIGIAWAGIITYPLTIVA
	310 320 330 340 350 360
m143.pep	370 380 390 400 410 420
	NALSGKHMCTYLGFLNGSICMPQIVASLLSFVLPMLGGLQATMFLVGGVLLLGAFSVF
g143	NALSGKHMDTYLGFLNGSVCMQIVASLLSFVLPMLGGHQATMFLVAGAVLLLGAFSVC
	370 380 390 400 410 420
m143.pep	430
	LIKETHGGVX
g143	LIKEIHGGVX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 569>:

```

a143.seq
1   ATGCTCAGTT TCGGCTTTCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAG
51  CTCGCAGATG AGCCGCATCT TCCAGACGCT CGGTGCCGAT CCGCACAGCC
101 TCGGCTGGTT CTTTATCCTG CCGCCGCTGG CGGGGATGCT GTGCAGCCG
151 ATTGTCGGCC ATTACTCCGA CCGCACTTGG AAGCCGCGTT TGGGCGGCCG
201 CCGTCTGCCG TATCTGCTTT ATGGCACGCT GATTGCGGTT ATTGTGATGA
251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG
301 GCTTTGTCTG TCGGCGCGCT GATGATTGCG CTGTTAGACG TGTCGTCAAA
351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGACATG GTCACGAGG
401 AGCAGAAAGG CTACGCCTAC GGGATTCAAA GTTCTTAGC GAATACGGGC
451 GCGGTCGTGG CGGCGATTCT GCCGTTTGTG TTTGCGTATA TCGGTTTGGC
501 GAACACCGCC GAGAAAGGCG TTGTGCCGCA GACCGTGGTC GTGGCGTTTT
551 ATGTGGGTGC GGCCTTGCTG GTGATTACCA GCGCGTTCAC GATTTTCAAA
601 GTGAAGGAAT ACAATCCGGA AACCTACGCC CGTTACCACG GCATCGATGT
651 CGCCGCGAAT CAGGAAAAAG CCAACTGGAT CGAACTCTTG AAAACCGCGC
701 CTAAGGCGTT TTGGACGGTT ACTTTGGTGC AATTCTTCTG CTGGTTCGCC

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407

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751 TTCCAATATA TGTGGACTTA CTCGGCAGGC GCGATTGCGG AAAACGTCTG
801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACGGT
851 ACGGCGTTTT GCGGCGGGTG CAGTCGGTTG CGGCGGTGAT TTGTTCTGTTT
901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGGCGGGTT ATTTCTGGCTG
951 TTTGGCTTTG GCGCGGCTCG GCTTTTTCTC CGTTTTCTTC ATCGGCAACC
1001 AATACGCGCT GGTGTTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC
1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CGGGCAAGCA
1101 TATGGGCACT TACTTGGGCC TGTTTAACGG CTCTATCTGT ATGCCGCAAA
1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG
1201 CAGGCCACTA TGTTCTTGGT AGGGGGCGTC GTCCTGCTGC TGGGCGCGTT
1251 TTCCGTGTTC CTGATTAAAG AAACACACGG CGGGGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 570; ORF 143.a>:

```

a143.pep
1  ML$FGFLGVQ TAFTLQSSQM SRIFQTLGAD PHSLGWFFIL PPLAGMLVQP
51  IVGHYSDRTW KPRLGGRRLP YLLYGTLI$V IVMILMPNSG SFGFGYASLA
101 ALSFGALMIA LLDVSSNMAM QPFKMMVGDM VNEEQKGAY GIQSFLANTG
151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSAFTIFK
201 VKEYNPETYA RYHGIDVAAN QEKANWIELL KTAPKAFWTV TLVQFFCWFA
251 FQYMWTSAG AIAENVWHTT DASSVGYQEA GNWYGVLA$V Q$VA$VICSF
301 VLA$VPNKYH KAGYFGCLAL GALGFFSVFF IGNQYALVLS YTLIGIAWAG
351 IITYPLTIVT NALSGKHMGT YLGLFNGSIC MPQIVASLLS FVLF$PMLGGL
401 QATMFLVGGV VLLLGA$SVF LIKETHGGV*

```

m143/a143 99.5% identity in 429 aa overlap

```

              10      20      30      40      50      60
m143.pep      ML$FGFLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW
|||||
a143           ML$FGFLGVQTAFTLQSSQMSRIFQTLGADPHSLGWFFILPPLAGMLVQPIVGHYSDRTW
              10      20      30      40      50      60

              70      80      90      100     110     120
m143.pep      KPRLGGRRLPYLLYGTLI$VIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
|||||
a143           KPRLGGRRLPYLLYGTLI$VIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
              70      80      90      100     110     120

              130     140     150     160     170     180
m143.pep      QPFKMMVGDMVNEEQKGAYGIQSFLANTGAVVAAILPFVFAYIGLANTA$EKGVPQTVV
|||||
a143           QPFKMMVGDMVNEEQKGAYGIQSFLANTGAVVAAILPFVFAYIGLANTA$EKGVPQTVV
              130     140     150     160     170     180

              190     200     210     220     230     240
m143.pep      VAFYVGAALLVITSAFTIFKVKEYDPETYARYHGIDVAANQ$KANWIELLKTAPKAFWTV
|||||
a143           VAFYVGAALLVITSAFTIFKVKEYNPETYARYHGIDVAANQ$KANWIELLKTAPKAFWTV
              190     200     210     220     230     240

              250     260     270     280     290     300
m143.pep      TLVQFFCWFAFQYMWTSAG$AIAENVWHTTDASSVGYQ$EAGN$WYGVLA$VQ$VA$VICSF
|||||
a143           TLVQFFCWFAFQYMWTSAG$AIAENVWHTTDASSVGYQ$EAGN$WYGVLA$VQ$VA$VICSF
              250     260     270     280     290     300

              310     320     330     340     350     360
m143.pep      VLA$VPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT
|||||
a143           VLA$VPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT
              310     320     330     340     350     360

              370     380     390     400     410     420
m143.pep      NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLF$PMLGGLQATMFLVGGVVLLLGA$SVF

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```

a143      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLPMLGGLQATMFLVGGVVLLLGAFSVF
          370      380      390      400      410      420

          430
m143.pep  LIKETHGGVX
          |||||||||
a143      LIKETHGGVX
          430

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 571>:

```

g144.seq
1  ATGAGCGATA CCCCGCTAC CCGCGATTTC GGCCTGATCG ACGGGCGGGC
51 CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGTGC GTCTTCGTGC
101 TGGACTTGGG CGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC CCGTGGTGTC GTTCGACGAT GCGGCTTCCT ATCGGGACAA
201 TCCGTTTCAG ATTAACAAGC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGTAGGACTT ACCGCGTGGG GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTTCGCAC GGGCTGGCCG TTACCggtTT
351 CAACGCGGTG GCGGCAGACG GccgacggTt atCCCAACGA TTTGGatatt
401 TCctaccgCT TGGACGAGGA CGGCCGGCTT ACCGTtaccT ATCGCGCCAC
451 CGCgctCGGC GACACGGTGT TCGACCCGAC GCTGCACATT TACTGGCGGC
501 TGGACGCGGG CCTGCACGAT GCGGTTCTGC ATATTCCGCA GGGCGGACAT
551 ATTCGGCCG ATGCCGAAAA ACTGCCCGTC TTAACGGTTT CAGACGGCCT
601 CGAAGTATTT GA

```

This corresponds to the amino acid sequence <SEQ ID 572; ORF 144.ng>:

```

g144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTC VFVLDLGGIV QEFVSLADGV
51 RENPVVSFDD AASYADNPFQ INKQIGRVAG RIRGAAFDIN GRTYRVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRRLSQR FGYFLPLGRG RPAYRYLSRH
151 RARRHGVRPD AAHLLAAGRG PARCGSAYS A GRTYSGRCRK TARLNGFRRP
201 RSI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 573>:

```

m144.seq
1  ATGAGCGATA CCCCGCTAC CCGCGATTTC GGTCTGATCG ACGGGCGTGC
51 CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGCGT GTCTGCGTGC
101 TGGACTTGGG CGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC TCGTGGTGTC GTTCGATGAT GCGGCTTCCT ATCGGGACAA
201 TCCGTTTCAG ATTAACAAAC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGCAGGACTT ACCGCGTGGG GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTTCGCAC GGGCTGGCCG TTACCCGTTT
351 CAACGCGGTG GCGGCAGACG GCCGTTTCGGT GGTGCTGCGC AGCCGCTGg
401 CAACAGTCGG CCGACGGTTA TCCCAACGAT TTGGATTGG ATATTTCTTA
451 CCGCTTGGAC GAGGACGACC GGCTTACCGT TAcCTATCGC GCCACCGCGC
501 TCGGCGACAC GGTGTTTCGAC CCGACGCTGC ACATTTACTG GCGGCTGGAC
551 GCGGGCCTGC ACGATGCGGT TCTGCATATT CCGCAGGGCG GACATATGCC
601 GGCCGATGCC GAAAACTGC CCGTCTCAAC GGTTCAGAC GACCTCGAAG
651 TATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 574; ORF 144>:

```

m144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTR VCVLDLGGIV QEFVSLADGV
51 RENLVVSFDD AASYADNPFQ INKQIGRVAG RIRGAAFDIN GRTYRVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRSVVLR SRLATVGRRL SQRFQFGYFL
151 PLGRGRPAYR YLSRHRARRH GVRPDAAHLL AAGRGPARCG SAYSAGRTYA
201 GRCRKARLN GFRRPRSI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m144 / g144 91.3% identity in 218 aa overlap

```

      10      20      30      40      50      60
m144.pep  MSDTPATRD FGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEF SVLADGVREN LVVSFDD
          |||||||
g144      MSDTPATRD FGLIDGRAVTGYVLSNRRGTCVFVLDLGGIVQEF SVLADGVREN PVVSFDD
          10      20      30      40      50      60

      70      80      90     100     110     120
m144.pep  AASYADNPFQINKQIGRVAGRIRGA AFDINGRTYRVEANE GRNALHGGSHGLAVTRFNAV
          |||||||
g144      AASYADNPFQINKQIGRVAGRIRGA AFDINGRTYRVEANE GRNALHGGSHGLAVTRFNAV
          70      80      90     100     110     120

      130     140     150     160     170     180
m144.pep  AADGRSVVLR SRLATVGRRLSQRFGFGYFLPLGRGRPAYR YLSRHRARRHGVRPDAAHLL
          |||
g144      AAD-----GRRLSQRFG--YFLPLGRGRPAYR YLSRHRARRHGVRPDAAHLL
          130     140     150     160

      190     200     210     219
m144.pep  AAGRGPARGSAYSAGRTYAGRCRK TARLNGFRPRSIX
          |||||||
g144      AAGRGPARGSAYSAGRTYSGRCRK TARLNGFRPRSIX
          170     180     190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 575>:

```

a144.seq
1   ATGAGCGATA CCCCCGCTAC CCGCGATTTTC GGCCTGATCG ACGGGCGTGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGCGT GTCTGCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC TCGTGGTGTC GTTCGACGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAGC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGCAGGACTT ACCGCGTGGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTCGCAC GGGCTGGCCG TTACCCGTTT
351 CAACGCGGTG GCGGCAGACG GCCGTTTCGGT GGTGCTGCGC AGCCGCCTG.
401 CAACAGTCGG CCGACGGTTA TCCCAACGAT TTGGATTGG ATATTTCCTA
451 CCGCTTGGAC GAGGACGACC GGCTTACCGT TACCTATCGC GCCACCGCGC
501 TCGGCGACAC GGTGTTTCGAC CCGACGCTGC ACATTACTG GCGGCTGGAC
551 GCGGGCCTGC ACGATGCGGT TCTGCATATT CCGCAGGGCG GACATATTCC
601 GGCCGATGCC GAAAACTGC CCGTCTCAAC GGTTCAGAC GACCTCGAAG
651 TATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 576; ORF 144.a>:

```

a144.pep
1   MSDTPATRDF GLIDGRAVTG YVLSNRRGTR VCVLDLGGIV QEF SVLADGV
51  RENLVVSFDD AASYADNPFQ INKQIGRVAG RIRGA AFDIN GR TYRVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRSVVLR SRLXTVGRRL SQRFGFGYFL
151 PLGRGRPAYR YLSRHRARRH GVRPDAAHLL AAGRGPARGC SAYSAGRTYS
201 GRCRK TARLN GFRRPRSI*

```

m144/a144 99.1% identity in 218 aa overlap

```

      10      20      30      40      50      60
m144.pep  MSDTPATRD FGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEF SVLADGVREN LVVSFDD
          |||||||
a144      MSDTPATRD FGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEF SVLADGVREN LVVSFDD
          10      20      30      40      50      60

      70      80      90     100     110     120
m144.pep  AASYADNPFQINKQIGRVAGRIRGA AFDINGRTYRVEANE GRNALHGGSHGLAVTRFNAV

```

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```

|||||
a144      AASYADNPQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV
              70          80          90          100          110          120

              130          140          150          160          170          180
m144.pep  AADGRSVVLSRLATVGRRLSQRFQFGYFLPLGRGRPAYRYLSRHRARRHGVRPDAHLL
|||||
a144      AADGRSVVLSRLXTVGRRLSQRFQFGYFLPLGRGRPAYRYLSRHRARRHGVRPDAHLL
              130          140          150          160          170          180

              190          200          210          219
m144.pep  AAGRGPARGCSAYSAGRTYAGRCRKRTARLNGFRRPRSIX
|||||
a144      AAGRGPARGCSAYSAGRTYSGRCRKRTARLNGFRRPRSIX
              190          200          210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 577>:

```

g146.seq
1  ATGAAGCAAA TCCCCCTCCG CTTTCTCCAG GTCGTCATTG ACCACGACAA
51 AGTCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCCCTT CGACAGCCTC
101 CTTTGGATAA ctTCCCGACT GTCCGTCCCG CGCctTTGA GGCGCGCGGC
151 AAGCACGTCG AAAGAAGGCG GCAGGATAAA GATACCGACA GCTTCGGCA
201 GCGCGTTGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCACG
251 TCATAGCCTG CCGCCGCCAA CGCATTACAG CCCTCCGTGC TTGTGCCGTA
301 ATAGTTGCCG AATACGTCTG CGTATTCCAA AAAAGCTTCC TGCGCGATAA
351 GCGATTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGGCGGGCG CGTCGTATGC GACACGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTC CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAA CCGATTGTAT CACAACGAC ACCCTATTTT
601 ATATTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 578; ORF 146.ng>:

```

g146.pep
1  MKQIPLRLQ VVIDHDKVEQ YGLFDFMPCL RQPPLDNFPT VRPAPFEARG
51 KHVERRRQDK DTDSFRQVA NLRRALNVDF QNHVIACRRQ RIHALRACAV
101 IVAEYVCVFQ KSLLRDKREF LFFGNKVIMY AVCFAFTRRA RMRHGNAT
151 VMVCQQRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQRTPYF
201 IFADAHILPL LF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 579>:

```

m146.seq
1  ATGGCGCAAA TCCTCCTCCG CTCGCGCCAA GTCGTCATTG ACCACGACAA
51 AGTCAAACAA TACGGACTGC TCGATTTCAT GCCTTGCCCTT CGACAGCCTC
101 CTTTGGATAA CTTCCCGACT GTCCGTCCCG CGTCCGTTGA GGCGCGCGGC
151 AAGTACGTCG AAAGAAGGCG GCAGGATAAA GATGCCGACG GCTTCGGGCA
201 GCGCGTCGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCACG
251 TCATAGCCTG CCGCCGCCAA CGCATTACAC CCCTCCGCGC CTGTGCCGTA
301 ATAGTTGCCA AATACGTCCG CGTATTCCAA AAAAGCTTCC TGCGCGATAA
351 GCGACTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGGCGGGCG CGTCGTGTGC GACACGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTC CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAG CCGATTGTAT CACAATGGAC ACCCAGTTTC
601 CTATTGCGG ATGCCCATAT TTTGCCGCTA TTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 580; ORF 146>:

```

m146.pep
1  MAQILLRSRQ VVIDHDKVKQ YGLLDFMPCL RQPPLDNFPT VRPASVEARG
51 KYVERRRQDK DADGFGQVA NLRRALNVDF QNHVIACRRQ RIHTLRACAV
101 IVAKYVGVFQ KSFLRDKRLK LFFGNKVIMY AVCFAFTRRA RVRHGNAT
151 VMVCQQRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQWTPSF
201 LFADAHILPL LF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m146 / g146 90.1% identity in 212 aa overlap

	10	20	30	40	50	60
m146.pep	MAQILLRSRQVVIDHDKVKQYGLLDFMPCLRQPPLDNFPTVRPASVEARGKYVERRRQDK					
g146	MKQIPLRLQVVIDHDKVEQYGLDFMPCLRQPPLDNFPTVRPAPFEARGKHVERRRQDK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m146.pep	DADGFGQRVANLRRALNVDFQNHVIACRRQRIHTLRACAVIVAKYVGVFQKSFLRDKRLK					
g146	DTDSFRQVRANLRRALNVDFQNHVIACRRQRIHALRACAVIVAEYVCVFQKSLLRDKRKF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m146.pep	LFFGNKVIMYAVCFATRRARRVRHGNATVMVCQQPRHQGFARAGSGRNDKDVAFSIS					
g146	LFFGNKVIMYAVCFATRRARRMRHGNATVMVCQQPRHQGFARAGSGRNDKDVAFSIS					
	130	140	150	160	170	180
	190	200	210			
m146.pep	GHIFYLYIFQPIVSQWTPSFLFADAHILPLLFX					
g146	GHIFYLYIFQPIVSQRTPYFIFADAHILPLLFX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 581>:

```

a146.seq
  1  ATGGCGCAAA TCCTCCTCCG CCCGCGCCAA GTCATCATTG ACCACGACAA
 51  AATCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCCTT CGACAGCCTC
101  CTTTGGATAA CTCCCGACT GTCCGTCCCG CGTCCGTGA GACGCGCAGC
151  AAGCACATCG AAAGACGGCG GCAGGATAAA GATGCCGACG GCTTCGGGCA
201  GCGCATCTCG AACCTGAGCC GCGCCCTGAA CGTCGATTTC CAAATCAGC
251  TCATAACCTG CCGCCGCCAA CGCATTCA CA CCTCCGCGC TTGTGCCGTA
301  ATAGTTGCCG AACACGTCCG CGTATTCCAA AAAAGCCTCC TCGCGGATAA
351  GCGACTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401  TCGCCTTCAC GCGGCGGACG CGTCGTGTGC GACACGAAA CGCGCAAACC
451  GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTC CCCGTGCCGG
501  AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551  TTTACCTGTA TATTTTCCAG CCGATTGTAT CACAACGGAC ACCCGGTTTC
601  CTATTTGCCG ATGCCCATAT TTGCGCGCTA TTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 582; ORF 146.a>:

```

a146.pep
  1  MAQILLRPRQ VIIDHDKIEQ YGLDFMPCL RQPPLDNFPT VRPASVETRS
 51  KHIERRRQDK DADGFGQRIS NLSRALNVDF QNHVITCRRQ RIHTLRACAV
101  IVAEHVRVFQ KSLLRDKRLK LFFGNKVIMY AVCFAFTRRT RVRHGNAT
151  VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQRTPGF
201  LFADAHILPL LF*

```

m146/a146 90.6% identity in 212 aa overlap

	10	20	30	40	50	60
m146.pep	MAQILLRSRQVVIDHDKVKQYGLLDFMPCLRQPPLDNFPTVRPASVEARGKYVERRRQDK					
a146	MAQILLRPRQVIIDHDKIEQYGLDFMPCLRQPPLDNFPTVRPASVETRSKHIERRRQDK					
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m146.pep  DADGFGQRVANLRRALNVDFQNHVIACRRQRIHTLRACAVIVAKYVGVFQKSFLRDKRLK
           |||||::|| |||||::|||:|||||::|||:| |||||::|||
a146       DADGFGQRI SNLSRALNVDFQNHVITCRRQRIHTLRACAVIVA EHVRFQKSLLRDKRLK
           70      80      90      100     110     120

           130     140     150     160     170     180
m146.pep  LFFGNKVIMYAVCFATRRARRVRHGN AQTVMVCQQPRHQRFARAGSGRNDKDVAFSIS
           |||||::|||:|||||::|||:| |||||::|||
a146       LFFGNKVIMYAVCFATRRARRVRHGN AQTVMVCQQPRHQRFARAGSGRNDKDVAFSIS
           130     140     150     160     170     180

           190     200     210
m146.pep  GHIFYLYIFQPIVSQWTPSFLFADAHILPLLFX
           |||||::|||:|||||::|||:| |||||::|||
a146       GHIFYLYIFQPIVSQRTPGFLFADAHILPLLFX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 583>:

```

g147.seq (partial)
1  ..ATGCGACGAG AAGCCAAAAT GGCACAAATC ACAC TCAAAC CCATTGTTTT
51  ATCAATTCTT TTAATCAACA CACCCTCCT CGCCCAAGCG CATGAAACTG
101 AGCAATCGGT GGGCTTGGA ACGGTCAGCG TCGTCGGCAA AAGCCGTCCG
151 CGCGCGACTT CGGGGCTGCT GCACACTTCG ACCGCCTCCG ACAAATCAT
201 CTCCGGCGAT ACTTTGCGCC AAAAAGCCGT CAACTTGGGC GACGCTTGG
251 ACGGCGTACC GGGCATCCAC GCTTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC GGGCAGACGG ATTAAAGTAT TGAACCATCA
351 CGGCGAAACG GCGGATATGG CGGACTTTTC TCCGATCAC GCCATTATGG
401 TAGATACCGC CTTGTCGCAA CAGGTGAAA TCCTGCGCGG GCCGGTTACG
451 CTCTTGTA CA GCTCGGgcaa tgtggccgGG GCTGGtcaat gttgccgatg
501 gAAAAAtccc ccaaaaAAtg cc..

```

This corresponds to the amino acid sequence <SEQ ID 584; ORF 147.ng>:

```

g147.pep (partial)
1  ..MRREAKMAQI TLKPIVLSIL LINTPLLAQA HETEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRGQTGRR IKVLNHHGET GDMADFS PDH AIMVDTALSQ QVEILRGPVT
151 LLYSSGNVAG AGQCCRWNKP PKNA..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 585>:

```

m147.seq (partial)
1  ..CCGCATAAAA CTGAGCAATC GGTGGATTTG GAAACGGTCA GCGTCGTCGG
51  CAAAAGCCGT CCGCGCGCCA CGTCGGGGCT GTTGACACT TCGACCGCCT
101 CCGACAAAAT CATCTCCGGC GATACCTTGC GCCAAAAGC CGTCAACTTG
151 GGCGACGCTT TAGACGGCGT ACCGGGCATC CACGCTTCG AATACGGCGG
201 CGGCGCGTCT GCTCCCGTCA TTCGCGGTCA AACAGGCAGG CGGATTAAAG
251 TGTTGAACCA TCACGGCGAA ACAGGCGATA TGGCGGATTT TTCGCCGAT
301 CACGCCATTA TGGTAGATAC CGCCTTGTCG CAACAGGTCG AAATCCTGCG
351 CGGGCCGGTT ACGCTCTTGT ACAGCTCGG CAATGTGGCG GGGCTGGTCG
401 ATGTTGCCGA TGGCAAAATC CCCGAAAAA TGCCTGAAAA CGGCGTATCG
451 GGCGAACTCG GATTGCGTTT GAGCAGCGGC AATCTGAAA AACTCACGTC
501 CGGCGGCATC AATATCGGTT TGGGCAAAA CTTGTATTG CACACGGAAG
551 GGCTGTACCG CAAATCGGGG GATTACGCCG TACCGCGTTA CCGCAATCTG
601 AAACGCCTGC CCGAGCCA CGCGATTTC CAAACGGGCA CCGCGGCT
651 GTCTTGGGTT GGCGAAAAG GTTTTATCGG CGTAGCGTAC AGCGACGTC
701 GCGACCAATA TGGTCTGCCT GCCCAGACC ACGAATACGA TGATTGCCAC
751 GCCGACATCA TCTGGCAAAA GAGCTTGATT AACAAACGCT ATTTACAGCT
801 TTATCCGCAC CTGTTGACCG AAGAAGACAT CGATTACGAC AATCCGGGCT
851 TGAGCTGCGG CTTCCACGAC GACGATAATG CACACGCACA CACCCACAGC
901 GGCAGACCGT GGATAGACCT GCGCAACAAA CGCTACGAAC TCCGTGCCGA
951 ATGGAAGCAA CCGTTCCTCG GTTTTGAAGC CCTGCGCGTA CACCTGAACC
1001 GCAACGACTA CCGCCACGAC GAAAAGCAG GCGATGCAGT CGAAAACCTT
1051 TTAAACAACC AAACGCAAAA CGCCCGCATC GAGTTGCGCC ACCAACCCAT

```



```

1101 AGGTCGTCTG AAAGGCAGCT GGGGCGTGCA ATATTTACAA CAAAATCCA
1151 GTGCTTTATC TGCCATATCC GAAGCGGTTA AACAAACGAT GCTGCTTGAC
1201 AACAAAGTGC AACATTACAG CTTTTTCGGT GTAGAACAGG CAAACTGGGA
1251 CAACTTCACG CTTGAAGGAG GCGTACGCGT GGAAAAACAA AAAGCCTCCA
1301 TTCAGTACGA CAAAGCATTG ATTGATCGGG AAAACTACTA CAACCACCCC
1351 CTGCCCCGACC TCGGCGCGCA CCGCCAAACC GCCCGCTCAT TCGCACTTTC
1401 GGGCAACTGG TATTTACACG CACAACACAA ACTCAGCCTG ACCGCCTCCC
1451 ATCAGGAACG CCTGCCGTCA ACGCAAGAGC TGTACGCACA CGGCAAACAC
1501 GTCGCCACCA ACACCTTTGA AGTCGGCAAC AAACACCTCA ACAAAGAGCG
1551 TTCCAACAAT ATCGAACTCG CGCTGGGCTA CGAAGGCGAC CGCTGGCAAT
1601 ACAATCTGGC ACTCTACCGC AACCGCTTCG GTAACCTACAT TTACGCCCAA
1651 ACCTTAAACG ACGGACGCGG CCCCAAATCC ATCGAAGACG ACAGCGAAAT
1701 GAAGCTCGTG CGCTACAACC AATCCGGCGC CGACTTCTAC GCGCGGGAAG
1751 GCGAAATCTA CTTCAAACCG ACACCGCGCT ACCGCATCGG CGTTTCCGGC
1801 GACTATGTAC GAGGCCGTCT GAAAAACCTG CCTTCCCTAC CCGGCAGAGA
1851 AGATGCCTAC GGCAACCGTC CTTTCATCGC ACAGGACGAC CAAAATGCCC
1901 CCCGTGTTCC GGCTGCGCGC CTCGGCTTCC ACCTGAAAGC CTCGCTGACC
1951 GACCGTATCG ATGCCAATTT GGACTACTAC CGCGTGTTCC CCCAAAACAA
2001 ACTCGCCCGC TACGAAACGC GCACGCCCGG ACACCATATG CTCAACCTCG
2051 GCGCAAACCTA CCGCCGCAAT ACGCGCTATG GCGAGTGGAA TTGGTACGTC
2101 AAAGCCGACA ACCTGCTCAA CCAATCCGTT TACGCCACAA GCAGCTTTCT
2151 CTCTGATACG CCGCAAATGG GCCGCAGCTT TACCGGCGGC GTGAACGTGA
2201 AGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 586; ORF 147>:

```

m147.pep (partial)
1 ..PHKTEQSVDL ETVSVVGKSR PRATSGLLHT STASDKIISG DTLRQKAVNL
51 GDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGE TGDMAFSPD
101 HAIMVDTALS QQVEILRGPV TLLYSSGNVA GLVDVADGKI PEKMPENGVS
151 GELGLRLSSG NLEKLTSGGI NIGLGKNFVL HTEGLYRKSG DYAVPRYRNL
201 KRLPDSHADS QTGSIGLSWV GEKGFIVGAY SDRRDQYGLP AHSHEYDDCH
251 ADIIWQKSLI NKRYLQLYPH LLTEEDIDYD NPGLSCGFHD DDNAHAHTS
301 GRPWIDLRNK RYELRAEWKQ PFPGFALRV HLNRRNDYRHD EKAGDAVENF
351 FNNQTQNARI ELRHQPIGRL KGSWGVQYLQ QKSSALS AIS EAVKQPMMLD
401 NKVQHYSFFG VEQANWDNFT LEGGVRVEKQ KASIQYDKAL IDRENNYHNP
451 LPDLGAHROT ARSFALSGNW YFTPQHKLSL TASHQERLPS TOELYAHGKH
501 VATNTFEVGN KHLNKRSEN IELALGYEGD RWQYNLALYR NREFGNYIYAQ
551 TLNDGRGPKS IEDDSEMKLV RYNQSGADFY GAEGEIFYFK TPRYRIGVSG
601 DYVRGLKNL PSLPGREDAY GNRPFIAQDD QNAPRVPAAR LGFHLKASLT
651 DRIDANLDYY RVFAQNKLAR YETRTPGHHM LNLGANYRRN TRYGEWNWYV
701 KADNLLNQSV YAHSSFLSDT PQMGRSFTGG VNVKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m147 / g147 92.3% identity in 142 aa overlap

```

                                10      20      30
m147.pep                      PHKTEQSVDL ETVSVVGKSR PRATSGLLHTS
                                |:||||| |
g147                          MRREAKMAQITLKPIVLSILLINTPLLAQAHE TEQSVGLE TVSVVGKSR PRATSGLLHTS
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m147.pep                      TASDKIISGDTLRQKAVNLGDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGET
                                |
g147                          TASDKIISGDTLRQKAVNLGDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGET
                                70      80      90      100     110     120

                                100     110     120     130     140     150
m147.pep                      GDMADFSPDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGLVDVADGKI PEKMPENGVS
                                |
g147                          GDMADFSPDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGAGQCCRWKNPPKNA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 587>:

```

a147.seq
1   ATGCGACGAG AAGCCAAAAT GGCACAAACT AACTCAAAC CCATTGTTTT
51  ATCAATTCTT TTAATCAACA CACCCCTCCT CTCCAAGCG CATGGAAGTG
101 AGCAATCAGT GGGCTTGGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTCGG
151 CGCGCCACTT CGGGGCTGCT GCACACTTCT ACCGCCTCCG ACAAATCAT
201 CAGCGGCGAC ACCTTGCAGC AAAAAGCCGT CAACTTGGGT GATGCTTTAG
251 ACGGCGTACC GGGCATTTCAT GCCTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC AGGCAGACGG ATTAAGTGT TGAACCATCA
351 CGGCGAAACG GGCACATGG CCGACTTCTC TCCAGACCAT GCAATCATGG
401 TGGACAGCGC CTTGTTCGAA CAGGTCGAAA TCCTGCGCGG TCCGTTACG
451 CTCTTGTAACA GCTCGGGCAA TGTGGCGGGG CTGGTCGATG TTGCCGATGG
501 CAAAATCCCC GAAAAAATGC CTGAAAACGG CGTATCGGGC GAACTCGGAT
551 TGCGTTTGAG CAGCGGCAAT CTGGA AAAAC TCACGTCCGG CGGCATCAAT
601 ATCGGTTTGG GCAAAAACCT TGTATTGCAC ACGGAAGGGC TGTACCGCAA
651 ATCGGGGGAT TACGCCGTAC CGCGTTACCG CAATCTGAAA CGCTGCCCG
701 ACAGCCACGC CGATTTCGAA ACGGCGAGCA TCGGGCTGTC TTGGGTTGGC
751 GAAAAAGGCT TTATCGGCGC AGCATAACAG GACCGTCGCG ACCAATATGG
801 TCTGCCTGCC CACAGCCACG AATACGATGA TTGCCACGCC GACATCATCT
851 GGCAAAAGAG TTTGATTAAC AAACGCTATT TGCAGCTTTA TCCGCACCTG
901 TTGACCGAAG AAGACATCGA TTACGACAAT CCGGGCTTGA GCTGCGGCTT
951 TCACGACGAC GATGATGCAC ACGCCCATGC CCACAACGGC AAACCTTGGA
1001 TAGACCTGCG CAACAAACGC TACGAACTCC GCGCCGAATG GAAGCAACCG
1051 TTCCCCGGTT TTGAAGCCCT GCGCGTACAC CTGAACCGCA ACGACTACCG
1101 CCACGACGAA AAAGCAGGCG ATGCAGTAGA AAACCTTTTT AACAACTAAA
1151 CGCAAAACGC CCGTATCGAG TTGCGCCACC AACCCATAGG CCGTCTGAAA
1201 GGCAGCTGGG GCGTGCAATA TTTGGGACAA AAATCCAGTG CTTTATCTGC
1251 CACATCCGAA GCGGTCAAAC AACCGATGCT GCTTGACAAT AAAGTGCAAC
1301 ATTACAGCTT TTTCGGTGTA GAACAGGCAA ACTGGGACAA CTCACGCTT
1351 GAAGGCGGCG TACGCGTGGA AAAACAAAAA GCCTCCATCC GCTACGACAA
1401 AGCATTGATT GATCGGAAA ACTACTACAA CCATCCCCTG CCCGACCTCG
1451 GCGCGCACCG CCAAACCGCC CGCTCATTCG CACTTTCGGG CAACTGGTAT
1501 TTCACGCCAC AACACAAACT CAGCCTGACC GCCTCCATC AGGAACGCCT
1551 GCGTCAACG CAAGAGCTGT ACGCACACGG CAAACACGTC GCCACCAACA
1601 CCTTTGAAGT CGGCAACAAA CACCTCAACA AAGAGCGTTC CAACAATATC
1651 GAACTCGCGC TGGGCTACGA AGGCGACCGC TGGCAATACA ATCTGGCACT
1701 CTACCGCAAC CGCTTCGGCA ACTACATTTA CGCCCAAACC TTAAACGACG
1751 GACGCGGCCC CAAATCCATC GAAGACGACA GCGAAATGAA GCTCGTGCGC
1801 TACAACCAAT CCGGTGCGGA CTCTACGGC GCGGAAGGCG AAATCTACTT
1851 CAAACCGACA CCGCGCTACC GCATCGGCGT TTCCGGCGAC TATGTACGAG
1901 GCCGTCTGAA AAACCTGCCT TCCCTACCCG GCAGGGAAGA CGCCTACGGC
1951 AACCGCCAC TCATTGCCCA AGCCGACCAA AACGCCCCTC GCGTTCCGGC
2001 TGCGCGCCTC GGCGTCCACC TGAAAGCCTC GCTGACCGAC CGCATCGATG
2051 CCAATTTGGA CTACTACCGC GTGTTGCGCC AAAACAAACT CGCCGCTAC
2101 GAAACGCGCA CGCCCGGACA CCATATGCTC AACCTCGGCG CAACTACCG
2151 CCGCAATACG CGCTATGGCG AGTGAATTG GTACGTCAA GCGGACAACC
2201 TGCTCAACCA ATCCGTTTAC GCCACAGCA GCTTCCTCTC TGATACGCCG
2251 CAAATGGGCC GCAGCTTTAC CGGCGGCGTG AACGTGAAGT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 588; ORF 147.a>:

```

a147.pep
1   MRREAKMAQT TLKPIVLISIL LINTPLLSQA HGTEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRGQTGRR IKVLNHHGET GDMADFSPDH AIMVDSALSQ QVEILRGFVT
151 LLYSSGNVAG LVDVADGKIP EKMPENGVSQ ELGLRLSSGN LEKLTSGGIN
201 IGLKGNFVLH TEGLYRKSGD YAVPRYRNK RLPDSHADSQ TGSIGLSWVG
251 EKGFIGAAYS DRRDQYGLPA HSHEYDDCHA DIIWQKSLIN KRYLQLYPHL
301 LTEDIDIDYN PGLSCGFHDD DDAHAHAHNG KPWIDLNRKR YELRAEWKQP
351 FPGFEALRVH LNRNDYRHDE KAGDAVENFF NNQTQNAIE LRHQPIGRK
401 GSWGVOYLQK KSSALSATSE AVKQPMLLDN KVQHSFFGV EQANWDNFTL
451 EGGVRVEKQK ASIRYDKALI DRENYNHPL PDLGAHRQTA RSFALSGNWX
501 FTPQHKLSLT ASHQERLPST QELYAHGKHV ATNTFEVGNK HLNKERSNNI
551 ELALGYEGDR WQYNLALYRN RFGNYIYAQT LNDGRGPKSI EDDSEMKLVR

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601 YNQSGADFYG AEGEIYFKPT PRYRIGVSGD YVRGRLKNLP SLPGREDAYG
651 NRPLIAQADQ NAPRVPAARL GVHLKASLTD RIDANLDYYR VFAQNKLARY
701 ETRTPGHHML NLGANYRRNT RYGEWNWYVK ADNLLNQSVY AHSSFLSDTP
751 QMGRSFTGGV NVKF*

m147/a147 98.1% identity in 734 aa overlap

m147.pep				10	20	30
				PHKTEQSV	DLTVSVVGKSRPRATS	SGLLHTS
a147	MRREAKMAQTTLKPIVLSILLINTPLLSQA	HGTEQSVG	LET	TVSVVGKSRPRATS	SGLLHTS	
	10	20	30	40	50	60
m147.pep	40	50	60	70	80	90
	TASDKIISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGET				
a147	TASDKIISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGET				
	70	80	90	100	110	120
m147.pep	100	110	120	130	140	150
	GDMADFSPDHAIMVDTALSQQVEILRGPV	TLLYSSGNVAGLVDVADGKIPEKMPENGVS	G			
a147	GDMADFSPDHAIMVDSALSQQVEILRGPV	TLLYSSGNVAGLVDVADGKIPEKMPENGVS	G			
	130	140	150	160	170	180
m147.pep	160	170	180	190	200	210
	ELGLRLSSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRNKRLPDSHAD	SQ			
a147	ELGLRLSSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRNKRLPDSHAD	SQ			
	190	200	210	220	230	240
m147.pep	220	230	240	250	260	270
	TGSIGLSWVGEGKGFIVAYS	DRRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHL				
a147	TGSIGLSWVGEGKGFIVAYS	DRRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHL				
	250	260	270	280	290	300
m147.pep	280	290	300	310	320	330
	LTEEDIDYDNPGLSCGFHDDDDNAHAH	THSGRPWIDLNRKRYELRAEWKQPFPGFEALRVH				
a147	LTEEDIDYDNPGLSCGFHDDDDNAHAH	AHNGKPWIDLNRKRYELRAEWKQPFPGFEALRVH				
	310	320	330	340	350	360
m147.pep	340	350	360	370	380	390
	LNRNDYRHDEKAGDAVENFFNNQTQ	NARIELRHQPIGRKLGSGWGVQYLQOKSSALS	SAISE			
a147	LNRNDYRHDEKAGDAVENFFNNQTQ	NARIELRHQPIGRKLGSGWGVQYLQOKSSALS	SATSE			
	370	380	390	400	410	420
m147.pep	400	410	420	430	440	450
	AVKQPMLLDNKVQHYSFFGVEQANW	NFTLEGGVRVEKQKASIQYDKALIDRENYYNHPL				
a147	AVKQPMLLDNKVQHYSFFGVEQANW	NFTLEGGVRVEKQKASIRYDKALIDRENYYNHPL				
	430	440	450	460	470	480
m147.pep	460	470	480	490	500	510
	PDLGAHRQTARSFALSGNWFYTPQ	HKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK				
a147	PDLGAHRQTARSFALSGNWFYTPQ	HKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK				
	490	500	510	520	530	540
m147.pep	520	530	540	550	560	570
	HLNKERSNNIELALGYEGDRWQYN	LALYRNRFNGNYIYAQT	LNDGRGPKSIEDDSEM	KLVR		
a147	HLNKERSNNIELALGYEGDRWQYN	LALYRNRFNGNYIYAQT	LNDGRGPKSIEDDSEM	KLVR		

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	550	560	570	580	590	600
	580	590	600	610	620	630
m147.pep	YNQSGADFYGAEGEIFYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFFIAQDDQ					
a147						
	610	620	630	640	650	660
	640	650	660	670	680	690
m147.pep	NAPRVPAARLGFHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNT					
a147						
	670	680	690	700	710	720
	700	710	720	730		
m147.pep	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
a147						
	730	740	750	760		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 589>:

```

g148.seq
1  ATGGCGTTAA  AAACATCAAA  CTTGGAACAC  GCAATGctgg  ttcaTCCCGA
51  AgctATgagt  gtccgCGCGC  TTGccgAcaa  AATCCGCAAA  AtcgaAAact
101 gGCCGCAAAA  AGgcaTCTTA  TTCCACGACA  TCACGCCCCG  CCTGCAAAGT
151 GCGGAATACT  TCCGCCTTTT  GGTCGATTTG  CTGGTTTACC  GCTATATGGA
201 TCAGAAAATC  GACATCGTTG  CCGGCTTGGA  CGCGCGCGGC  TTCATTATCG
251 GCGCGGCACT  CGCCTACCAG  CTCAaCGtcg  gctTCGTCCC  CATCCGCAAA
301 AAAGGCAAGC  TGCCTTTTGA  AACCGTATCG  CAAAGCTAcg  cgcTCGAATA
351 CGGGGAAGCT  GCGGTGGAa  TCCACACCGa  tgccgTCAAA  CCCGTTTCGC
401 GCGTCCTGCT  GGTCGATGAT  TTGGTTGCCA  CGGGCGGCAC  AATGCTTGCC
451 GGGCTGGAAC  TGATCCGCAA  ACTCGGCGGG  GAAATTGTCT  AAgccgccgC
501 CATTTTGGAA  TTTACCGACC  TTCAAGGCGG  CAAGAATATC  CGCGCAAGTG
551 GCGCGCCCTT  ATTTACCCTG  CTTCAAAACG  AAGGCTGCAT  GAAAGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 590; ORF 148.ng>:

```

g148.pep
1  MALKTSNLEH  AMLVHPEAMS  VGALADKIRK  IENWPQKGIL  FHDITPVLQS
51  AEYFRLLVDL  LVYRYMDQKI  DIVAGLDARG  FIIGAALAYQ  LNVGFVPIRK
101 KGKLPFETVS  QSYALEYGEA  AVEIHTDAVK  PGRVLLVDD  LVATGGTMLA
151 GLELIRKLGG  EIVEAAAILE  FTDLQGGKNI  RASGAPLFTL  LQNEGCMKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 591>:

```

m148.seq
1  ATGGCGTTAA  AAACATCAAA  CTTGGAACAC  GCAATGCTGG  TTCATCCCGA
51  AGCTATGAGT  GTCGGCGCGC  TTGCCGACAA  AATCCGCAAA  ATCGAAAAC
101 GGCCGCAAAA  AGGCATCTTA  TTCCACGACA  TCACGCCCCG  CCTTCAAAGC
151 GCGGAATACT  TCCGCCTTTT  GGTGATTGTA  TTGGTTTACC  GCTATATGGA
201 TCAGAAAATC  GACATCGTTG  CCGGTTTGGA  CGCGCGCGGC  TTCATTATCG
251 GCGCGGCACT  CGCCTACCAG  CTCAACGTCG  GTTTCGTCCC  CATCCGCAAA
301 AAAGGCAAGC  TGCCTTTTGA  AACCGTATCG  CAAAGCTACG  CGCTCGAATA
351 CGGGGAAGCT  GCGGTGGAa  TCCACACCGa  TGCCGTCAAA  CTCGGTTTCG
401 GCGTGCTGCT  GGTCGATGAT  TTGATTGCCA  CGGGCGGCAC  GATGCTTGCC
451 GGACTGGAAC  TGATCCGCAA  ACTCGGCGGA  GAAATTGTCT  AAGCCGCCGC
501 CATTTTGGAA  TTTACCGACC  TTCAAGGCGG  CAAGAATATC  CGTGAAGCG
551 GCGCGCCCTT  ATTTACCCTG  CTTCAAAACG  AAGGCTGTAT  GAAGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 592; ORF 148>:

```

m148.pep
1  MALKTSNLEH  AMLVHPEAMS  VGALADKIRK  IENWPQKGIL  FHDITPVLQS
51  AEYFRLLVDL  LVYRYMDQKI  DIVAGLDARG  FIIGAALAYQ  LNVGFVPIRK

```

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101 KGKLPFETVS QSYALEYGEA AVEIHTDAVK LGSRVLLVDD LIATGGTMLA
 151 GLELIRKLGG EIVEAAAILE FTDLQGGKNI RASGAPLFTL LQNEGCMKG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m148 / g148 99.0% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
g148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m148.pep	LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
g148	LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m148.pep	AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
g148	AVEIHTDAVKPGSRVLLVDDLVATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
	130	140	150	160	170	180
	190	200				
m148.pep	RASGAPLFTLLQNEGCMKGX					
g148	RASGAPLFTLLQNEGCMKGX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 593>:

a148.seq

1	ATGGCGTTAA	AAACATCAAA	CTTGAACAC	GCAATGCTGG	TTCATCCCGA
51	AGCTATGAGT	GTCGGTGCGC	TTGCCGACAA	AATCCGCAAA	ATCGAAAAC
101	GGCCGCAAAA	AGGCATCTTA	TTCCACGACA	TCACGCCCCG	CCTGCAAAGC
151	GCGGAATACT	TCCGACTTTT	GGTTGATTTA	TTGGTTTACC	GCTATATGGA
201	TCAGAAAATC	GACATCGTTG	CCGGTTTGGA	CGCGCGCGGC	TTCATTATCG
251	GCGCGGCACT	CGCCTACCAG	CTCAACGTCG	GTTTCGTCCC	CATCCGCAAA
301	AAAGGCAAGC	TGCCTTTTGA	AACCGTATCG	CAAAGCTACG	CGCTCGAATA
351	CGGGGAAGCT	GCGGTGGAAA	TCCACACCGA	TGCCGTCAAA	CTCGGTTTCG
401	GCGTGCTGCT	GGTCGATGAT	TTGGTTGCCA	CGGGCGGCAC	GATGCTTGCC
451	GGACTGGAGC	TGATCCGCAA	ACTCGGCGGG	GAAATTGTCT	AAGCCGCCGC
501	CATTTTGGA	TTTACCGACC	TTCAAGGCGG	CAAGAATATC	CGTGCAAGCG
551	GCGCGCCCTT	ATTTACCCTG	CTTCAAAACG	AAGGCTGTAT	GAAGGGCTGA

This corresponds to the amino acid sequence <SEQ ID 594; ORF 148.a>:

a148.pep

1	MALKTSNLEH	AMLVHPEAMS	VGALADKIRK	IENWPQKGIL	FHDITPVLQS
51	AEYFRLLVDL	LVYRYMDQKI	DIVAGLDARG	FIIGAALAYQ	LVNVGFVPIRK
101	KGKLPFETVS	QSYALEYGEA	AVEIHTDAVK	LGSRVLLVDD	LVATGGTMLA
151	GLELIRKLGG	EIVEAAAILE	FTDLQGGKNI	RASGAPLFTL	LQNEGCMKG*

m148/a148 99.5% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
a148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120

418

```

m148.pep      LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a148          LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA
               70      80      90      100     110     120

               130     140     150     160     170     180
m148.pep      AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
               ||||||||||||||||:||||||||||||||||||||||||||||||||||||
a148          AVEIHTDAVKLGSRVLLVDDLVATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
               130     140     150     160     170     180

               190     200
m148.pep      RASGAPLFTLLQNEGCMKGX
               ||||||||||||||||||
a148          RASGAPLFTLLQNEGCMKGX
               190     200

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 595>:

```

g149.seq
1   ATGTTGATTG ACAACAATGT CCGCCATTAC AGCTTTTTTCG GTGTAGAACA
51  GGCAAATTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGAAAAAC
101 AAAAAGCCTC CATCCGGTAC GACAAAGCAT TGATTGATCG AGAAAACCTAC
151 TACAACCAGC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201 GTTCGCACTT TCGGGCAACT GGTATTTTAC GCCACACCAC AAACCTCAGCC
251 TGACCGCCTC CCATCAGGAA cgCCTGCCGT CAACGCaagA actGtACgca
301 cacggcAAGC ACGtcgccac CAACACCTTT GAagtcggca acaaACACCT
351 CAACAAAGaG CgttccaacA atatcgaACT CGCGCTGGgc tAcaaaggcg
401 accGCTGGCA ATACAATCTG GCAGCCTACC GCAACCGAtT CGGCAACTAC
451 ATTTACGCCC AAACCTTAaa cgacggacgC GGCCCAAAAT CCATCgaaga
501 cgacagcgaa ATGaagcTCG TGCGCTACAA CCAATCCGGT GCCGACTTCT
551 ACGgcgcgga aggcgaaatc tACTTcaaaC CGACACCGCG CTACCGCATC
601 GGTGTTTCCG GCGACTatgt acgaggccgT CTGAAAAACC TGCCGTCCCT
651 ACCCGGCAGG gaagatccCT AcggcAAACG TCccttcaTC GCACAAGCCG
701 ACCAAAACGC CCCCCGATT ceggcTGGC GCCTCGGCTT CCACCTGAAA
751 ACCTCGCTAA CCGACCGTAT CGATGCCAAT TTGGACTACT ACCGCGTGTT
801 CGCCCAAAAC AAACCTCGCCC GCTACGAAAC GCGTACGCCC GGACACCATA
851 TGCTCAACCT CGGTGCAAAc TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901 AATTGGTACG TCAAAGCCGA CAACCTGctc aACcaatCcg tTTACGCCCCa
951 cAGCAGCTTC CTCTCTGATA CGCCGCAAAc gGGCCGCAGC TTtgccgGCg
1001 gcgtaAACGT GaAGTTttaA

```

This corresponds to the amino acid sequence <SEQ ID 596; ORF 149.ng>:

```

g149.pep
1   MLIDNNVRHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY
51  YNQPLPDLGA HRQTARSFAL SGNWYFTPHH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YKGDWRQYNL AAYRNRFGNY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201 GVSVDYVRGR LKNLPSLPGR EDPYGKRPFi AQADQNApRI PAARLGfHLK
251 TSLTDRIDAN LDYYRVFAQN KLARYETRTP GHMLNLGAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FAGGVNVKF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 597>:

```

m149.seq
1   ATGCTGCTTG ACAACAAAGT GCAACATTAC AGCTTTTTTCG GTGTAGAACA
51  GGCAAACCTG GACAACTTCA CGCTTGAAGG AGGCGTACGC GTGGAAAAAC
101 AAAAAGCCTC CATTCAGTAC GACAAAGCAT TGATTGATCG GGAAAACCTAC
151 TACAACCACC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201 ATTCGCACTT TCGGGCAACT GGTATTTTAC GCCACAACAC AAACCTCAGCC
251 TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA
301 CACGGCAAAC ACGTCGCCAC CAACACCTTT GAAGTCGGCA ACAACACCTT
351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGGCG
401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGTAACCTAC

```

```

451 ATTTACGCCC AAACCTTAAA CGACGGACGC GGCCCCAAAT CCATCGAAGA
501 CGACAGCGAA ATGAAGCTCG TGCCTACAA CCAATCCGGC GCCGACTTCT
551 ACGGCGCGGA AGGCGAAATC TACTTCAAAC CGACACCGCG CTACCGCATC
601 GCGGTTTTCCG GCGACTATGT ACGAGGCCGT CTGAAAAACC TGCCTTCCCT
651 ACCCGGCAGA GAAGATGCCT ACGGCAACCG TCCTTTCATC GCACAGGACG
701 ACCAAAATGC CCCCCGTGTT CCGGCTGCGC GCCTCGGCTT CCACCTGAAA
751 GCCTCGCTGA CCGACCGTAT CGATGCCAAT TTGGACTACT ACCGCGTGTT
801 CGCCCCAAAC AAACCTGCCC GCTACGAAAC GCGCACGCCC GGACACCATA
851 TGCTCAACCT CGGCGCAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901 AATTGGTACG TCAAAGCCGA CAACCTGCTC AACCATCCG TTTACGCCCA
951 CAGCAGCTTT CTCTCTGATA CGCCGCAAAAT GGGCCGCAGC TTTACCGGCG
1001 GCGTGAACGT GAAGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 598; ORF 149>:

m149.pep

```

1  MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEQKASIQY DKALIDRENY
51  YNHPLPDLGA HRQTARSFAL SGNWYFTPQH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YEGDRWQYNL ALYRNRFNGY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201 GVSGDYVRGR LKNLPSLPGR EDAYGNRPFI AQDDQNAPRV PAARLGFHLK
251 ASLTDRIAN LDYYRVFAQN KLARYETRTP GHMLNLGAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FTGGVNVKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 149 shows 95.9% identity over a 339 aa overlap with a predicted ORF (ORF 149.ng) from *N. gonorrhoeae*:

m149/g149

m149.pep	10	20	30	40	50	60
	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQASIQYDKALIDRENYNHPLPDLGA					
g149	MLIDNNVRHYSFFGVEQANWDNFTLEGGVRVEKQASIRYDKALIDRENYNQPLPDLGA					
	10	20	30	40	50	60
m149.pep	70	80	90	100	110	120
	HRQTARSFALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
g149	HRQTARSFALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
	70	80	90	100	110	120
m149.pep	130	140	150	160	170	180
	RSNNIELALGYEGDRWQYNLALYRNRFNGYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
g149	RSNNIELALGYKGRWQYNLAAYRNRFNGYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
	130	140	150	160	170	180
m149.pep	190	200	210	220	230	240
	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRRLKNLPSLPGREDAYGNRPFI AQDDQNAPRV					
g149	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRRLKNLPSLPGREDPYGRPFIAQADQNAPRI					
	190	200	210	220	230	240
m149.pep	250	260	270	280	290	300
	PAARLGFHLKASLTDRIANLDYYRVFAQNKLARYETRTPGHMLNLGAN YRRNTRYGEW					
g149	PAARLGFHLKSLTDRIDANLDYYRVFAQNKLARYETRTPGHMLNLGAN YRRNTRYGEW					
	250	260	270	280	290	300
m149.pep	310	320	330	340		
	NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					

420

g149 NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFAGGVNVKFX
 310 320 330 340

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 599>:

a149.seq
 1 ATGCTGCTTG ACAATAAAGT GCAACATTAC AGCTTTTTTCG GTGTAGAACA
 51 GGCAAACTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGAAAAAC
 101 AAAAAGCCTC CATCCGCTAC GACAAAGCAT TGATTGATCG GGAAACTAC
 151 TACAACCATC CCCTGCCCCG CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
 201 ATTCGCACTT TCGGGCAACT GGTATTTTAC GCCACAACAC AAACCTAGCC
 251 TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA
 301 CACGGCAAAC ACGTCGCCAC CAACACCTTT GAAGTCGGCA ACAAACACCT
 351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGGCG
 401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGCAACTAC
 451 ATTTACGCCC AAACCTTAAA CGACGGACGC GGCCCCAAAT CCATCGAAGA
 501 CGACAGCGAA ATGAAGCTCG TCGCTACAA CCAATCCGGT GCGGACTTCT
 551 ACGGCGCGGA AGGCGAAATC TACTTCAAAC CGACACCGCG CTACCGCATC
 601 GGCGTTTCCG GCGACTATGT ACGAGGCCGT CTGAAAAACC TGCCTTCCCT
 651 ACCCGGCAGG GAAGACGCCT ACGGCAACCG CCCACTCATT GCCCAAGCCG
 701 ACCAAAACGC CCCTCGCGTT CCGGCTGCGC GCCTCGGCGT CCACCTGAAA
 751 GCCTCGCTGA CCGACCGCAT CGATGCCAAT TTGGACTACT ACCGCGTGTT
 801 CGCCCCAAAAC AAACTCGCCC GCTACGAAAC GCGCACGCCC GGACACCATA
 851 TGCTCAACCT CGGCGCAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
 901 AATTGGTACG TCAAAGCCGA CAACCTGCTC AACCAATCCG TTTACGCCCA
 951 CAGCAGCTTC CTCTCTGATA CGCCGCAAAT GGGCCGCAGC TTTACCGGCG
 1001 GCGTGAACGT GAAGTTTAA

This corresponds to the amino acid sequence <SEQ ID 600; ORF 149.a>:

a149.pep
 1 MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY
 51 YNHPLPDLGA HRQTARFAL SGNWYFTPQH KLSLTASHQE RLPSTQELYA
 101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YEGDRWQYNL ALYRNRFNGNY
 151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
 201 GVS GDYVRGR LKNLPSLPGR EDAYGNRPLI AQADQNAPRV PAARLGVLHLK
 251 ASLTDRIDAN LDYYRVFAQN KLARYETRTP GHMMLNLGAN YRRNTRYGEW
 301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FTGGVNVKF*

m149/a149 98.8% identity in 339 aa overlap

	10	20	30	40	50	60
m149.pep	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIYQYDKALIDRENYNHPLPDLGA					
a149	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHPLPDLGA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m149.pep	HRQTARFALSGNWYFTPQHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
a149	HRQTARFALSGNWYFTPQHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m149.pep	RSNNIELALGYEGDRWQYNLALYRNRFNGNYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
a149	RSNNIELALGYEGDRWQYNLALYRNRFNGNYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m149.pep	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRRLKNLPSLPGREDAYGNRPLIAQDDQNAPRV					
a149	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRRLKNLPSLPGREDAYGNRPLIAQADQNAPRV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m149.pep	PAARLGFLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHMMLNLGANYYRRNTRYGEW					

[illegible]

g149-1.seq

1	ATGGCACAAA	TCACACTCAA	ACCCATTGTT	TTATCAATTTC	TTTTAATCAA
51	CACACCCCTC	CTCGCCCAAG	CGCATGAAAC	TGAGCAATCG	GTGGGCTTGG
101	AAACGGTCACT	CGTCGCTGGC	AAAAGCCGTC	CGCGCGCGAC	TTCCGGGGCTG
151	CTGCACACTT	CGACCGCTCT	GCACAAAATC	ATCTCCGGCG	ATATCTTTGGC
201	CCAAAAAGCC	GTCAACTGGG	GCGACGCTTT	GGACGGCGTA	CCGGGCATCC
251	ACGCTTCGCA	ATACCGCTGC	GGCGCATCCG	CTCCCGTTAT	TCGCGGTCAA
301	ACGGGCACAG	GGATTAAAGT	ATTGAACCAT	CACGGCGAAA	CGCCGATATC
351	GGCGGACTTT	TCTCCCGATC	ACGCCATTAT	GGTAGATACC	GCCTTGTCG
401	AACAGGTTGA	AATCTCTGCG	GGGCGGGTTA	CGCTCTTGTA	CAGCTCGGGC
451	AATGTGGCGG	GATCTGGTCA	TGTTGCCGAT	GGAAAAATCC	CGGAAAAATC
501	GCCTGAAAAC	GGCGTATCGG	GCGaagccgG	ATTGCGTTTG	AGCAGCGCCA
551	ATTTAGAAAA	ACTGACATCC	GCAGGCATCA	ATATCGGACT	GGGCAAAAAC
601	TTCTGTCTGC	ATACCCGAAG	CTTGTAACCG	AAATCGGGCG	ATTACCGCGT
651	ACCGCGTTAC	CGCAATCTGA	AAACGCTGCC	CGACAGCCAT	CGCGATTTCG
701	AAACGGGCGC	CATCGGGCTG	TCTTTGGGTG	GCGAAAAAGG	CTTTATCGGC
751	GCAGCATACA	GCGACCGTCG	CGACCGCCTAC	GGCCTGCCTG	CCCCACGCCA
801	CGAATACGAT	GATTGCCACG	CCGACATCAT	CTGGCAAAAAG	AGTTTGATCA
851	ACAACCGCTA	TTTGCAGCTT	TATCCGCATC	TGTTGACCGA	AGAAGACATC
901	GATTACGACA	ATCCGGGCTT	GAGCTGCGGT	TTCCACGACG	CGCAGCGGTG
951	ACACGCCACAC	ACCCACAACG	GCAAACCCGT	GATAGACCTG	GCGCAACCAAT
1001	GCTACGAACT	CCGCGCCGAA	TGGAAGCAGC	CATTCCCCGG	TTTTGAAGCC
1051	CTGCGCGTAC	ATCTGAACCC	CAATGACTAC	CACCACGACG	AAAAAGCAGG
1101	CGATGCGAGTA	GAAAACTTCT	TCAACACAAC	AACACACAAC	CCCCGTATCG
1151	AGTTGCGCCA	CCAACCCATA	GGCCGTCTGA	AAGGCAGCTG	GGGCGTGCAA
1201	TATTTGGGAC	AAAAATCCAG	CGCGCTTTCC	GCCATTTCCG	AAACCGTCCA
1251	ACAACCCATG	TTGATTGACA	ACAATTTCGG	CCATTACAGC	TTTTTCGGTG
1301	TAGAACAGGC	AAATTGGGAC	AACTTGACGC	TTGAAGGGCG	GTACCGCGTG
1351	GAAAAACAAA	AAGCCTCCAT	CCGGTACGAC	AAAGCATGTA	TTGATCGAGA
1401	AAACTACTAC	AACCAGCCCC	TGCCCGACCT	CGGCGCGCAC	CGCCAAACCC
1451	CCCGTCGTT	CGCACTTTTC	GGCAACTGGT	ATTTACAGCC	ACCCACAACA
1501	CTAGCCTGTA	CGCGCTCCCA	TCAGGACACG	CTGCCGTCAA	CGCAAGAACT
1551	GTACGCGACG	GGCAAGCAGC	TCGCCACCAA	TCCAGTTGAA	GTCCGGCAAT
1601	AACACCTCAA	CAAGAGCGCT	TCCAACAATA	TCAACTCGC	GTCGGGCTAC
1651	GAAGGCGACC	GCTGGCAATA	CAATCTGGCA	GCCTACCGCA	ACCGATTTCG
1701	CAACTACAT	TACGCCCCAA	CTTTAAACGA	CGGACGCGGC	CCCCAAATCA
1751	TCGAAGACGA	CAGCGAAATG	AAGCTCGTGC	GCTACAACCA	TTCGGTGGCC
1801	GACTTCTACG	GCGCGGAAGG	CGAAATCTAC	TTCAAACCGA	CACCCGCGCTA
1851	CCGCACTCGT	GTTTCCGGCG	ACTATGTACG	AGGCCGTCTG	AAAAAAGCTG
1901	CGTCCCTACC	CGGCAGGGAA	GATCCCTACG	GCAAAAGTCC	CTTCATCGCA
1951	CAAGCGGACC	AAAACGCCCC	CGCATTTCCG	CGTGCAGCGC	TCGGGTTCCA
2001	CCTGAAAACC	TCGCTAACC	ACCGTATCGA	TGCCAATTTG	GACTACTACC
2051	CGGTGTTTCG	CCAAAACAAA	CTCGCCCGCT	ACGAAACGCG	TACGCCCGGA
2101	CACCATATGC	TCAACCTCGG	TGCAAACTAC	CGCCGCAATA	CGCGCTATGG
2151	CGAGTGGAA	TGGTAGCTCA	AAGCGACAAA	CCTGCTCAAC	CAATCCGTTT
2201	ACGCCACACG	CAGCTTCTCT	TCTGATACGC	GCGAAATGGG	CCCGAGCTTT
2251	ACCGCGCGCG	TAAACGTGAA	GTTTTTAA		

g149-1.pep

	1	MAQITLKPIV	LSILLINTPL	LAQAHETEQS	VGLETVSVVG	KSRPRATSGL
51	LHTSTASDKI	ISGDTLRQKA	VNLGDALDVT	PGIHASQYGG	GASAPVIRSQ	
101	TGRRIKVLNH	HGETGDMADF	SPDHAIMDVD	ALSQQVEILR	GPVTLLYSSG	
151	NVAGLVVDVA	GKIPEKMEN	GVSGEAGRLR	SSGNLEKLTS	AGINIGLGKN	
201	FVLHTEGLRY	KSGDYAVPPI	RNLKRLPDSH	ADSQTSGISL	SWVGEGKFIF	
251	AAYSDRRDRY	GLPAHSHEYD	DCHADIIWQK	SLENKRIYLQ	YPHLLTDEDI	
301	DDYNPCLSCG	FHDGDGAHAH	THNGKPWIDL	RNKRYELREA	WKOPFPFEAA	

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351 LRVHLNRNDY HHDEKAGDAV ENFFNNKTHN ARIELRHQPI GRLKGSWGVQ
401 YLGQKSSALS AIPETVQQPM LIDNNVRHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIRYD KALIDRENY NQPLPDLGAH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
551 EGDWRQYNLA AYRNRFNGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEII FKPTPRYRIG VSGDYVRGRL KNLPSPGPRE DYPGKRPFIA
651 QADQNAPRIP AARLGFHLKT SLTDRIDANL DYYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 603>:

m149-1.seq

```

1 ATGGCACAAA CTACACTCAA ACCCATTGTT TTATCAATTC TTTTAATCAA
51 CACACCCCTC CTCGCCCAAG CGCATGAAAC TGAGCAATCG GTGGATTGG
101 AAACGGTCAG CGTCGTCGGC AAAAGCCGTC CGCGCGCCAC GTCGGGGCTG
151 TTGCACACTT CGACCGCCTC CGACAAATC ATCTCCGGCG ATACCTTGCG
201 CCAAAAGGCC GTCAACTTGG GCGACGCTT AGACGGCGTA CCGGGCATCC
251 ACGCTTCGCA ATACGGCGGC GCGCGCTCG CTCCCCTCAT TCGCGGTCAA
301 ACAGGCAGGC GGATTAAAGT GTTGAACCAT CACGGCGAAA CAGGCGATAT
351 GCGGGATTTT TCGCCCGATC ACGCCATTAT GGTAGATACC GCCTTGTCGC
401 AACAGGTCGA AATCCTGCGC GGGCCGGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCGA TGTGCGGAT GGCAAAATCC CCGAAAAAAT
501 GCCTGAAAAC GCGGTATCGG GCGAACTCGG ATTGCGTTG AGCAGCGGCA
551 ATCTGAAAAA ACTCACGTCC GCGGGCATCA ATATCGGTTT GGGCAAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCGGT
651 ACCGCGTTAC CGCAATCTGA AACGCGTGCC CGACAGCCAC GCCGATTGCG
701 AAACGGGCAG CATCGGGCTG TCTTGGGTTG GCGAAAAAGG TTTTATCGGC
751 GTAGCGTACA GCGACCGTCG CGACCAATAT GGTCTGCGTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGCTTGATTA
851 ACAAAACGTA TTTACAGCTT TATCCGCACC TGTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTCCACGACG ACGATAATGC
951 ACACGCACAC ACCCACAGCG GCAGACCGTG GATAGACCTG CGCAACAAAC
1001 GCTACGAAC TCGTGCCGAA TGGAAGCAAC CGTTCGCCGG TTTGAAGCC
1051 CTGCGCGTAC ACCTGAACCG CAACGACTAC CGCCACGACG AAAAAGCAGG
1101 CGATGCAGTC GAAACTTTT TTAACAACCA AACGCAAAAC GCCCGCATCG
1151 AGTTGCGCCA CCAACCCATA GGTCGTCTGA AAGGCAGCTG GGGCGTGCAA
1201 TATTTACAAC AAAAATCCAG TGCTTTATCT GCCATATCCG AAGCGGTTAA
1251 ACAACCGATG CTGCTTGACA ACAAAAGTGA ACATTACAGC TTTTTCGGTG
1301 TAGAACAGGC AAATGGGAC AACTTCACGC TTGAAGGAGG CGTACGCGTG
1351 GAAAAACAAA AAGCCTCCAT TCAGTACGAC AAAGCATTGA TTGATCGGGA
1401 AAATACTAC AACCACCCCC TGCCCGACCT CGGCGCGCAC CGCCAAACCG
1451 CCCGCTCATT CGCACTTTCG GGCAACTGGT ATTTACGCCC ACAACACAAA
1501 CTCAGCCTGA CCGCCTCCCA TCAGGAACGC CTGCCGTCAA CGCAAGAGCT
1551 GTACGCACAC GGCAAAACAG TCGCCACCAA CACCTTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGCTAC
1651 GAAGGCGACC GCTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 TAACTACATT TACGCCCAAA CCTTAAACGA CGGACGCGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GCTACAACCA ATCCGGCGCC
1801 GACTTCTACG GCGCGGAAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGC GTTTCGGCGC ACTATGTACG AGGCCGTCTG AAAAACCTGC
1901 CTTCCTTACC CGGCAGAGAA GATGCCTACG GCAACCGTCC TTTCTATCGC
1951 CAGGACGACC AAAATGCCCC CCGTGTTCGG GCTGCGCGCC TCGGCTTCCA
2001 CCTGAAAGCC TCGCTGACCG ACCGTATCGA TGCCAAATTG GACTACTACC
2051 GCGTGTTCGC CCAAAACAAA CTCGCCCGCT ACGAAACGCG CACGCCCGGA
2101 CACCATATGC TCAACCTCGG CGCAACTAC CGCCGCAATA CGCGCTATGG
2151 CGAGTGGAAT TGGTACGTCA AAGCCGACAA CCTGCTCAAC CAATCCGTTT
2201 ACGCCACAG CAGCTTCTC TCTGATACGC CGCAATGGG CCGCAGCTTT
2251 ACCGGCGGCG TGAACGTGAA GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 604; ORF 149-1>:

m149-1.pep

```

1 MAQTTLKPIV LSILLINTPL LAQAHETEQS VDLETVSUVG KSRPRATSGL
51 LHTSTASDKI ISGDTLRQKA VNLGDALDGV PGIHASQYGG GASAPVIRGQ
101 TGRRIKVLNH HGETGDMADF SPDHAIMVDT ALSQQVEILR GPVTLLYSSG
151 NVAGLVDVAD GKIPEKMPEN GVSGLGLRL SSGNLEKLTG GGINIGLGKN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGEKGFIG
251 VAYSDDRRDQY GLPAHSHEYD DCHADIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPGLSGC FHDDDNAHAH THSGRPWIDL RNKRYELRAE WKQFPFGFEA
351 LRVHLNRNDY HHDEKAGDAV ENFFNNQTON ARIELRHQPI GRLKGSWGVQ
401 YLGQKSSALS AISEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIYD KALIDRENY NHPLPDLGAH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY

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551 EGDRWQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEIIY FKPTPRYRIG VSGDYVRGRL KNLPSPGRE DAYGNRPFFIA
651 QDDQNAPRVP AARLGFHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

m149-1/g149-1 96.2% identity in 758 aa overlap

m149-1.pep	10	20	30	40	50	60
	MAQTTLKPIVLSILLINTPLLAQAHETE	QSV	DLET	VS	VVGKSRPRAT	SGLLHTSTASDKI
g149-1	MAQITLKPIVLSILLINTPLLAQAHETE	QSV	GLET	VS	VVGKSRPRAT	SGLLHTSTASDKI
	10	20	30	40	50	60
m149-1.pep	70	80	90	100	110	120
	ISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF				
g149-1	ISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF				
	70	80	90	100	110	120
m149-1.pep	130	140	150	160	170	180
	SPDHAIMVDTALSQQVEILRG	PVTLLYSSGNVAGLVDVADGKIPEKMPENGVS	GELGLRL			
g149-1	SPDHAIMVDTALSQQVEILRG	PVTLLYSSGNVAGLVDVADGKIPEKMPENGVS	GEAGLRL			
	130	140	150	160	170	180
m149-1.pep	190	200	210	220	230	240
	SSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRN	LKRLPDSHADSQTGSIGL			
g149-1	SSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRN	LKRLPDSHADSQTGSIGL			
	190	200	210	220	230	240
m149-1.pep	250	260	270	280	290	300
	SWVGEKGFIVAYS	DRRDQYGLPAHSHEYDDCHADI	IWKSLINKRYLQLYPHLLTEEDI			
g149-1	SWVGEKGFIGAAYS	DRRDQYGLPAHSHEYDDCHADI	IWKSLINKRYLQLYPHLLTEEDI			
	250	260	270	280	290	300
m149-1.pep	310	320	330	340	350	360
	DYDNPLSCGFHDDNAHAH	THSGRPWIDLNRKRYELRAEWKQFP	PGFEALRVHLNRNDY			
g149-1	DYDNPLSCGFHDDNAHAH	THSGRPWIDLNRKRYELRAEWKQFP	PGFEALRVHLNRNDY			
	310	320	330	340	350	360
m149-1.pep	370	380	390	400	410	420
	RHDEKAGDAVENFFN	QTNARIELRHQPIGR	LKGSWGVQYLQOKSSALSAISEAVKQPM			
g149-1	HHDEKAGDAVENFFN	KNTHNARIELRHQPIGR	LKGSWGVQYLQOKSSALSAIPETVQQPM			
	370	380	390	400	410	420
m149-1.pep	430	440	450	460	470	480
	LLDNKVQHY	SFFGVEQANW	NFTLEGGVRVEKQKASI	QYDKALIDRENYNHP	LDLGAH	
g149-1	LIDNNVRHY	SFFGVEQANW	NFTLEGGVRVEKQKASIRYDKALIDRENYNQ	PLDLGAH		
	430	440	450	460	470	480
m149-1.pep	490	500	510	520	530	540
	RQTAR	SFALSGN	WYFTPHHKL	SLTASHQERLPSTQELYAHGKHVATNT	FEVGNKHLNKER	
g149-1	RQTAR	SFALSGN	WYFTPHHKL	SLTASHQERLPSTQELYAHGKHVATNT	FEVGNKHLNKER	
	490	500	510	520	530	540
m149-1.pep	550	560	570	580	590	600
	SNNIELALGYEGDRWQYN	LALYRNRFGNYIYAQTLNDGRGPKSIEDDSEM	KLVRYNQSGA			
g149-1	SNNIELALGYEGDRWQYN	LALYRNRFGNYIYAQTLNDGRGPKSIEDDSEM	KLVRYNQSGA			
	550	560	570	580	590	600
m149-1.pep	610	620	630	640	650	660
	DFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLP	SLPGREDAYGNRPFFIAQDDQNAPRVP				
g149-1	DFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLP	SLPGREDPYGKRPFIAQADQNAPRIP				
	610	620	630	640	650	660

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	670	680	690	700	710	720
m149-1.pep	AARLGFLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN					
g149-1	AARLGFLKTSLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN					
	670	680	690	700	710	720
	730	740	750	759		
m149-1.pep	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
g149-1	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
	730	740	750			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 605>:

a149-1.seq

```

1  ATGGCACAAA CTACACTCAA ACCCATTGTT TTATCAATTC TTTAATCAA
51  CACACCCCTC CTCTCCCAAG CGCATGGAAC TGAGCAATCA GTGGGCTTGG
101 AAACGGTCAG CGTCGTCGGC AAAAGCCGTC CGCGCGCCAC TTCGGGGCTG
151 CTGCACACTT CTACCGCTC CGACAAAATC ATCAGCGGCG ACACCTTGCG
201 ACAAAAAGCC GTCAACTTGG GTGATGCTTT AGACGGCGTA CCGGGCATTC
251 ATGCCCTCGCA ATACGGCGGC GGCGCATCCG CTCCCGTTAT TCGCGGTCAA
301 ACAGGCAGAC GGATTAAAGT GTTGAACCAT CACGGCGAAA CGGGCGACAT
351 GGCGGACTTC TCTCCAGACC ATGCAATCAT GGTGGACAGC GCCTTGTCGC
401 AACAGGTCTGA AATCCTGCGC GGTCCGGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCGA TGTGCGCAT GGCAAAATCC CCGAAAAAAT
501 GCCTGAAAAC GCGGTATCGG CGGAACCTCG ATTGCGTTG AGCAGCGGCA
551 ATCTGGAAAA ACTCAGCTCC GGCGGCATCA ATATCGGTTT GGGCAAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCCGT
651 ACCGCGTTAC CGCAATCTGA AACGCCTGCC CGACAGCCAC GCCGATTCGC
701 AAACGGGCAG CATCGGGCTG TCTTGGGTTG GCGAAAAGG CTTTATCGGC
751 GCAGCATACA GCGACCGTCG CGACCAATAT GGTCTGCCTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGTTTGATTA
851 ACAAACGCTA TTTGCAGCTT TATCCGCACC TGTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTTCACGACG ACGATGATGC
951 ACACGCCCAT GCCACAACG GCAAACCTTG GATAGACCTG CGCAACAAAC
1001 GCTACGAACT CCGCGCCGAA TGGAAGCAAC CGTCCCCGG TTTGAAGCC
1051 CTGCGCGTAC ACCTGAACCG CAACGACTAC CGCCACGACG AAAAAGCAGG
1101 CGATGCAGTA GAAACTTTT TTAACAACCA AACGCAAAAC GCCCGTATCG
1151 AGTTGCGCCA CCAACCCATA GGCCGTCTGA AAGGCAGCTG GGGCGTGCAA
1201 TATTGGGAC AAAATCCAG TGCTTTATCT GCCACATCCG AAGCGGTCAA
1251 ACAACCGATG CTGCTTGACA ATAAAGTGCA ACATTACAGC TTTTTCGGTG
1301 TAGAACAGGC AAATGGGAC AACTTCACGC TTGAAGCGCG CGTACGCGTG
1351 GAAAAACAAA AAGCCTCCAT CCGCTACGAC AAAGCATTGA TTGATCGGGA
1401 AAATACTAC AACCATCCCC TGCCCGACCT CGGCGCGCAC CGCCAAACCG
1451 CCGGCTCAT CGCACTTTCG GGCAACTGGT ATTTACGCC ACAACACAAA
1501 CTCGCTCGTA CCGCTCCCA TCAGGAACGC CTGCCGTCAA CGCAAGAGCT
1551 GTACGCACAC GGCAACACG TCGCCACCAA CACCTTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGCTAC
1651 GAAGGCGACC GCTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 CAACTACATT TACGCCAAA CCTTAAACGA CGGACGCGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GCTACAACCA ATCCGGTGCG
1801 GACTTCTACG CGCGGAAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGC GTTTCGGCG ACTATGTACG AGGCCGTCTG AAAAACCTGC
1901 CTTCCCTACC CGGCAGGGAA GACGCCTACG GCAACCGCCC ACTCATTGCC
1951 CAAGCCGACC AAAACGCCCC TCGCGTTCCG GCTGCGCGCC TCGGCGTCCA
2001 CCTGAAAGCC TCGCTGACCG ACCGCATCGA TGCCAATTG GACTACTACC
2051 GCGTGTTCGC CCAAAACAAA CTCGCCGCT ACGAAACGCG CACGCCCGGA
2101 CACCATATGC TCAACCTCGG CGCAACTAC CGCCGCAATA CGCGCTATGG
2151 CGAGTGGAAT TGGTACGTCA AAGCGACAA CCTGCTCAAC CAATCCGTTT
2201 ACGCCACAG CAGCTTCCTC TCTGATACGC CGCAATGGG CCGCAGCTTT
2251 ACCGCGGCG TGAACGTGAA GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 606; ORF 149-1.a>:

a149-1.pep

```

1  MAQTTLKPIV LSILLINTPL LSOAHGTEQS VGLETVSVVG KSRPRATSGL
51  LHTSTASDKI ISGDTLRQKA VNLGDALDGV PGIHASQYGG GASAPVIRGQ
101 TGRRIKVLNH HGETGDMADF SPDHAIMVDS ALSQQVEILR GPVTLTYSSG
151 NVAGLVDVAD GKIPEKMPEN GVSSELGLRL SSGNLEKLTG GGINIGLGKN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGEKGFIG
251 AAYSDDRDQY GLPAHSHEYD DCHADIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPLSCG FHDDDDAHAH AHNGKPWIDL RNKRYELRAE WKQFPFGFEA

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351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTON ARIELRHQPI GRLKGSWGVSQ
401 YLGQKSSALS ATSEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIRYD KALIDRENY NHPPLDLGAH RQTARSFALS GNWYFTPOHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
551 EGDWRQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEII FKPTPRYRIG VSGDYVRGRL KNLPSPGRE DAYGNRPLIA
651 QADQNAAPRV AARLGVHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

```

a149-1/m149-1 98.0% identity in 758 aa overlap

	10	20	30	40	50	60
a149-1.pep	MAQTTLKPIVLSILLINTPLLSQA	HGTEQSVGLET	VS	VVGKSRPRATS	GLLHTSTASDKI	
m149-1	MAQTTLKPIVLSILLINTPLLAQA	HETEQSVDELET	VS	VVGKSRPRATS	GLLHTSTASDKI	
	10	20	30	40	50	60
	70	80	90	100	110	120
a149-1.pep	ISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRI	KVLNHHGETGDMADF			
m149-1	ISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRI	KVLNHHGETGDMADF			
	70	80	90	100	110	120
	130	140	150	160	170	180
a149-1.pep	SPDHAIMVDSALSQQVEILRGPV	TLTYSSGNVAGLVDVADGKIPEK	MPENGVS	GELGLRL		
m149-1	SPDHAIMVDTALSQQVEILRGPV	TLTYSSGNVAGLVDVADGKIPEK	MPENGVS	GELGLRL		
	130	140	150	160	170	180
	190	200	210	220	230	240
a149-1.pep	SSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRNLK	RLPDSHAD	SGTSGISGL		
m149-1	SSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRNLK	RLPDSHAD	SGTSGISGL		
	190	200	210	220	230	240
	250	260	270	280	290	300
a149-1.pep	SWVGEKGFIGAAYS	DRRDQYGLPAHSHEYDDCHADI	IWQKSLINKRYLQLYPHLLTEEDI			
m149-1	SWVGEKGFIVAYS	DRRDQYGLPAHSHEYDDCHADI	IWQKSLINKRYLQLYPHLLTEEDI			
	250	260	270	280	290	300
	310	320	330	340	350	360
a149-1.pep	DYDNPLGLSCGFHDDDDAH	AHANGKPWIDLRNKRYELRAEWKQ	FFPGFEALRVHLNRNDY			
m149-1	DYDNPLGLSCGFHDDDDAH	AHATHSGRPWIDLRNKRYELRAEWKQ	FFPGFEALRVHLNRNDY			
	310	320	330	340	350	360
	370	380	390	400	410	420
a149-1.pep	RHDEKAGDAVENFFNNQTON	ARIELRHQPIGRLKGSWGVSQY	LGQKSSALSATSEAVKQPM			
m149-1	RHDEKAGDAVENFFNNQTON	ARIELRHQPIGRLKGSWGVSQY	LQKSSALSATSEAVKQPM			
	370	380	390	400	410	420
	430	440	450	460	470	480
a149-1.pep	LLDNKVQHYSFFGVEQANWDN	FTLEGGVRVEKQKASIRYDK	KALIDRENYNHPPLDLGAH			
m149-1	LLDNKVQHYSFFGVEQANWDN	FTLEGGVRVEKQKASIQYDK	KALIDRENYNHPPLDLGAH			
	430	440	450	460	470	480
	490	500	510	520	530	540
a149-1.pep	RQTARSFALSGN	WYFTPOHKLSLTASHQERLP	STQELYAHGKHVATNTFEVGNKHLNKER			
m149-1	RQTARSFALSGN	WYFTPOHKLSLTASHQERLP	STQELYAHGKHVATNTFEVGNKHLNKER			
	490	500	510	520	530	540
	550	560	570	580	590	600
a149-1.pep	SNNIELALGYEGDRWQYN	LALYRNRFGNYIYAQTLNDGRG	PKSIEDDSEM	KLVRYNQSGA		
m149-1	SNNIELALGYEGDRWQYN	LALYRNRFGNYIYAQTLNDGRG	PKSIEDDSEM	KLVRYNQSGA		
	550	560	570	580	590	600
	610	620	630	640	650	660

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a149-1.pep  DFYGAEGEIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPLIAQADQNAPRVP
              |||
m149-1       DFYGAEGEIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFFIAQDDQNAPRVP
              610      620      630      640      650      660

              670      680      690      700      710      720
a149-1.pep  AARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
              |||
m149-1       AARLGFHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
              670      680      690      700      710      720

              730      740      750      759
a149-1.pep  WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
              |||
m149-1       WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
              730      740      750

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 607>:

```

g150.seq (partial)
1  ..TACTGCAAGG CAGACCCCTT TCCCGCCGCC CTGCTGGCCA ATCAGAAAAT
51  CACCGCCCGC CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTTGA
101 GCGGTTTCGGA TTTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGTTT
151 GACAACGATC CGGCACTGGT CGGGGAAATC CTAGACCTGC TCGGCATCAA
201 TCCGGCAACG GAAATACAGG CGGGCGGAAA AACCCTGCCG GTTGCCTCCG
251 CACTGTTATC CCATTTTCGAA CTCACGCAAA ACACCCCGCG CTTTGTCAAA
301 GGCTATGCCA CGTTCGCCGA TAATGACGAA CTCGACCGTA TTGCTGCCGA
351 CAACGCCGTT TTGCAAGGCT TTGTGCAAAG CACGCCGATT GCCGGTGTGC
401 TGCACCGCTT CCGGCAAAA CTGACGGCGG AACAATTTCG CGGCCTGCTG
451 CGCCCGCTTG CGCCGCGCCT GTATTTCGATT TCCTCGTCGC AGGCGGAAGC
501 GGGGGACGAA GTGCACCTGA CCGTCGGCGC AGTGCGTTTC GAACACGAAG
551 GGCGCGCCAG GGCGGGCGGC GCATCGGGTT TCTTTGCCGA CCGGCTGGAA
601 GAGGACGGCA CGGTGCGCGT GTTTGCGGAA CGCAACGACG GCTTCAGGCT
651 GCCCGAAGAC AGCCGCAAGC CGATTGTGAT GATCGGCTCC GGTACCGGCG
701 TCGCACCGTT CCGCGCCTTC GTCCAACAAC GTGCCGAGA AAATGCGGAA
751 GGCAGAAACT GGCTGATTTT CGGCAATCCG CATTTTGCCG CCGACTTCCT
801 CTATCAGACC GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGAT
851 ATGACTTCGC CTGGTCGCGC GATCAGGAAG AAAAAATCTA TGTGCAGGAC
901 AAAATCCCGC AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC
951 GCATATCTAT GTGTGCGGCG ATCGGCAAAA AATGGCAAAA GAAGTGGAAG
1001 CCGCCTTGCT GGATGTGATT ATCGGGGCGG GGCATTTCGA CGAAGACGGC
1051 GCAGAAAGAT ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA
1101 TGTTTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 608; ORF 150.ng>:

```

g150.pep (partial)
1  ..YCKADPFPA LLANQKITAR QSDKDVRHIE IDLSGSDLHY LPGDALGVWF
51  DNDPALVGEI LDLLGINPAT EIQAGGKTL P VASALLSHFE LTQNTPAFVK
101 GYATFADNDE LDRIAADNAV LQGFVQSTPI AGVLHRFPK LTAEQFAGLL
151 RPLAPRLYSI SSSQAEAGDE VHLTVGAVRF EHEGRARAGG ASGFFADRLE
201 EDGTVRVFAE RNDGFRLPED SRKPIVMIGS GTGVAPFRAF VQQRAAENAE
251 GRNWLIFGNP HFAADFLYQT EWQQFAKDF L HRYDFAWSR DQEEKIYVQD
301 KIREQAEGLW OWLQEGAHY VCGDAAKMAK EVEAALLDVI IGAGHSDEDEG
351 AEGYLDMLRE EKRYQRDVY*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 609>:

```

m150.seq
1  ATGCAGAACA CAAATCCGCC ATTACCGCCT CTGCCGCCCG AAATCACGCA
51  GCTCCTGTCG GGGCTGGACG CGGCACAATG GGCGTGCTG TCCGGCTACG
101 CTTGGGCAAA AGCAGGAAAC GGGGCATCTG CAGGACTGCC CGCGCTTCAG
151 ACGGCATTGC CGGCGGCAGA ACCTTTTTCG GTAACCGTCC TTTCCGCCTC
201 GCAAACCGGC AATGCGAAAT CCGTTGCCGA CAAAGCGGCG GACAGCCTGG
251 AAGCCGCCGG CATCCAAGTC AGTCGCGCCG AACTGAAAGA CTATAAGGCG
301 AAAAAACATC CCGGCGAAGC CCGCCTGCTG CTGGTTACCT CCACCCAGG
351 CGAAGGCGAA CCGCGAAAG AAGCCGTCTG GCTGCACAAA CTGCTGAACG
401 GCAAAAAGC CCCGAAATTG GACAAACTCC AATTTGCCGT ACTGGGTTTG

```

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451 GCGGACAGTT CCTATCCGAA TTTCTGTCAG GCAGGTAAAG ATTTGACCG
501 GCGTTTTGAA GAATTGGGCG CAAAACGGCT GCTCGAACGC GTTGATGCGG
551 ATTTGGACTT TACCGCCTCC GCAAACGCCT GGACAGATAA TATCGCCGCA
601 CTCTTAAAG AAGAAGCCGC AAAAAACCGG GCAACGCCCC CGCCGCAGAC
651 AACGCCCCC GCGGCGCTTC AGACGGCACC GGATGGCAGG TACTGCAAGG
701 CAGCCCCCTT TCCCGCCGCC CTGCTGGCCA ATCAGAAAAT CACCGCCCCG
751 CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTGGA GCGGTTCCGA
801 TTTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGGTTT GACAACGATC
851 CGGCACTGGT CAGGGAATC CTAGACCTGC TCGGCATCGA TCCGGCAACG
901 GAAATACAGG CGGGCGGAAA GATGATGCCG GTTGCGCGCG CACTTTCATC
951 TCATTTGCAA CTCACGCAA ACACCTCCGC TTTCGTCAA GGCTATGCCG
1001 CGTTCGCCCCA TTATGAAGAA CTCGATAAAA TCATTGCCGA TAACGCCGTT
1051 TTGCAGGATT TCGTGCAAAA CACGCCTATT GTCGATGTGC TGCACCGCTT
1101 CCCGGCAAGC CTGACGGCAG AACAATTCAT CCGTTTACTG CGTCCGCTTG
1151 CACCCCGTTT GTATTGATT TCTTCAGCAC AGGCGGAAGT GGGCGATGAA
1201 GTGCATTAA CTGTCGGCGT GGTTTCGTTT GAACACGAAG GCCGCGCCAG
1251 AACGGGCGGC GCATCGGGTT TCCTTGCCGA CCGGCTGGAA GAGGACGGCA
1301 CGGTGCGCGT GTTTGTGGAA CGCAACGACG GCTTCAGGCT GCCCGAAGAC
1351 AGCCGCAAGC CGATTGTGAT GATCGGCTCG GGCACCGCGC TCGCACCGTT
1401 CCGCGCTTTC GTCCAACAAC GTGCCGAGA AAATGCGGAA GGCAAAAAC
1451 GGCTGATTTT CCGCAATCCG CATTTTGCCC GTGATTTTCT CTATCAAACC
1501 GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGGT ACGATTTTCG
1551 CTGGTCCCGC GATCAGGAAG AAAAAATCTA TGTGCAGGAC AAAATCCGCG
1601 AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC GCATATCTAT
1651 GTGTGCGGCG ATGCGGCAAA AATGGCAAAA GACGTGGAAG CCGCCTTGCT
1701 GGATGTGATT ATCGGGGCG GACATTTGGA CGAAGAGGGC GCAGAAGAAT
1751 ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA TGTTTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 610; ORF 150>:

m150.pep

```

1  MQNTNPPLPP LPPEITQLLS GLDAAQWAWL SGYAWAKAGN GASAGLPALQ
51  TALPAAEPFS VTVLSASQTG NAKSVADKAA DSLEAAGIQV SRAELKDYKA
101 KNIAGERRLL LVTSTQGEGE PPKEAVVLHK LLNGKKAPKL DKLQFAVLGL
151 GDSSYPNFCQ AGKDFDRRFE ELGAKRLLER VDADLDFTAS ANAWTDNIAA
201 LLKEEAAKNR ATPAPQTTPP AGLQTAPDGR YCKAAPFPAA LLANQKITAR
251 QSDKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI LDLLGIDPAT
301 EIQAGGKMMP VARALSSHFE LTQNTPAFVK GYAAFAHYEE LDKIIADNAV
351 LQDFVQNTPI VDLVHRFPAS LTAEQFIRLL RPLAPRLYSI SSAQAEVGDE
401 VHLTVGVVRF EHEGRARTGG ASGFLADRLE EDGTVRVFVE RNDGFRLPED
451 SRKPIVMIGS GTGVAPFRAF VQORAAENAE GKNWLI FGNP HFARDFLYQT
501 EWQQFAKDFG LHRDYFAWSR DQEEKIYVQD KIREQAELGW QWLQEGAHYI
551 VCGDAAKMAK DVEAALLDVI IGAGHLDEEG AEEYLDMLRE EKRYQRDVY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 150 shows 91.3% identity over a 369 aa overlap with a predicted ORF (ORF 150.ng) from *N. gonorrhoeae*:

m150/g150

```

                210      220      230      240      250      260
m150.pep      LLKEEAAKNRATPAPQTTPAGLQTAPDGRYCKAAPFPAALLANQKITARQSDKDVRHIE
                |||||
g150                YCKADPFPAALLANQKITARQSDKDVRHIE
                        10      20      30

                270      280      290      300      310      320
m150.pep      IDLSGSDLHYLPGDALGVWFDNDPALVREILDLLGIDPATEIQAGGKMMPVARALSSHFE
                |||||
g150                IDLSGSDLHYLPGDALGVWFDNDPALVGEILDLLGINPATEIQAGGKTLPVASALLSHFE
                        40      50      60      70      80      90

                330      340      350      360      370      380
m150.pep      LTQNTPAFVKGYAAFAHYEELDKIIADNAVLDQDFVQNTPIVDVLHFRFPASLTAEQFIRLL

```

a150.seq

a150.seq	1	51	101	151	201	251	301	351	401	451	501	551	601	651	701	751	801	851	901	951	1001	1051	1101	1151	1201	1251	1301	1351	1401	1451	1501	1551	1601	1651	
	ATGCAGAACA	CAAATCCGCC	ATTACCGCCT	ATGCCGCCCC	AAATCACGCA																														
	GCTCCTGTCT	GGGCTGGACG	CGGCACAATG	GGCGTGGCTG	TCCGGCTACG																														
	CTTGGGCAAA	AGCAGGAAC	GGGGCATCTG	CAGGACTGCC	CTGCGCTTAC																														
	ACGGCATTGC	CGACGGCAGA	ACCTTTTTTC	GTAACCGTCC	TTTCCGCCTC																														
	GCAAACCGGC	AATGCGAAAT	CCGTTGCCGA	CAAAGCGGCG	GACAGCCTGG																														
	AAGCCGCCGG	CATCCAAGTC	AGTCGCGCCG	AACCTGAAAG	CTATAAGGCG																														
	AAAAACATCG	CCGGCGGAAC	CCGCCCTGCT	CTGGTTACCT	CCACCCAAGG																														
	CGAAGGCGAA	CCGCCGAAG	AAGCCGTCGT	GCTGCACAAA	CTGCTGAACG																														
	GCAAAAAAGC	CCGGAATATG	GACAAACTCC	AATTTGCCGT	ACTGGGTTTG																														
	GGCGACAGCT	CCTATCCGAA	TTTCTGCCGG	GCGGGCAAAG	ATTTTCGACAA																														
	ACGTTTTGAA	GAATTGGGCG	CAAAACGCCT	GCTCGAACGC	GTTGATGCGG																														
	ATTTGGACTT	TGCCGCCGCG	GCAGACGGAT	GGACAGATAA	TATCGCCGCA																														
	CTCTTAAAG	AAGAAGCCGC	AAAAAACCCG	GCAACGCCCG	CGCCGCGAGC																														
	AACGCCCCCC	GCCGCCCTTC	AGACGGCACC	GGAATGGCAG	TACTGCAAGG																														
	CAGACCCCTT	TCCCGCCGCC	CTGCTGGCCA	ATCAGAAAAT	CACCGCCCGC																														
	CAATCCGATA	AAGACGTGCG	CCACATCGAA	ATCGATTTGA	GCGGTTCTGA																														
	TTTGCACTAC	CTCCCGGGCG	ACGCGCTCGG	CGTTTGTTT	GACAACGATC																														
	CGGCACTGGT	CAGGGAATAT	CTAGACCTGC	TCCGATCGAT	TCAGCAACG																														

1701 GGATGTGATT ATCGGGGCAG GACATTTGGA CGAAGAGGGC GCAGAAGAAT
 1751 ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA TGTTTATTGA

This corresponds to the amino acid sequence <SEQ ID 612; ORF 150.a>:

a150.pep
 1 MQNTNPPLPP MPPEITQLLS GLDAAQWAWL SGYAWAKAGN GASAGLPALQ
 51 TALPTAEPFS VTVLSASQTG NAKSVADKAA DSLEAAGIQV SRAELKDYKA
 101 KNIAGERRLL LVTSTQGEGE PPEEAVVLHK LLNGKKAPKL DKLQFAVLGL
 151 GDSSYPNFCR AGKDFDKRFE ELGAKRLLER VDADLDFAAA ADGWTDNIAA
 201 LLKEEAANKR ATPAPQTTPP AGLQTAPDGR YCKADPFPAAL LANQKITAR
 251 QSDKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI LDLLGIDQAT
 301 EIQAGGKTLF VASALLSHFE LTQNTPAFVK GYAPFADDDDE LDRIAADNAV
 351 LQGFVQSTPI ADVLHRFPFAK LTAEQFAGLL RPLAPRLYSI SSSQAEVGDE
 401 VHLTVGAVRF EHEGRARAGG ASGFLADRLE EDGTVRVFVE RNDGFRLPED
 451 SRKPIVMIGS GTGVAPFRAF VQRAAENAE GKNWLFFGNP HFARDFLYQT
 501 EWQQFAKDGFLHRYDFAWSR DQEEKIYVQD KIREQAEGLW QWLQEGAHIY
 551 VCGDAAKMAK DVEAALLDVI IGAGHLDEEG AEEYLDMLRE EKRYQRDVY*

m150/a150 94.8% identity in 599 aa overlap

	10	20	30	40	50	60
m150.pep	MQNTNPPLPP	MPPEITQLLS	GLDAAQWAWL	SGYAWAKAGN	GASAGLPALQ	TALPAAEPFS
a150	MQNTNPPLPP	MPPEITQLLS	GLDAAQWAWL	SGYAWAKAGN	GASAGLPALQ	TALPAAEPFS
	70	80	90	100	110	120
m150.pep	VTVLSASQTG	NAKSVADKAA	DSLEAAGIQV	SRAELKDYKA	KNIAGERRLL	LVTSTQGEGE
a150	VTVLSASQTG	NAKSVADKAA	DSLEAAGIQV	SRAELKDYKA	KNIAGERRLL	LVTSTQGEGE
	130	140	150	160	170	180
m150.pep	PPKEAVVLHK	LLNGKKAPKL	DKLQFAVLGL	GDSSYPNFCR	AGKDFDRRFE	ELGAKRLLER
a150	PPKEAVVLHK	LLNGKKAPKL	DKLQFAVLGL	GDSSYPNFCR	AGKDFDRRFE	ELGAKRLLER
	190	200	210	220	230	240
m150.pep	VDADLDFTA	ASANAWTDN	IAALLKEEA	AKNRATPAP	QTTPPAGLQ	TAPDGRYCKA
a150	VDADLDFTA	ASANAWTDN	IAALLKEEA	AKNRATPAP	QTTPPAGLQ	TAPDGRYCKA
	250	260	270	280	290	300
m150.pep	LLANQKITAR	QSDKDVRHIE	IDLSGSDLHY	LPGDALGVWF	DNDPALVREI	LDLLGIDPAT
a150	LLANQKITAR	QSDKDVRHIE	IDLSGSDLHY	LPGDALGVWF	DNDPALVREI	LDLLGIDPAT
	310	320	330	340	350	360
m150.pep	EIQAGGKMP	VARALSSHF	ELTQNTPAF	VKGYAAFAH	EELDKIADN	AVLQDFVQNT
a150	EIQAGGKMP	VARALSSHF	ELTQNTPAF	VKGYAAFAH	EELDKIADN	AVLQDFVQNT
	370	380	390	400	410	420
m150.pep	VDVLRFPAS	LTAEQFIRLL	RPLAPRLYS	ISSAQAEVG	DEVHVTGVR	FEHEGRARTGG
a150	VDVLRFPAS	LTAEQFIRLL	RPLAPRLYS	ISSAQAEVG	DEVHVTGVR	FEHEGRARTGG
	430	440	450	460	470	480
m150.pep	ASGFLADRLE	EDGTVRVF	VERNDGFR	LPEDSRKPI	VMIGSGTG	VAPFRAFVQ
a150	ASGFLADRLE	EDGTVRVF	VERNDGFR	LPEDSRKPI	VMIGSGTG	VAPFRAFVQ
	490	500	510	520	530	540
m150.pep	GKNWLIFGN	PHFARDFLY	QTEWQQFA	KDGFLHRYD	FAWSRDQEE	KIYVQDKIRE
a150	GKNWLIFGN	PHFARDFLY	QTEWQQFA	KDGFLHRYD	FAWSRDQEE	KIYVQDKIRE

```

a150      GKNWLFFGNPHFARDFLYQTEWQQFAKDGLHRYDFAWSRDQEEKIYVQDKIREQAEGWL
           490      500      510      520      530      540

           550      560      570      580      590      600
m150.pep  QWLQEGAHIIYVCGDAAKMAKDVEAALLDVIIGAGHLDEEGAEYLDMLREEKRYQRDVYX
           |||||
a150      QWLQEGAHIIYVCGDAAKMAKDVEAALLDVIIGAGHLDEEGAEYLDMLREEKRYQRDVYX
           550      560      570      580      590      600

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 613>:

```

g151.seq
1   ATGAAACAAA   TCCGCAACAT   CGCCATCATC   GCACACGTCG   ACCACGGCAA
51  AACCACATTG   GTCGACCAAC   TGCTGCGCCA   ATCCGGCACA   TTCCGCGCCA
101 ACCAGCAGGT   TGACGAGCGC   GTGATGGACA   GCAACGACCT   TGAAAAAGAA
151 CGCGGCATCA   CCATCCTCGC   CAAAAACACC   GCCATCGATT   ACGAAGGCTG
201 CCACATCAAT   ATCGTCGACA   CGCCGGGACA   CGCCGACTTC   GGCGGCGAAG
251 TGGAGCGCGT   TTTGGGGATG   GTGGATTGCG   TCGTCTTGTT   GGTGGACGCA
301 CAGGAAGGTC   CGATGCCGCA   AACCCGTTTC   GTGACCAAAA   AAGCCTTGCG
351 TTTGGGGCTG   AAACCGATTG   TCGTCATCAA   CAAAATCGAC   AAACCGTCCG
401 CCCGTCCGAG   CTGGGTATATC   GACCAGACTT   TCGAGTTGTT   CGACAACCTG
451 GGTGCGACCG   ACGAGCAGTT   GGATTTCCTG   ATTGTTTACG   CTTCAGGTTT
501 GAGCGGCTTT   GCCAAGCTGG   AAGAAAacga   CGAGAGCAGC   GATATGCCCC
551 CGCtggttcga   CACCATCCTA   AAATACAcgc   ctgCACCGAG   CGGCAGCGCG
601 GACGAGCCGC   TGCAACTGCA   AATTTCCCAA   CTCGACTACG   ACAACTACAC
651 CGGCCGCCCTC   GGTATCGGTC   GTATCTTGAA   CGGACGCATC   AAACCCGGCC
701 AAACCGTTGC   CGTGATGAAC   CACGAGCAGC   AAATCGCCCA   AGGCCGCATC
751 AACCAGCTTT   TGGGTTTCAA   AGGCTTGGA   CGCGTGCCGC   TTGAAGAAGC
801 CGAAGCCGGC   GACATTGTGA   TTATTTCCGG   TATCGAAGAC   ATCGGCATCG
851 GCGTAACCAT   CACCGACAAA   GACAACCCCA   AAGGCTGCC   GATGTTGAGC
901 GTGGACGAAC   CGACGCTGAC   GATGGACTTT   ATGGTAAACA   CCAGCCCGCT
951 CGCAGGTACA   GAAGGCAAAT   TCGTGACCAG   CCGCCAAATC   CGCGACCGCC
1001 TGCAAAAAGA   ATTGCTGACC   AACGTGCCC   TGCGCGTGGA   AGACACCGCC
1051 GatgCCGACG   TGTTCCGCGT   ATCcgGGCGC   GGCGAACTGC   ACCTGACGAT
1101 TTTGCTGGAA   AATATGCGCC   GCGAAGGCTA   CGAACTCGCC   GTCGGCAAGC
1151 CGCGCGTCGT   GTACCGAGAC   ATCGACGGTC   AAAAATGCGA   ACCTTATGAA
1201 AACCTGACTG   TGGACGTACc   cgacgacAAC   CAAGGCGCGG   TAATGGAAGA
1251 ACTCGGCCGC   CGCCGTGGCG   AACTGACCAA   TATGGAAGC   GACGGCAACG
1301 GacgCACCCG   CCTCGAATAC   CATATTCCAG   CGCGCGGCTT   GATCGGTTTC
1351 CAAGCGAAT   TCATGACCCT   GACGCGCGGC   GTCGGGCTGA   TGAgccacGT
1401 GTTcgacgac   tacgcgcccg   tcaAACCCGA   TATGCCCGGC   CGCCACAACG
1451 GCGTactggt   GtcccaAGAG   CAGGGCGAGG   CGGTTGCTTA   CGCCTTGTGG
1501 AATCTTGAAG   ACCGCGGCCG   TATGTTGTA   TCGCCCAACG   ACAAATCTA
1551 CGAAGGTATG   ATTATCGGCA   TCCACAGCCG   CGACAACGAT   TTGGTGGTCA
1601 ACCCGCTCAA   AGGCAAAAAA   CTCACCAATA   TCCGTGCCAG   CGGTACCGCA
1651 GAAGCGGTGC   GCCTGACCAC   GCCGATCAAA   CTGAcgcTGG   AAGGCGCGGT
1701 CGAGTTTATC   GACGATGACG   AGCTGGTGGA   AATCACGCCG   CAAtccatcc
1751 gcctgcgcat   gcgttacctG   AGCGaattgg   aacgccgccc   tcaTTTTAAA
1801 AagctgGATT   AA

```

This corresponds to the amino acid sequence <SEQ ID 614; ORF 151.ng>:

```

g151.pep
1   MKQIRNIAII  AHVDHGKTTL  VDQLLRQSGT  FRANQQVDER  VMDSNDLEKE
51  RGITILAKNT  AIDYEGCHIN  IVDTPGHADF  GGEVERVLGM  VDCVLLVDA
101 QEGPMPQTRF  VTKKALALGL  KPIVVINKID  KPSARPSWVI  DQTFELFDNL
151 GATDEQLDFP  IVYASGLSGF  AKLEETDESS  DMRPLFDTIL  KYTPAPSGSA
201 DEPLQLQISQ  LDYDNYTGRL  GIGRILNGRI  KPGQTVAVMN  HEQQIAQGRI
251 NQLLGFKGLE  RVPLEBAEAG  DIVIISGLIED  IGIGVTITDK  DNPKGLPMLS
301 VDEPTLTMDF  MVNTSPLAGT  EGKFVTSRQI  RDRLQKELLT  NVALRVEDTA
351 DADVFRVSGR  GELHLTILLE  NMRREGYELA  VGKPRVVYRD  IDGQKCEPYE
401 NLTVDPDDN  QGAVMEELGR  RRGELTNMES  DGNRTRLEY  HIPARGLIGF
451 QGEFMTLTRG  VGLMSHVFD  YAPVKPDMPG  RHNGVLVSQE  QGEAVAYALW

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431

501 NLEDGRGMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD
 551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRMYL SELERRRHF
 601 KLD*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 615>:

m151.seq
 1 ATGAAACAAA TCCGCAACAT CGCCATCATC GCCACGTCG ACCACGGCAA
 51 AACCATATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
 101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA
 151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA
 201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GGCGGCGAAG
 251 TAGAGCGCGT TTTGGGGATG GTGGACTGCG TCGTCTTGTT GGTGGACGCG
 301 CAGGAAGGCC CGATGCCGCA AACCCGTTTC GTGACCAAAA AAGCCTTGGC
 351 TTTGGGGCTG AAACCGATTG TCGTCATCAA CAAAATCGAC AAGCCGTCCG
 401 CTCGTCCGAG CTGGGTATAT GACCAAACTT TCGAGCTGTT CGACAACTTG
 451 GGCAGCAGCG ACGAGCAGTT GGATTTCCCG ATTGTTTACG CTTCAGGGTT
 501 GAGCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC
 551 CGCTGTTCGA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG
 601 GACGAAACGC TGCAACTGCA AATTTCCTCA CTCGACTACG ACAACTACAC
 651 CGGCCGCTC GGTATCGGTC GTATCTTGAA CGGACGCATC AAACCCGGCC
 701 AAACCGTTGC CGTCATGAAC CACGATCAGC AAATCGCCCA AGGCCGCATC
 751 AACAGCTTT TGGGTTTCAA AGGTTTGAA CGCGTGCCGC TTGAAGAAGC
 801 CGAAGCCGGC GACATCGTGA TTATTTCCGG TATCGAAGAC ATCGGTATCG
 851 GCGTAACCAT CACCGACAAA GACAATCCCA AAGGCCTACC GATGTTGAGC
 901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGCT
 951 GCGGGGTACG GAAGGCAAAAT TCGTAACCAG CCGCAAATC CGCGACCGCC
 1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TCGCGTGGA AGATACCGCC
 1051 GATGCCGACG TGTTCCGCGT ATCCGGGCGC GCGAGCTGC ACCTGACCAT
 1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAAC
 1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAATGCGA ACCGTATGAA
 1201 AACCTGACCG TGGATGTACC CGACGACAAC CAAGCGCGG TAATGGAAGA
 1251 ACTCGGCCGC CGCCGTGGCG AACTGACTAA TATGGAAAGC GACGGCAACG
 1301 GACGCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGTTTC
 1351 CAAGCGAAT TTATGACCT GACGCGCGG GTCGGGCTGA TGAGCCACGT
 1401 GTTCGACGAT TACGCGCCCG TCAAACCCGA TATGCCCGGC CGCCACAACG
 1451 GCGTGCTGGT GTCCCAAGAG CAGGGCGAGG CAGTCGCTTA CGCCTTGTTG
 1501 AATCTGGAAG ACCCGGGCCG TATGTTGTA TCGCCCAACG ACAAATCTA
 1551 CGAAGGCATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
 1601 ACCCGCTCAA AGGCAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC
 1651 GAAGCCGTTT GCCTGACCAC GCCAATCAAG CTGACGCTGG AAGGTGCGGT
 1701 TGAGTTTATC GACGATGACG AACTCGTTGA AATCACGCCG CAATCCATCC
 1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCCGCCG CCACTTTAAA
 1801 AAGCTGGATT GA

This corresponds to the amino acid sequence <SEQ ID 616; ORF 151>:

m151.pep
 1 MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQOQVDER VMDSNDLEKE
 51 RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVLLVDA
 101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
 151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDITL KYTPAPSGSA
 201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQTVAVMN HDQQIAQGRI
 251 NQLLFPKGLF RVPLEEAEAG DIVIISGIED IGIGVTITDK DNPKGLPMLS
 301 VDEPTLTMDP MVNTSPLAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
 351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
 401 NLTVDPDDN QGAVMEELGR RRGELTNMES DGNRTRLEY HIPARGLIGF
 451 QGEFMTLTRG VGLMSHFDD YAPVKPDMPG RHNGVLVSQE QGEAVAYALW
 501 NLEDGRGMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD
 551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRMYL SELERRRHF
 601 KLD*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 151 shows 99.2% identity over a 603 aa overlap with a predicted ORF (ORF 151.ng) from *N. gonorrhoeae*:

m151/g151

	10	20	30	40	50	60
m151.pep	MKQIRNIAIIAHVDHGKTTLVLDQLLRQSGTFRANQQVDERVMDSDNLEKERGITILAKNT					
g151	MKQIRNIAIIAHVDHGKTTLVLDQLLRQSGTFRANQQVDERVMDSDNLEKERGITILAKNT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m151.pep	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
g151	AIDYEGCHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m151.pep	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN					
g151	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m151.pep	DMRPLFDITILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN					
g151	DMRPLFDITILKYTPAPSGSADEPLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m151.pep	HDQQIAQGRINQLLGFKGLERVPLEEAAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
	:					
g151	HEQQIAQGRINQLLGFKGLERVPLEEAAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m151.pep	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLOKELLTNVALRVEDTADADVFRVSGR					
g151	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLOKELLTNVALRVEDTADADVFRVSGR					
	310	320	330	340	350	360
	370	380	390	400	410	420
m151.pep	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDVPDDNQAVMEELGR					
g151	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDVPDDNQAVMEELGR					
	370	380	390	400	410	420
	430	440	450	460	470	480
m151.pep	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG					
g151	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m151.pep	RHNGVLVSQEQGEAVAYALWNLEDGRGMFVSPNDKIYEGMIIGIHSRDNDLVNPLKGKK					
g151	RHNGVLVSQEQGEAVAYALWNLEDGRGMFVSPNDKIYEGMIIGIHSRDNDLVNPLKGKK					
	490	500	510	520	530	540
	550	560	570	580	590	600
m151.pep	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK					
g151	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRMYLSELERRRHFK					
	550	560	570	580	590	600

433

m151.pep KLDX
 ||||
 g151 KLDX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 617>:

a151.seq
 1 ATGAAACAAA TCCGCAACAT CGCCATCATC GCCACGTCG ACCACGGCAA
 51 AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
 101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGA AAAAGAA
 151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA
 201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GGCGGCGAAG
 251 TAGAGCGAGT TTTGGGGATG GTGGACTGCG TCGTCTTGTT GGTGGACGCG
 301 CAGGAAGGCC CGATGCCGCA AACCCTTTTC GTGACCAAAA AAGCCTTGGC
 351 TTTGGGGCTG AAACCGATTG TCGTCATCAA TAAAATCGAC AAACCGTCCG
 401 CCCGTCCGAG CTGGGTCATC GACCAAACTT TCGAGCTGTT CGACAACCTG
 451 GGCGCGACCG ACGAGCAGTT GGATTTCCCG ATTGTTTATG CTTCCGGTCT
 501 GTCCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC
 551 CGCTGTTCTGA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG
 601 GACGAAACGC TGCAACTGCA AATTTCCCAA CTCGACTACG ACAACTACAC
 651 CGGCGCGCTC GGTATCGGTC GTATCTTGAA CGGACGTATC AAGCCCGGTC
 701 AAGTTGTTGC CGTCATGAAC CACGATCAAC AAATCGCCCA AGGCCGATC
 751 AACCAGCTTT TGGGTTTCAA AGGTTTAGAA CGCGTGCCGC TTGAAGAAGC
 801 CGAAGCCGGC GACATCGTGA TTATTTCCGG TATTGAAGAC ATCGGCATCG
 851 GCGTAACCAT CACCGACAAA GACAACCCCA AAGGCCTGCC GATGTTGAGC
 901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGTT
 951 GGCAGGTACG GAAGGCAAAT TCGTAACCG CCGCAAATC CGCGACCGCC
 1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TCGCGTGGA AGATACCGCC
 1051 GATGCCGACG TGTTCCGCGT ATCCGGGCGC GGCGAGCTGC ACCTGACCAT
 1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAC
 1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAAATGCGA ACCGTATGAA
 1201 AACCTGACCG TGGACGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
 1251 ACTCGCCGCG CGCCGTGGCG AACTGACTAA TATGGAAAGC GACGGCAACG
 1301 GACGCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGCTTC
 1351 CAAGGCGAAT TTATGACCTT GACGCGCGGG GTCGGGCTGA TGAGCCACGT
 1401 GTTCGACGAT TACGCGCCCG TCAAACCCGA TATGCCTGGC CGCCACAACG
 1451 GCGTGCTGGT GTCCCAAGAG CAGGGCGAGG CAGTCGCTTA CGCCTTGTGG
 1501 AATCTGGAAG ACCGCGGCCG TATGTTTCGTA TCGCCCAACG ACAAATCTA
 1551 CGAAGGTATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
 1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC
 1651 GAAGCCGTTT GCCTGACCAC GCCGATTAAG CTGACGCTGG AAGGTGCGGT
 1701 CGAGTTTATC GACGATGATG AGCTGGTAGA AATCACGCCG CAATCCATCC
 1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCCGCCG CCATTTCAAA
 1801 AAGCTAGATT GA

This corresponds to the amino acid sequence <SEQ ID 618; ORF 151.a>:

a151.pep
 1 MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
 51 RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVLLLVDA
 101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
 151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDLIL KYTPAPSGSA
 201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQVVAVMN HDQQAQAGRI
 251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IGIGVTITDK DNPKGLPMLS
 301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLOKELLT NVALRVEDTA
 351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
 401 NLTVDVPDDN QGAVMEELGR RRGELTNMES DNGRTRLEY HIPARGLIGF
 451 QGEFMTLTRG VGLMSHVFD YAPVKPDMPG RHNGVLVSQE QGEAVAYALW
 501 NLEDRGRMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGGK LTNIRASGTD
 551 EAVRLTTFIK LTLEGAVEFI DDDELVEITP QSIRLRKRYL SELERRRHFK
 601 KLD*

m151/a151 99.8% identity in 603 aa overlap

10

20

30

40

50

60

434

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m151.pep  MKQIRNIAIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT
a151      MKQIRNIAIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT
           10      20      30      40      50      60

           70      80      90      100     110     120
m151.pep  AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL
a151      AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL
           70      80      90      100     110     120

           130     140     150     160     170     180
m151.pep  KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN
a151      KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN
           130     140     150     160     170     180

           190     200     210     220     230     240
m151.pep  DMRPLFDTILKYTPAPSGSADETLLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN
a151      DMRPLFDTILKYTPAPSGSADETLLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN
           190     200     210     220     230     240

           250     260     270     280     290     300
m151.pep  HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS
a151      HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS
           250     260     270     280     290     300

           310     320     330     340     350     360
m151.pep  VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR
a151      VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR
           310     320     330     340     350     360

           370     380     390     400     410     420
m151.pep  GELHLTILLENMRREGYELAVGKPRVVYRIDIGQKCEPYENLTVDPDDNQGAVMEELGR
a151      GELHLTILLENMRREGYELAVGKPRVVYRIDIGQKCEPYENLTVDPDDNQGAVMEELGR
           370     380     390     400     410     420

           430     440     450     460     470     480
m151.pep  RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG
a151      RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG
           430     440     450     460     470     480

           490     500     510     520     530     540
m151.pep  RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVVNPLKGKK
a151      RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVVNPLKGKK
           490     500     510     520     530     540

           550     560     570     580     590     600
m151.pep  LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK
a151      LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK
           550     560     570     580     590     600

m151.pep  KLDX
a151      KLDX

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 619>:

g152.seq

```

1  ATGAAAAaca aACCaaagt ctgGGacttc cCaccccgcc ttTTCactG
51 GctgcttgCC gCATCCctgc CCTTTATGTG gtatagCGCA AAAGCCGGCG
101 GcgataTGCT GcaatgGCAC ACGCGCGTCG GGCTGCTCGT CCTTTTCCTG

```

g152.pcp

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 621>:

1	ATGAAAAACA	AAACCAAAGT	CTGGGACCTC	CCCACCCGCC	TTTTCCA CTG
51	GCTGCTTGCC	GCGTCCTGTC	CCTTTATGTG	GTATAGCGCG	AAAGCCGGCG
101	GCGATATGCT	GCAATGGCAG	ACGCGCGTCG	GGCTGTTCTG	CCTTTTCTGT
151	CTCGTATTTC	GCGCTTGCTG	GGGCACTTTG	GGCAGCGATA	CCGCCGCTTT
201	TTCCCGTTTT	GTCCAAGGCT	GGGCAGGCAT	ACGCGGCTAT	CTGAAAAACG
251	GTATTCCCGA	ACACATCCAG	CCCGGACACA	ACCCCTTGGG	CGCACTGATG
301	GTCGTTTGCG	TTTTTGCCCG	CGTGTCTCTC	CAAGTCGGGA	CCGGGCTTTT
351	TGCCGCGCAT	GAACCAACCT	TCAAGACCAA	CGGCTACCTC	AACCAATTTG
401	TTTCCGAACA	TACGGGCAGC	CTTATGCGGA	AAATCCACCT	CAACTTTTTT
451	AAGCTGCTCG	CCGTTTTTTT	TGCAATCCAC	ATCGCCGCCG	TCGCCGCATA
501	CCGCGTATTC	AAAAAGAAAA	ACCTCATCCT	CCCGATGATA	ACCGGCTTCA
551	AATACATCGA	AGGCAAAACC	TCAATCCGCT	TTGCAGGCAA	AGCCGCGCTT
601	GCCGCCGCAT	TATCGGTTGC	CTCGCTTGCC	GCAGCCGCCA	TCCTGCTCCT
651	GTCCTGA				

m152.pcp

Computer analysis of this amino acid sequence gave the following results:

ORF 152 shows 95.4% identity over a 218 aa overlap with a predicted ORF (ORF 152.ng) from *N. gonorrhoeae*:

m152/g152

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFHWLLAASLPFMWYSAKAGGDMQLQWHTRVGLFVLFLLVFRLCWGIW					
	:					
g152	MKNKTKVWDFPTRLFWHLLAASLPFMWYSAKAGGDMQLQWHTRVGLLVFLFLLVFRLCWGIW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	:					
g152	GSDTARFSRFVRGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAN					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSIAIHIAAVAAYRVFKKKNLILPMI					
	: : : :					
g152	ENTFSTNGYLNHLVSEHTGSLIRKIHLNFFKLLAVFSAVHIAAVAAYRIFKKKNLVRPMI					
	130	140	150	160	170	180

	190	200	210	219
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVASLAAAAIILLSX			
	:			
g152	TGFKYIEGKTSIRFAGKAALAAALSVAAALAAAAIILLSX			
	190	200	210	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 623>:

```

a152.seq
  1  ATGAAAAACA AAACCAAGT CTGGGACTTC CCCACCCGCC TTTTCCACTG
 51  GCTGCTTGCC GCATCCCTAC CCTTTATGTG GTATAGCGCG AAAACCGGCG
101  GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTTAT CCTTTTCCTG
151  CTCGTATTCC GCCTCTGCTG GGCATTTTGG GGCAGCGATA CCGCCCGTTT
201  CTCCCGTTTC GTCCGCGGAT GGTGCGGTAT CAGAGAGTAT ATGAAAAACG
251  GTATTCCCGA ACACGTCCAA CCCGGACACA ACCCCTTGGG CGCAGTGATG
301  GTCGTTGCGC TTTTGGCCGC CGTGTGCTTC CAAGTCGGCA CAGGGCTTTT
351  TGCCGCCGAT GTAAACACCT TCAGCACCAA CGGCTACCTC AACCATTGGG
401  TTTCCGAACA TACGGGCAGC CTTATGCGGA AAATCCATCT CAACTTTTTC
451  AAAGTGTCTG CCGTTTTTTC CGCAGTCCAC ATCGCCGNCG TCGCCGCATA
501  CCGCGTGTTT AAAAAGAAAA ACCTCGTCCT CCCGATGATA ACCGGCTTCA
551  AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGGCAA AGCCGCGCTT
601  GCCGCCGCAT TATCGGTTGC CGCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651  GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 624; ORF 152.a>:

```

a152.pep
  1  MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KTGGDMLQWH TRVGLFILEL
 51  LVFRLCWGIW GSDTARFSRF VRGWSGIREY MKNGIPEHVQ PGHNPLGALM
101  VVALLAAVSF QVGTGLFAAD VNTFSTNGYL NHLVSEHTGS LMRKIHLNFF
151  KLLAVFSAVH IAXVAAYRVF KKKNLVLPMI TGFKYIEGKT SIRFAGKAAL
201  AAALSVAALA AAAIILLS*

```

m152/a152 94.0% identity in 218 aa overlap

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFHWLLAASLPFMWYSAKAGGDMQLQWHTRVGLFVLFLLVFRLCWGIW					
	: : : :					
a152	MKNKTKVWDFPTRLFHWLLAASLPFMWYSAKTGGDMLQWHTRVGLFILFLLVFRLCWGIW					
	10	20	30	40	50	60

	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNIGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	: : : :					
a152	GSDTARFSRFVRGWSGIREYMKNGIPEHVQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	70	80	90	100	110	120

	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSIAIHIAAVAAYRVFKKKNLILPMI					
	: : : :					
a152	VNTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSAVHIAAXVAAYRVFKKKNLVLPMI					
	130	140	150	160	170	180

	190	200	210	219
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVASLAAAAIILLSX			
	:			
a152	TGFKYIEGKTSIRFAGKAALAAALSVAAALAAAAIILLSX			
	190	200	210	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 625>:

```
g153.seq
1  atgggggtttg cttacAgat gacgtatatc gaggtCGGga taccggaggc
51  ggcacccgctc ctttCgctGC CCGAGATgat gcgcctgatG GTGTTtCagg
101 attATGGTTT TttggcCGAA GTGATGTTTG TGctgaCTTT cGGCGcgcCG
151 GTTCTGTTtC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GGCAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCACTCT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AAAGGTTTCG TTCGGGCCGG CGTTTTATCT
351 GATGTTCCGC CTGTCGGTTA TGCTGATTCT GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTCCAA ATCGGCGGGC TGACGGGGAA TAATGCGGTT
451 CAGACGGCAT CGGAAGGCAA AACCTGTTGC AGCCGCTGCC TGTATTtccg
501 cgacAGTgcc gaatccCCCT GCGGGGTGTg cgGCGcggaa CTgtacggcg
551 gacggccgaa aagtCTGAGt atttCgtCGG CGTTTCTgac ggcggcggtT
601 GTTTTGTATT TCCctgCcaa TATCctgccc attaTGAttt cgtccAATCc
651 tgcgcgccag GAGGcCAACA CCATCTTTAG CGGCATCGCT TATATGTGGG
701 ACGaggcgA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTG
751 GTGCCGGTGC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGGCGGCACG
801 GTTCGCTTTG CCGGCGGGCG CAAAGAAATT GTCGCACCTC tacCGCATCA
851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGTG GATTATTATT
901 TTGATGTGTT CGTTCCaCaC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTTT GACGATGCTG TCCGCCTATT
1001 ATTTCGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAACGAAA CGGAAAAATA TGACTGA
```

This corresponds to the amino acid sequence <SEQ ID 626; ORF 153.ng>:

```
g153.pep
1  MGFAYSMTYI EVGIPEAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRVM VRLRQAMMVD VFFVSTLVAY
101 IKLSSVAKVR FGPAPFLMFA LSVMLIRTSV SVPQHWVYFQ IGRLTGNNAV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYGGRPKSLs ISSAFLTAaV
201 VLYFPANILP IMISSNPAAT EANTIFSGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIAAARFAL PAGAKKLSHL YRITEAVGRW SMIDIFVIlI
301 LMCSFHTYAA RVIPGSAaVY FCLVVLITML SAYYFDPRLl WDKRASDGIA
351 FNETEKYD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 627>:

```
m153.seq
1  ATGGCGTTTG CTTACGGTAT GACGTATATC GAGGTCGGGA TACCGGGTGC
51  GGCATCCGTC CTTTCGCTGC CCGAGATGAT GCGCCTGATG GTGTTTCAGG
101 ATTATGGTTT TTTGGCCGAA GTGATGTTTG TGCTGACTTT CGGCGCGCCG
151 GTTCTGTTTC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 ACAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCACTTT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AGAGGTTTCG TTCGGGCCGG CGTTTTATCT
351 GATGTTCCGC CTGTCACTTA TGCTGATTCT GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTTCAA ATCGGCGGGC TGACGGGGGA TAATGCGGTT
451 CAGACGGCAT CGGAAGGTAA AACCTGTTGC AGCCGCTGCC TGTATTTCCG
501 CGACAGTGCC GAATCCCCCT GCGGCGTGTG CGGTGCGGAA CTGTACCGCC
551 GACGCGCGAA AAGTCTGAGT ATTTCTGCGG CGTTTCTGAC GGCGGCGGTT
601 ATTTTGTATT TCCCTGCCAA TATCCTGCCG ATTATGATTT CGTCCAATCC
651 TTCCCGCACG GAGGTCAATA CCATCCTTAA CGGCATCGCT TATATGTGGG
701 ACGAGGGCGA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGGTAC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGTCCGCCCC
801 CTTCGCTTTG CCAACGGGTG CAAAGAAATT GTCGCACCTC TACCGCATCA
851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGTG GATTATTATT
901 TTGATGTGTT CGTTCCACAC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTCGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGACTGA
```

This corresponds to the amino acid sequence <SEQ ID 628; ORF 153>:

```
m153.pep
1  MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRVM VRLRQAMMVD VFFVSTLVAY
```

438

```

101 IKLSSVAEVR FGPAFYLMFA LSVMLIRTSV SVPQHWVYFQ IGRLTGDNAV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSLs ISSAFLTAAV
201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIII
301 LMCSFHYYAA RVIPGSAAVY FCLVVILTML SAYYFDPRLW WDKRASDGIA
351 FNETEKHD*

```

m153 / g153 96.1% identity in 358 aa overlap

```

              10      20      30      40      50      60
m153.pep    MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFDYGFLEVMFVLTFGAPVLFLLCLYV
              |||:|||||
g153        MGFAYSMTYIEVGIPGAASVLSLPEMMRLMVFDYGFLEVMFVLTFGAPVLFLLCLYV
              10      20      30      40      50      60

              70      80      90      100     110     120
m153.pep    YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA
              |||:|||||
g153        YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAKVRFGPAFYLMFA
              70      80      90      100     110     120

              130     140     150     160     170     180
m153.pep    LSVMLIRTSVSVSPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE
              |||:|||||
g153        LSVMLIRTSVSVSPQHWVYFQIGRLTGNNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE
              130     140     150     160     170     180

              190     200     210     220     230     240
m153.pep    LYRRRPKSLsISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI
              |||:|||||
g153        LYGGRPKSLsISSAFLTAAVILYFPANILPIMISSNPAATEANTIFSGIAYMWDEGDRLI
              190     200     210     220     230     240

              250     260     270     280     290     300
m153.pep    AAVIFSASILVPVLKIAAMS VLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII
              |||:|||||
g153        AAVIFSASILVPVLKIAAMS VLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII
              250     260     270     280     290     300

              310     320     330     340     350     359
m153.pep    LMCSFHYYAARVIPGSAAVYFCLVVILTML SAYYFDPRLW WDKRASDGIAFNETEKHD
              |||:|||||
g153        LMCSFHYYAARVIPGSAAVYFCLVVILTML SAYYFDPRLW WDKRASDGIAFNETEKYD
              310     320     330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 629>:

a153.seq

```

1  ATGGCGTTTG CTTACGGTAT GACGTATATC GAGGTCGGGA TACCGGGTGC
51  GGCATCCGTC CTTTCGCTGC CCGAGATGAT GCGCCTGATG GTGTTTCAGG
101 ATTATGGTTT TTTGGCCGAA GTGATGTTTG TGCTGACCTT CGGCGCGCCG
151 GTTCTGTTTC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GACAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCACTTT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AGAGGTTTCG TTCGATCGG CGTTTATCT
351 GATGTTTCGC CTGTCGGTTA TGCTGATTCT GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTTCAA ATCGGGCGGC TGACGGGGGA TAATGCGGTT
451 CAGACGGCAT CGGAAGGTAA AACCTGTTGC AGCCGCTGCC TGTATTTCCG
501 CGACAGTGCC GAATCCCCCT GCGGCGTGTG CGGTGCGGAA CTGTACCGCC
551 GACGGCCGAA AAGTCTGAGT ATTTCGTGCG CGTTTCTGAC GCGGCGGTT
601 ATTTGTATT TCCCTGCCAA TATCCTGCCG ATTATGATTT CGTCCAATCC
651 TGCCGCCACG GAGGTCAATA CCATCCTTAA CGGCATCGCT TATATGTGGG
701 ACGAGGGCGA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGGTAC TGAAGATTGC GGCAATGTCT GTTTTGATTG CGTCCGCCCG
801 CTTGCTTTG CCAACGGGTG CAAAGAAATT GTCGCACCTC TACCGCATCA

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439

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851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGT GATTATTATT
901 TTGATGTGTT CGTTCCACAC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTTCGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 630; ORF 153.a>:

```

a153.pep
  1 MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
 51 VLFLLLCLYV YAALIRKQAY PALRLATRV M VRLRQAMMVD VEFVSTLVAY
101 IKLSSVAEVR FGSAYFLMFA LSVMLIRTSV SVPQHWVYFQ IGRLTGDNV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSL S ISSAFLTAAV
201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIII
301 LMCSFHYYAA RVIPGSAAVY FCLVVILTML SAYYFDPRL WDKRASDGIA
351 FNETEKHD*

```

m153/a153 99.7% identity in 358 aa overlap

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLLCLYV					
a153	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLLCLYV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m153.pep	YAALIRKQAYPALRLATRV M VRLRQAMMVDV FEFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
a153	YAALIRKQAYPALRLATRV M VRLRQAMMVDV FEFVSTLVAYIKLSSVAEVRFGSAFYLMFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m153.pep	LSVMLIRTSV SVPQHWVYFQ IGRLTGDNV QTASEGKTCCSRCLYFRDSAESPCGVCGAE					
a153	LSVMLIRTSV SVPQHWVYFQ IGRLTGDNV QTASEGKTCCSRCLYFRDSAESPCGVCGAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m153.pep	LYRRRPKSL S ISSAFLTA AVILYFPANILP IMISSNPAATEVNTILNGIAYMWDEGDRLI					
a153	LYRRRPKSL S ISSAFLTA AVILYFPANILP IMISSNPAATEVNTILNGIAYMWDEGDRLI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m153.pep	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII					
a153	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII					
	250	260	270	280	290	300
	310	320	330	340	350	359
m153.pep	LMCSFHYYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGIAFNETEKHDX					
a153	LMCSFHYYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGIAFNETEKHDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 631>:

```

g154.seq
  1 ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCTCAAG CACGCGTCCG
 51 CAAAAACAAC accttctct CCGCGTCTG GCTGGTCCCG CTGATCGCGC
101 TGATTGCCG CGGCTGGCTT TGGGTAAAG AAATCCGCA CAGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGA GGCATCGAAG TCAACAATAC
201 GGTCATTAAG GTATTGAGCA TCGATGTCG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CAAAAAGGC GTGGAAGTTA CTGCCCAACT CAATGCGGAC
301 GTATCCGGC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGcgtAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT

```

```

401 ACATCGCTTT TACACCCGGC AAAAGCGGCG AGGCAAAAGA CGTGTTCCTAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGcg GGCTGCGCTT
501 GAATTTGATT GGTA AAAACG AccgCATCCT CAACGTcaaC AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAATCG AAAGCGCGCA TTTCGAcccG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACACAGG CAGCGGCATC AAACCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTCAGGCG CGATTTCATT TGATTCGCGG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAGC GAGGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAATCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT cggTTCGCCT GTcgaATACA AAGGGctgaA
951 TGTcggCATG GTTTCGGATG TCCCTTATTT TGACCGCAAt gacagCCTGC
1001 ACCTcgtTTGA aaacggcgtg aTTcccGtac gCATCCGCAT cgagccTTCC
1051 CGTTTGAAAA TCAATGCCGA CGAGCAAAGC AAAGAGCATT GGAAACAACA
1101 ATTCAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCGGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCAAAGC TGCGACCGCA TACCGTTTAT GCAGGCGATA CCGTCATCGC
1251 CACACGGGGC GCGGTTTGG ATGACTTGCA GGTCAAATTG GCGGATTTCG
1301 TGGACaaatT CAACAATCTG CCATTggata aaACCGTTGC CGAATTGAAC
1351 GGCTCGCTCG CCGAACTCAA GTCCGCATC AAATCCGCCA ATGCCGCCCT
1401 AAGTCCATT GacaAACTGG TCGgcaatCC GCAGACGCAA AACATCCCGA
1451 ACGAACTGAA CCAAACTCTG AAAGAGTTGC GCATAACCCT GCAAGGCGTA
1501 TCGcctCAAT CGCCTATCTa cgGAgacgta caAAATAcgc tgCaAAGTTT
1551 GGACAAAACC TTAAAgacg TtcaACCCGT CATTAACT TTGAAAGAAa
1601 aacCCaaCgc actGATTtTc aacaACAGCA GCAAAGacc tatCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 632; ORF 154.ng>:

g154.pep

```

1 MTDNSPPPNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51 VTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTL LSGSYIAFTPG KSGEAKDVFQ
151 VQDIPPVTAI QQSGLRLNLI GKNDRIILNVN SPVLVENFMV GQIESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLNSAPLPAL
251 LSGATLSFDSF KTKNSKNVKS EDSFTLYDSR SEIANLPDDR SLYYTAFKQ
301 SVRGLTVGSP VEYKGLNVGM VSDVPYFDRN DSLHLFENGW IPVIRIEPS
351 RLEINADEQS KEHWKQQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATRG GGLDDLQVKL ADLLDKFNNL PLDKTVAELN
451 GSLAELKSAL KSANAALSSI DKLVGNPQTQ NIPNELNQTL KELRITLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NNSSKDPIPK
551 GSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 633>:

m154.seq

```

1 ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51 CAAAAACAAC ACCTTCCTCT CTGCCGCTCTG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTAAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTATCAAAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCTAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTA AAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGATGAAAAA TTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACACAGG CAGCGGCATC AAACCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTCGGCG CGATTTCATT TGATTCGCGG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GCCTGACCGT CGGTTTCGCC GTCGAGTACA AAGGGCTGAA
951 TGTCCGGCTG GTTTCGACG TCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATACCCGTAC GCATCCGCAT TGAACCTTCC
1051 CGTTTGAAAA TCAATGCCGA CGAACAAAGC AAAGAACATT GGAAACAACA
1101 ATTCAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGAAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCA

```

```

1201 TCACCTAAGC TGCACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTGCA GGTCAAATTG GCGGATTTGC
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTGCTTG CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAACCTG AAAGAGTTGC GCACAACCTT GCAAGGCGTA
1501 TCGCCGCAAT CGCCTATCTA CGGCGACGTA CAAAATACGC TGCAAAGTTT
1551 GGACAAAAC TTAAGACG TTCAACCCGT GATTAATACT TTGAAAGAAA
1601 AACCCAACGC GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 634 ORF 154.a>:

m154.pep

```

1  MTDNSPPPNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVFG
151 VQDIPPVTAI QSGGLRLNLI GKNDRIILNVN SPVLYENFMV QVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTGSGI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINAEQSK KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN
451 GSLAEKSTL KSANAALSSI DKLVGKPTQ NIPNELNQT KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*

```

m154 / g154 97.8% identity in 553 aa overlap

m154.pep	10	20	30	40	50	60
	MTDNSPPPNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE					
g154	MTDNSPPPNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE					
	10	20	30	40	50	60
m154.pep	70	80	90	100	110	120
	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
g154	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
	70	80	90	100	110	120
m154.pep	130	140	150	160	170	180
	SGVTGLGTLT SGSYIAFTPG KSDEAKDVFG VQDIPPVTAI QSGGLRLNLI GKNDRIILNVN					
g154	SGVTGLGTLT SGSYIAFTPG KSDEAKDVFG VQDIPPVTAI QSGGLRLNLI GKNDRIILNVN					
	130	140	150	160	170	180
m154.pep	190	200	210	220	230	240
	SPVLYENFMV QVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTGSGI					
g154	SPVLYENFMV QVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTGSGI					
	190	200	210	220	230	240
m154.pep	250	260	270	280	290	300
	KLNSAPLPALLSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDRS SLYYTAFKQ					
g154	KLNSAPLPALLSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDRS SLYYTAFKQ					
	250	260	270	280	290	300
m154.pep	310	320	330	340	350	360
	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINAEQSK					
g154	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINAEQSK					
	310	320	330	340	350	360
m154.pep	370	380	390	400	410	420
	KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATQG					
g154	KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATRG					

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	370	380	390	400	410	420
	430	440	450	460	470	480
m154 . pep	GGLDDDLQVKLADLLDKFDKLPDKTVAEI NGSLAELKSTLKSANAALSSIDKLVGKPQTQ					
g154	GGLDDDLQVKLADLLDKFNNLPDKTVAEI NGSLAELKSALKSANAALSSIDKLVGNPQTQ					
	430	440	450	460	470	480
	490	500	510	520	530	540
m154 . pep	NIPNELNQTLKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVPVINTLKEKPNALIF					
g154	NIPNELNQTLKELRITLQGVSPQSPIYGDVQNTLQSLDKTLKDVPVINTLKEKPNALIF					
	490	500	510	520	530	540
	550					
m154 . pep	NSSSKDPIPKGSRX					
g154	NNSSKDPIPKGSRX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 635>:

```

a154 . seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGTCGT GCTGGTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCAACAAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCCG TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTA AAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTGACCCG
601 TCCGACCAAA GCGTGCAATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTCTGGCTT GGAAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAAT CCGCCCTCTT GCCTGCCCTG
751 CTGTGCGGCG CGATTTTATT TGATTCGCGG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGATGACCGT TCGCTGTACT ACACCGCGTT TTTCAAAACA
901 TCCGTGCGCG GACTGACCGT CGGTTGCGCT GTCGAGTACA AAGGGCTGAA
951 TGTCGGCGTG GTTTCGATG TTCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATTCCCGTAC GCATCCGTAT TGAGCCTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAACAAGC AAAGAACATT GGAACAACA
1101 ATTTAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TGCGACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGCG GGCGGTTTGG ACGATTGCA GGTCAAATTG GCGGATTGTC
1301 TGGACAAGTT CGACAAACTG CCTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTTCGCTT CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAACCTTG AAAGAGTTGC GCACAACCTT GCAAGGCGTA
1501 TCGCCTCAAT CGCCTATCTA CGGCGACGTA CAAATACGCG TGCAAAGTTT
1551 GGACAAAACC TTAAAAGACG TTCAACCCGT CATTAACACT TTGAAAGAAA
1601 AACCCAACGC GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 636; ORF 154.a>:

```

a154 . pep
1  MTDNSPPPNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVFDQ

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151 VQDIPPVTAI QSGRLRLNLI GKNDRIILNVN SPVLYENFMV QQVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTGSIGI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN
451 GSLAELKSTL KSANAALSSI DKLVGKPGTQ NIPNELNQTQ KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*
```

m154/a154 100.0% identity in 553 aa overlap

```
m154.pep      10      20      30      40      50      60
MTDNSPPENGHAQARVRKNNTFLSAVWLVPILIALIAGGWLWVKEIRNRGPVVTLLMDSAE
|||||
a154          10      20      30      40      50      60
MTDNSPPENGHAQARVRKNNTFLSAVWLVPILIALIAGGWLWVKEIRNRGPVVTLLMDSAE

m154.pep      70      80      90     100     110     120
GIEVNNTVIKVLSDVGRVTRIKLRDDQKGEVETAQLNADVSGLIRSDTQFWVVKPRIDQ
|||||
a154          70      80      90     100     110     120
GIEVNNTVIKVLSDVGRVTRIKLRDDQKGEVETAQLNADVSGLIRSDTQFWVVKPRIDQ

m154.pep     130     140     150     160     170     180
SGVTGLGTLTLLSGSYIAFTPGKSDEAKDVFOVDIPPVTAIGQSGRLRLNLIGKNDRIILNVN
|||||
a154         130     140     150     160     170     180
SGVTGLGTLTLLSGSYIAFTPGKSDEAKDVFOVDIPPVTAIGQSGRLRLNLIGKNDRIILNVN

m154.pep     190     200     210     220     230     240
SPVLYENFMVGQVESAHFDPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTGSIGI
|||||
a154         190     200     210     220     230     240
SPVLYENFMVGQVESAHFDPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTGSIGI

m154.pep     250     260     270     280     290     300
KLNSAPLPALLSGAISFDSPKTKNSKNVKS EDSFTLYDSRSEVANLPDDRSLYYTAFFKQ
|||||
a154         250     260     270     280     290     300
KLNSAPLPALLSGAISFDSPKTKNSKNVKS EDSFTLYDSRSEVANLPDDRSLYYTAFFKQ

m154.pep     310     320     330     340     350     360
SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS
|||||
a154         310     320     330     340     350     360
SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS

m154.pep     370     380     390     400     410     420
KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATQG
|||||
a154         370     380     390     400     410     420
KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATQG

m154.pep     430     440     450     460     470     480
GGLDDLQVKLADLLDKFDKLPLDKTVAELNGSLAELKSTLKSANAALSSIDKLVGKPGTQ
|||||
a154         430     440     450     460     470     480
GGLDDLQVKLADLLDKFDKLPLDKTVAELNGSLAELKSTLKSANAALSSIDKLVGKPGTQ

m154.pep     490     500     510     520     530     540
NIPNELNQTQKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF
|||||
a154         490     500     510     520     530     540
NIPNELNQTQKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF
```

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                    550
m154.pep      NSSSKDPIPKGSRX
              |||||
a154          NSSSKDPIPKGSRX
                    550

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 637>:

```

g155.seq
1  atGAAaatcg GtateCCACG CGAGTCatta tcCGGCGAAA cccgcgtagc
51  ctgcAcgccc gCCACCGTTG CCctgctggg caAactAGGC TTTGAAACCG
101 TTGtcgaAAG CGGTGCAggt TTGGCGGCAA GTTtgaCGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGCCTGCCC
201 TTTAATTTAT AAGGTCAACG CGCCGTCCGA AGGCGAGCTG CCGCTGTCTA
251 AAGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAGG CCTTGCGCGC CAAGAAAGTC AACGCGCTGG CGATGGACAT
351 GGTTCCCCGC ATTTCCCGCG CTCAGGCCTT GGACGCTTTG TCTTCAATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT CACTGCCGCC GGCAAAGTGC CGCCTGCGCA
501 GGTTTTGGTG ATTGGCGCCG GTGTGGCGGG TTTGGCGGCA ATCGGTACGG
551 CAAATTCGCT CGGCGCAGTG GTGCGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGTAAG TTcctGAAAC TCGACTTCCT
651 GCAAGAATCG GCGGCGAGCG GAGACGgctA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAAATG AAGCTCTTTG CCGAACAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CTCCCAAGCT
801 GATTACCAAA GAAATGTTGG AAAGCATGAA ATCCGGATCC GTCATCGTCG
851 ATTTGGCGGC GACGGGCGGC AACTGCGAAC TCACCCGACC GGGCGAATTG
901 TCCGTAACCG GCAACGGCGT GAAAATCATC GGCTACACCG ACATGGCAAA
951 CCGCCTTGCC GGACAGTCTT CCCAGCTTTA CGCCACCAAC TTGGTGAACC
1001 TGACCAAGCT GTTAAGCCCG AACAAAGAcg gcgAATCAC GCTGGACTTC
1051 GAAGacgtGA TTATCCGCAA TATGACCGTT ACCCGcgacg gcgaaATCAC
1101 CTCCCGCCT CCGccgaTtC aggtTTCgc cggccgCAG CAAAcgccgt
1151 ctgaAAAagc cgcGCCTGCC GCCAagccc AgccGaaacc tgttCCcctg
1201 tggaAAAAaac tcgCGCCCGC CGCcatcgCC GCCGTATTGG tgctgtgGgt
1251 cggCgcggtc gcacccgcag CATTCCTGAA CCACTTTATC GTCTTCGTCC
1301 TCGCTGCGT CATCGGTAC CATGTCGTTT GgaacgTCAG CCACTCGCTG
1351 CACACACCGC TGAtgtcggT aaccaaCgcc atctccGGCA tcatggtcgt
1401 cggCGCGCTG CTGCAAAATCG GTCAGGGcaa cggcttcgtT TCgctGCTGT
1451 CGTTTGTGTC CATCTGATT GCCGGCATCA ATATCTTCGG CGGCTTTGCG
1501 GTTACACGGC GTATGCTGAA TATGTTTAAG AAAGGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 638; ORF 155.ng>:

```

g155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWACPLIY KVNAPSEGEL PLLKEGQTIIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMVPR ISRAQALDAL SSMANISGYR AVIEAANAFG
151 RFFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDRLEV
201 AEQIESMGGK FLKLDLQES GSGDGYAKV MSDEFIAAEM KLFAEQAKEV
251 DIIITTAaip GKPAKLITK EMVESMKSGS VIVDLAATGG NCELTRPGEL
301 SVTNGVKIi GYTDMANRLA GQSSQLYATN LVNLTkLLSP NKDGEITLDF
351 EDVIIRNMTV TRDGEITFPF PPIQVSARPO QTPSEKAAPA AKPEPKPVPL
401 WKKLAPAAIA AVLVLWVGAV APAaFLNHFI VFVLACVIGY HVVWNVSHSL
451 HTPLMSVTNA ISGIMVVGAL LQIGQGNGFV SLLSFVAILI AGINIFGGFA
501 VTRRMLNMFk KG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 639>:

```

m155.seq
1  ATGAAAATCG GTATCCACG CGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTGCAAAAG CGGTGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGTCTGCCCC
201 TTTGATTTAT AAGGTCAACG CGCCGTCCGA ACAGGAAGTG CCGCTTTTGA
251 ACGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT

```



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301 TTGGTCGAAG CCTTGC GCGC CAAGAAAGTG AACGCGCTGG CGATGGATAT
351 GGTGCCCCGC ATTTGCGCGC CGCAGGCTTT GGACGCTTTG TCTTCGATGG
401 CAAACATCAG CGGCTACGCG GCCGTAATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT TACCGCCGCC GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 ACAAGAATCG GGCGGAGCGG GAGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTATATCG AGCCGAGATG AAGCTCTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCT
801 GATTACCAAA GAAATGGTGG AAAGCATGAA ATCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGGACGGGC GGCAACTGCG AACTCACCCG CCCGGGCGAA
901 TTGTCCGTAA CCGGCAACGG CGTGAATATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTCCAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGTTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCACG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCCGA TTCAAGTTTC CGCCAGCCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGTGCCT GCCGCCAAGC CCGAGCCAAA ACCCGTTCCC
1201 CTGTGAAAAA AACTCGCGCC CGCCGTCATC GCCGCCGCT TGGTACTGTG
1251 GGTGCGGCGC GTCGCACCCG CAGCATTCTT GAACCACTT ATCGTGTTCG
1301 TTCTCGCCTG CGTCATCGGC TACTACGTCG TCTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTAACCAAC GCCATCTCCG GCATCATCGT
1401 CGTCGCGCGC CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCTG ATTGCCGCA TCAACATCT CGGCGGCTTT
1501 GCGGTAAACAC GCGTATGCT GAATATGTTT AAGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 640; ORF 155>:

```

m155.pep
  1 MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
 51 QTAGATVADK AAVWVCPLIY KVNAPSEQEL PLLNEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMPV ISRAQALDAL SSMANISGYR AVIEAANAFG
151 RFFTQGITA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDLPQES GSGDGYAKV MSDEFIAAEM KLF AEQAKEV
251 DIIITTAIP GKPAKPLTK EMVESMKSGS VIVDLAAATG GNCELTRPGE
301 LSVTGNVVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTHDGEITFP PPPIQVSAQP QQTPEKAVP AAKPEPKPVP
401 LWKKLAPAVI AAVLVLVWGA VAPAAFLNHF IVFVLACVIG YYVWNVVSHS
451 LHTPLMSVTN AISGIIVVGA LLQIGQNGF VSLLSFVAIL IAGINIFGGF
501 AVTRRMLNMF KKG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 155 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 155.ng) from *N. gonorrhoeae*:

```

m155 / g155 97.9% identity in 513 aa overlap
              10      20      30      40      50      60
m155.pep      MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              |||
g155           MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              10      20      30      40      50      60

              70      80      90      100     110     120
m155.pep      AAVWVCPLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPV
              |||:|||||
g155           AAVWACPLIYKVNAPSEGELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPV
              70      80      90      100     110     120

              130     140     150     160     170     180
m155.pep      ISRAQALDALSSMANISGYRAVIEAANAFGRFFTQITAAGKVPPAQVLVIGAGVAGLAA
              |||
g155           ISRAQALDALSSMANISGYRAVIEAANAFGRFFTQITAAGKVPPAQVLVIGAGVAGLAA

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	130	140	150	160	170	180
	190	200	210	220	230	240
m155.pep	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
g155	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m155.pep	KLFAEQAKEVDIIITTAaipgkPAPKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
g155	KLFAEQAKEVDIIITTAaipgkPAPKLITKEMVESMKSGSVIVDLAA-TGGNCELTRPGE					
	250	260	270	280	290	
	310	320	330	340	350	360
m155.pep	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
g155	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	300	310	320	330	340	350
	370	380	390	400	410	420
m155.pep	VTHDGEITFPPPIQVSAQPQPTSEKAVPAKPEPKPVPLWKKLAPAVIAAVLVLWVGA					
	: : : :					
g155	VTRDGEITFPPPIQVSARPQPTSEKAAPAAKPEPKPVPLWKKLAPAAIAAVLVLWVGA					
	360	370	380	390	400	410
	430	440	450	460	470	480
m155.pep	VAPAAFLNHFIVFVLACVIGYVWVNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF					
g155	VAPAAFLNHFIVFVLACVIGYHVVWVNVSHSLHTPLMSVTNAISGIMVVGALLQIGQGNGF					
	420	430	440	450	460	470
	490	500	510			
m155.pep	VSLLSFVAILIAGINIFGGFAVTRRMLNMFKKGX					
g155	VSLLSFVAILIAGINIFGGFAVTRRMLNMFKKGX					
	480	490	500	510		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 641>:

```

a155.seq
1  ATGAAAATCG GTATCCCACG TGAGTCATTA TCCGCGGAAA CCCGCGTCCG
51  CTGTACGCCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTCGAAAG CGGCGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAGCAGCAG GCGCAACCGT TGCCGACAAA GCAGCGGTTT GGGCATACCC
201 TTTAATTTAT AAGGTTAACG CGCCGTCCGA AGACGAGCTG CCGCTGCTCA
251 AAGAAGGACA GACCATCGTC AGCTTCCGTG GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAAG CCTTGCGCGC CAAGAAAGTG AACGCGCTGG CAATGGACAT
351 GGTGCCCCGC ATTCGCGCGC CGCAGGCTTT GGACGNTTTG TCTTNGATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTNTTCA CCGGCCAAAT TACTGCCGCA GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGTGT TCGATACCCG CCTG.AAGTG
601 GCGGAACAAT TAGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 GCAAGAATCG GCGCGCAGCG GCGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAGATG AAGCTTTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCN
801 NNTNANCAAA GAAATGGTCG AAAGCATGAA ACCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGGACGGGC GGCAACTGCG AACTCACCAA ACAGGGCGAA
901 TTGTTTCGTAA CCGGCAACGG CGTGAAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTGCGAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGCTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCGCG ACGGCGAAAT
1101 CACCTTCCCG CTTCCGCGCA TTCAAGTTTC CGCCCAACCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGCGCCT GCCGCCAAGC CCGAACCGAA ACCCGTTCCC

```

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1201 CTGTGGAAAA AACTCGCGCC CGCCNTNATC GCCGCCGTGT TGGTACTGTG
1251 GGTGCGCGCG GTCGCACCCG CAGCATTCCT GAACCACTTT ATCGTCTTCG
1301 TCCTCGCCTG CGTCATCGGC TACTATGTCG TTTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTGACCAAC GCCATTTCCG GCATCATCGT
1401 CGTCGCGCGC CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCAGCA TCAACATCTT CGGCGGCTTC
1501 TTTGTAACGC GCGGATGCT GAATATGTTT AGGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 642; ORF 155.a>:

```

a155.pep
  1 MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
 51 QAAGATVADK AAVWAYPLIY KVNAPSEDEL PLLKEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMPVR ISRAQALDXL SXMANISGYR AVIEAANAFG
151 RXFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRVFDTRLXV
201 AEQLESMGGK FLKLDFFQES GSGDGYAKV MSDEFIAAEM KLF AEQAKEV
251 DIIITTAaip GKPAKXXXXK EMVESMKPGS VIVDLAAATG GNCELTKQGE
301 LFVTGNGVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTRDGEITFP PPPIQVSAQP QQTPEKAAP AAKPEPKPVP
401 LWKKLAPAXI AAVLVLVWGA VAPAAFLNHF IVFVLACVIG YVYVWNVSHS
451 LHTPLMSVTN AISGIIIVGA LLQIGQGNGF VSLLSFVAIL IASINIFGGF
501 FVTRRMLNMF RKG*

```

m155/a155 95.3% identity in 513 aa overlap

m155.pep	10	20	30	40	50	60
	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK					
a155	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQAAGATVADK					
	10	20	30	40	50	60
m155.pep	70	80	90	100	110	120
	AAVWVCPLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR					
a155	AAVWAYPLIYKVNAPSEDELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR					
	70	80	90	100	110	120
m155.pep	130	140	150	160	170	180
	ISRAQALDALSSMANISGYRAVIEAANAFGRFFTGQITAAGKVPPAQVLVIGAGVAGLAA					
a155	ISRAQALDXLSXMANISGYRAVIEAANAFGRXFTGQITAAGKVPPAQVLVIGAGVAGLAA					
	130	140	150	160	170	180
m155.pep	190	200	210	220	230	240
	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDFFQESGSGDGYAKVMSDEFIAAEM					
a155	IGTANSLGAVVRVFDTRLXVAEQLESMGGKFLKLDFFQESGSGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
m155.pep	250	260	270	280	290	300
	KLF AEQAKEVDIIITTAaipGKPAKKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
a155	KLF AEQAKEVDIIITTAaipGKPAKXXXXKEMVESMKPGSVIVDLAAATGGNCELTKQGE					
	250	260	270	280	290	300
m155.pep	310	320	330	340	350	360
	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
a155	LFVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	310	320	330	340	350	360
m155.pep	370	380	390	400	410	420
	VTHDGEITFPPIQVSAQPQQTPEKAAPAAKPEPKVPPLWKKLAPAVIAAVLVLVWGA					
a155	VTRDGEITFPPIQVSAQPQQTPEKAAPAAKPEPKVPPLWKKLAPAXIAAVLVLVWGA					
	370	380	390	400	410	420

448

```

              430      440      450      460      470      480
m155.pep      VAPAAFLNHFIVFVLACVIGYYVWNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNF
              |||||
a155           VAPAAFLNHFIVFVLACVIGYYVWNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNF
              430      440      450      460      470      480

              490      500      510
m155.pep      VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX
              |||||:|||||
a155           VSLLSFVAILIASINIFGGFFVTRMLNMFRKGX
              490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 643>:

```

g156.seq
1  ATGACTTTCG CCTATTGGTG CATTCTGATT GCCTGCCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCTCG CGGTTTCTG GCACATACGC AAGGCGCAGC CGCCCGTGCC
151 CAGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCCGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG ATTGTTTCATC CTGTTCCGCC TCGCCTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT GCGCTCGCTG ATGTGGGCGG GCGGATTTCG
351 CTGCACCGTC GGACTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 644; ORF 156.ng>:

```

g156.pep
1  MTFAYWCILI ACLLPFLCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51 HAAQONGFEA FAPFAAAVLT AHATGNAGQA TVNTLAGLFI LFRLAFIWCY
101 IADKAALRSL MWAGGFACTV GLFVAAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 645>:

```

m156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTGCCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCGCG CGGTTTCTA GCGCACACGC AAGGCGCAGC CGCCCGTGCC
151 CAGCCGCGAC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCCGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC GCGCAATCG ACCATCAACA
251 CGCTTGCCTG CCTGTTTCATC CTGTTCCGCC TCGCCTTAT CTGGTGCTAT
301 ATCGCCGACA AAGCCGCTAT GCGCTCACTG ATGTGGGCAG GCGGATTTCG
351 CTGCACCGTC GGGCTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 646; ORF 156>:

```

m156.pep
1  MTFAYWCILI ACLLPFLCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51 HAAQONGFEA FAPFAAAVLT AHATGNAAQS TINTLACLF LFRLAFIWCY
101 IADKAAMRSL MWAGGFACTV GLFVAAA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m156 / g156 96.1% identity in 127 aa overlap

```

              10      20      30      40      50      60
m156.pep      MTFAYWCILIACLLPFLCAAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQONGFEA
              |||||
g156           MTFAYWCILIACLLPFLCAAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQONGFEA
              10      20      30      40      50      60

              70      80      90      100     110     120
m156.pep      FAPFAAAVLTAAHATGNAAQSTINTLACLFILFRLAFIWCYIADKAAMRSLMWAGGFACTV
              |||||:|||||

```

449

```

g156      FAPFAAAVLTAHATGNAGQATVNTLAGLFI LFR LAFIWCYIADKAALRSLMWAGGFACTV
              70      80      90      100      110      120

m156.pep  GLFVAAAX
            |||||
g156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 647>:

```

a156.seq
  1  ATGACTTTTCG CCTATTGGTG TATTCTGATT GCCTACCTAT TGCCGCTTTT
 51  TTGTGCGGCG TATGCCAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101  ACAATCCGCG CGATTTTCTG GCGCGCACGC AAGGCACAGC CGCCCGTGCC
151  CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCAGCCGC
201  CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251  CGCTTGCCGG CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301  ATCGCAGACA AAGCAGCATT ACGCTCGCTG ATGTGGGTGG GCGGATTTGT
351  CTGCACCGTC GGGCTGTTT TCGTGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 648; ORF 156.a>:

```

a156.pep
  1  MTFAYWCILI AYLLPLFCAA YAKKAGGFRF KDNHNPRDFL ARTQGTAAARA
 51  HAAQONGFEA FAPFAAAVLTAHATGNAGQA TVNTLAGLFI LFR LAFIWCY
101  IADKAALRSL MWVGGFVCTV GLFVVAAX*

m156/a156  90.6% identity in 127 aa overlap

              10      20      30      40      50      60
m156.pep    MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAARAHAQONGFEA
            |||||
a156        MTFAYWCILIAYLLPLFCAAYAKKAGGFRFKDNHNPRDFLARTQGTAAARAHAQONGFEA
              10      20      30      40      50      60

              70      80      90      100     110     120
m156.pep    FAPFAAAVLTAHATGNAAQSTINTLACLFILFR LAFIWCYIADKAAMRSLMWAGGFACTV
            |||||
a156        FAPFAAAVLTAHATGNAGQATVNTLAGLFI LFR LAFIWCYIADKAALRSLMWVGGFVCTV
              70      80      90      100     110     120

m156.pep    GLFVAAAX
            |||||
a156        GLFVVAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 649>:

```

g157.seq
  1  atgaggaacg aggAAAAACg cgccctgcgc cgcgaaattgC gCgGgcggcg
 51  ttcgcAAATg GGgcgagacg tGCGgGCGC GCGGgCgatA Aaaatcaacc
101  gcctgctcaa aCGTtatatc AAGCGCggtc gGaAaatcgG CGTGTATTgg
151  cCGATGGGCA AGGAATTGcg TTTGGGCGgc tTgtcCGCG CGGCGCAAAA
201  ACGCgGCGCA AAactctatc tgccttATAT CGAACCGCAC ACGCGGCGGA
251  TGTGGTTTAC GCCGTATCCT GAACGCGGAA TGGAACGGGA ACGCAAGCGC
301  GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGGCGCA AAATCCGCGT
351  GCACGGTTTG TCGGTATTGC TCGTCCCCTG TGTCGGCATA GACCGCGAAG
401  GCTACCGTTT GGGGCAGGCA GGCGGCTATT ACGATGCGAC GCTTTCGGCG
451  ATGAAATACC GTTTGCAGGC GAAAACCGTG GGCGTGGGCT TTGCCTGCCA
501  GTTGGTGGAC AGGCTCCAC GCGAGGCGCA CGACCTGCCG CTGGACGGTT
551  TTGTATCGGA AGCGGGGATA TTGTGTTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 650; ORF 157.ng>:

```
g157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAAAI KINRLKRYI KRGRKIGVYW
 51 PMGKELRLGG FVRAAQKRG KLYLPYIEPH TRRMWFTYP ERGMRERKR
101 GRAKLHVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGAFACQLVD RLPREAHDL LDGFVSEAGI LCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 651>:

```
m157.seq
  1 ATGAGGAACG AGGAAAAACG CGCCCTGCGC CGCGAATTGC GCGGGCGGCG
 51 TTCGCAAATG GGGCGGGACG TCGGGGCGGC GGCAACGGTA AAAATCAACC
101 ACCTGCTCAA ACGTTATATT AAAAAAGGGC GGAAATCGG CGTGATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCG GAACTCTACC TGCCTTATAT CGAACCGCGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GCCGATGGAG TAAAAACAAGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGTCGGA AAAAGCGTGT
351 GCATGATTG AACCTCCTGC TTGTGCCAGT GGTCGGTATG GACAGGCTGG
401 GCTACCGCTT GGGACAGGCA GGCGGCTATT ACATGCGAC GCTTTCAGCG
451 ATGAAATACC GTTTCAGGCA AAAAACCCTG GCGGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTGCCGG TCGAGGCGCA CGACCGGTCT TTGACGGTT
551 TTGTGTCGGA GGCGGGGATA TTGTGTTTTT AG
```

This corresponds to the amino acid sequence <SEQ ID 652; ORF 157>:

```
m157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAATV KINHLLKRYI KKGRKIGVYW
 51 PMGKELRLDG FVRAAQKRG ELYLPYIEPR SRRMWFTYP ADGVKQERKR
101 GRAKLHVPQF AGRKKRVHDL NLLLVPPVGM DRLGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGAFACQLVD RLPVEAHDRS LDGFVSEAGI LCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m157 / g157 88.1% identity in 193 aa overlap

      10      20      30      40      50      60
m157.pep MRNEEKRALRRELGRRSQMGRDVRAAATVKINHLLKRYIKKGRKIGVYWPMGKELRLDG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g157      MRNEEKRALRRELGRRSQMGRDVRAAAAIKINRLKRYIKRGRKIGVYWPMGKELRLGG
      10      20      30      40      50      60

      70      80      90     100     110     120
m157.pep FVRAAQKRGAEKLYLPYIEPRSRMWFTYPADGVKQERKRGRAKLHVPQFAGRKKRVHDL
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g157      FVRAAQKRGAKLYLPYIEPHTRMWFTYPERGMERERKRGRAKLHVPQFAGRKIRVHGL
      70      80      90     100     110     120

      130     140     150     160     170     180
m157.pep NLLLVPPVGM DRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g157      SVLLVPLVGI DREGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPREAHDLP
      130     140     150     160     170     180

      190
m157.pep LDGFVSEAGILCFX
|||||:|||||
g157      LDGFVSEAGILCFX
      190
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 653>:

```
a157.seq
  1 ATGAGGAACG AGGAAAAACA CGCCTTGCGC CGAGAGTTGC GCCGCGCCCCG
 51 CGCGCAGATG GGCATCAAG GGCGGTTGGC GGCGGGGCAA ACGATTAAAC
```

451

```

101 GCCTGCTCAA ACGTTATATC AAGCGTGGTC GGAAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCA AAACCTTATC TGCCTTATAT CGAACCGCGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAAAGCGGAA TGGAACGGGA GCGCATACGG
301 GGCAGGGCGA AGTTGAACGT GCCGCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTGCGCATA GACCGCGAGG
401 GCTACCGCTT AGGACAGGCA GCGGCTATT ACGATGCGAC GCTTGCGGCG
451 ATGAAATACC GTTTGCAGGC AAAAACCGTG GCGGTGGGCT TTGCCTGCCA
501 GTTTGTGGAC AGGCTGCCGC GCGAACCGCA CGATCTGCTG CTGGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGCTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 654; ORF 157.a>:

a157.pep

```

1 MRNEEKHALR RELRRARAQM GHQGRLAAGQ TINRLLKRYI KRGRKIGVYW
51 PMGKELRLDG FVRAAQKRG A KLYLPYIEPR SRRMWFTYP ESGMERERIR
101 GRAKLNVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLAA
151 MKYRLQAKTV GVGFAQCFVD RLPREPHDLL LDGFVSEAGI LCF*

```

m157/a157 82.4% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALRRELRRRSQMGRDVR	AAATVKINHLLKRYIKKGRKIGVYW	PMGKELRLDG			
a157	MRNEEKHALRRELRRARAQM	GHQGRLAAGQTINRLLKRYIKRGRKIGVYW	PMGKELRLDG			
	10	20	30	40	50	60
	70	80	90	100	110	120
m157.pep	FVRAAQKRGAE	LYLPYIEPRSRMWFTYPADGVKQERK	GRAKLHVPQFAGRKKRVHDL			
a157	FVRAAQKRGAKLYLPYIEPRSRMWFTYP	PESGMERERIRGRAKLNVPQFAGR	KIRVHGL			
	70	80	90	100	110	120
	130	140	150	160	170	180
m157.pep	NLLLVFVVGMDRLGYRLGQAGGYDAT	LSAMKYRLQAKTVGVGFACQLVDRLPVEA	HDRS			
a157	SVLLVPLVGIDREGYRLGQAGGYDAT	LAAMKYRLQAKTVGVGFACQFVDRLPREPHDLL				
	130	140	150	160	170	180
	190					
m157.pep	LDGFVSEAGILCFX					
a157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 655>:

g158.seq

```

1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
51 CGGCAGCTTC AGCCGTGCGG CGgagcAGTT GGAGAtggCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGCGT GAAcCTGCTc
151 aACCGCACCA CGCGGCAACT CAATCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
251 TGCTGGCAGT GCACGAAGTA CCGCAAGGCG TGTTGCGCGT GGATTCCGCG
301 ATGCcgatgg TGCTGCATCT GCTGGCGCCG CTGGCAGCAA AATTCAACGA
351 ACGCTATCCG CATATCcgac TTTCGCTCGT TTCTTCCGAa ggctatatca
401 atctGattGA Acgcaaagtc gAtatTGCCT TACGGGCCGG AGAATTGGAC
451 GATTCCGGGC TGCGTGACG CCATCTGTTT GACAGCCACT TCCGCGtagt
501 cgCCAGTCCT GAATATTTAG CAAAACACGG CACGCCACAA TCTGCAGAAG
551 atcTTGCCAA CCATCAATGT TTAGGCTTCA CAGAACCCGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGAtgC GCAGGGAAAT CCCTATAAAA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAAGtt
701 gCGGTATTGC TTGCTTATCA GATTTTTTGG TTGACAACGA CATCACTGAA
751 GGAAAGTTAA TTCCcctatt cgCCGAACAA ACCTCCAATA AAACACACCC

```

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801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAACCTC CGCTTACGCG
 851 TATTTTTGGA TTTTATTAGT AAGGAACTGG GAAAAAATAT GAATAGAACG
 901 AATACCAAT AA

This corresponds to the amino acid sequence <SEQ ID 656; ORF 158.ng>:

g158.pep
 1 MKTNSEELTV FVQVVEGSGSF SRAAEQLEMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLNLT EEGAQYFERR QRILQEMAAA ETEMLAVHEV PQGVLRVDSA
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD
 151 DSGLRARHLF DSHFRVVASP EYLAKHGTPQ SAEDLANHQC LGFTEPGSLN
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSSCGIACLS DFLVDNDITE
 251 GKLIPLFAEQ TSNKTHPFNA VYYSKAVNL RLRVFLDFLV KELGKNMNR
 301 NTK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 657>:

m158.seq
 1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
 51 CGGCAGCTTC AGCCGTGCGG CGGAGCAGTT GGCGATGGCA AATTCTGCCG
 101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGTGT GAACCTGCTC
 151 AACCGCACCA CGCGGCAACT CAGTCTGACG GAAGAAGGCG CGCAATATTT
 201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGCGG GAAACCGAAA
 251 TGCTGGCAGT GCACGAAATA CCGCAAGGCG TGTGAGCGT GGATTCCGCG
 301 ATGCCGATGG TGCTGCATCT GCTGGCGCCG CTGGCAGCAA AATTCAACGA
 351 ACGCTATCCG CATATCCGAC TTTCTGCTCGT TTCTTCCGAA GGCTATATCA
 401 ATCTGATTGA ACGCAAAGTC GATATTGCCT TACGGGCCGG AGAATTGGAC
 451 GATTCCGGGC TCGGTGCACG CCATCTGTTT GACAGCCGCT TCCGCGTAAT
 501 CGCCAGTCCT GAATACCTGG CAAAACACGG CACGCCGCAA TCTACAGAAG
 551 AGCTTGCCGG CCACCAATGT TTAGGCTTCA CCGAACCCGG TTCTCTAAAT
 601 ACATGGGCGG TTTTAGATGC GCAGGAAAT CCCTATAAGA TTTACCCGCA
 651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAGSTT
 701 GCGGTATTGT TTGCTTATCA GATTTTTTGG TTGACAACGA CATCGCTGAA
 751 GGAAAGTTAA TTCCCCTGCT CGCCGAACAA ACCTCCGATA AAACACACCC
 801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAATCTC CGCTTACGCG
 851 TATTTTTGGA TTTTATTAGT GAGGAACTGG GAAACAATCT CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 658; ORF 158>:

m158.pep
 1 MKTNSEELTV FVQVVEGSGSF SRAAEQLAMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLSLT EEGAQYFERR QRILQEMAAA ETEMLAVHEI PQGVLSVDSA
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD
 151 DSGLRARHLF DSRFRVIASP EYLAKHGTPQ STEELAGHC LGFTEPGSLN
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSGCGIVCLS DFLVDNDIAE
 251 GKLIPLLAEQ TSDKTHPFNA VYYSKAVNL RLRVFLDFLV EELGNNLCG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m158 / g158 94.3% identity in 297 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVEGSGSF	SRAAEQLAMANS	AVSRIVKR	LEEKLGVNLL	NRTTRQLSLT	
g158	MKTNSEELTVFVQVVEGSGSF	SRAAEQLEMAN	AVSRIVKR	LEEKLGVNLL	NRTTRQLNLT	
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRRQRILQEMAAA	ETEMLA	VEI	PQGVLSVDS	SAMPMVLHLLAP	LAAKFNERYP
g158	EEGAQYFRRQRILQEMAAA	ETEMLA	VEVPQGVLRVDS	SAMPMVLHLLAP	LAAKFNERYP	
	70	80	90	100	110	120

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	130	140	150	160	170	180
m158.pep	HIRLSLVSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
	: : : : :					
g158	HIRLSLVSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSHFRVVASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
	: : : : : : : :					
g158	SAEDLANHQCLGFTEPGSLNTWAVLDAQNPYKISPHFTASSGEILRSLCLSSCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTS DKTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
	: : : : :					
g158	DFLVDNDITEGKLIPLFAEQTSNKNTHPFNAVYYSDKAVNLRRLRVFLDFLVKELGKNMNR					
	250	260	270	280	290	300
g158	NTKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 659>:

a158.seq

1	ATGAAAACCA	ATTCAGAAGA	ACTGACCGTA	TTTGTTC AAG	TGGTGGAAAG
51	CGGCAGCTTC	AGCCGTGCGG	CGGAGCAGTT	GGCGATGGCA	AATTCTGCCG
101	TAAGCCGCAT	CGTCAAACGG	CTGGAGGAAA	AGTTGGGTGT	GAACCTGCTC
151	AACCGCACCA	CGCGGCAACT	CAGTCTGACG	GAAGAAGGCG	CGCAATATTT
201	CCGCCGCGCG	CAGAGAATCC	TGCAAGAAAT	GGCAGCGGCG	GAAACCGAAA
251	TGCTGGCAGT	GCACGAAATA	CCGCAAGGCG	TGTTGCGCGT	GGATTCCGCG
301	ATGCCGATGG	TGCTGCATCT	GCTGGCGCCG	CTGGCAGCAA	AATTCAACGA
351	ACGCTATCCG	CATATCCGAC	TTTCGCTCGT	TTCTTCCGAA	GGCTATATCA
401	ATCTGATTGA	ACGCAAAGTC	GATATTGCCT	TACGGGCCGG	AGAATTGGAC
451	GATTCCGGGC	TGCGTGCACG	CCATCTGTTT	GACAGCCGCT	TCCGCGTAAT
501	CGCCAGTCCT	GAATACCTGG	CAAAACACGG	CACGCCGCAA	TCTACAGAAG
551	AGCTTGCCGG	CCACCAATGT	TTAGGCTTCA	CCGAACCCGG	TTCTCTAAAT
601	ACATGGGCGG	TTTTAGATGC	GCAGGGAAAT	CCCTATAAGA	TTTCACCGCA
651	CTTTACCGCC	AGCAGCGGTG	AAATCTTACG	CTCGTTGTGC	CTTTCAGGTT
701	GCGGTATTGC	TTGCTTATCA	GATTTTTTGG	TTGACAACGA	CATCGCTGAA
751	GGAAAGTTAA	TTCCCCTGCT	CGCCGAACAA	ACCTCCAATA	AAACGCACCC
801	CTTTAATGCT	GTTTATTACA	GCGATAAAGC	CGTCAACCTC	CGCTTACGCG
851	TATTTTTTGA	TTTTTTAGTG	GAGGAACCTG	GAAACAATCT	CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 660; ORF 158.a>:

a158.pep

1	MKTNSEELTV	FVQVVESGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL
51	NRTTRQLSLT	EEGAQYFRRA	QRILQEMAAA	ETEM LAVHEI	PQGVLRVDSA
101	MPMVLHLLAP	LAAKFNERYP	HIRLSLVSSE	GYINLIERKV	DIALRAGELD
151	DSGLRARHLF	DSRFRVIASP	EYLAKHGTPQ	STEELAGHQ	LGFTPEPGSLN
201	TWAVLDAQGN	PYKISPHFTA	SSGEILRSLC	LSGCGIACLS	DFLVDNDIAE
251	GKLIPLLAEQ	TSNKNTHPFNA	VYYSKAVNLR	RLRVFLDFLV	EELGNNLCG*

m158/a158 99.0% identity in 299 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVESGSFSRAAEQLAMANS AVSRIVKRLEEKLGVNLLNRTTRQLSLT					
	: : : : :					
a158	MKTNSEELTVFVQVVESGSFSRAAEQLAMANS AVSRIVKRLEEKLGVNLLNRTTRQLSLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRRAQRILQEMAAAE TEM LAVHEIPQGVLSVDSAMP MVLHLLAPLA AKFNERYP					
	: : : : :					
a158	EEGAQYFRRAQRILQEMAAAE TEM LAVHEIPQGVLRVDSAMP MVLHLLAPLA AKFNERYP					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m158.pep	HIRLSLSVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
a158	HIRLSLSVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
a158	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
a158	DFLVDNDIAEGKLIPLLAEQTSNKTTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 661>:

```

g160.seq
1  ATGGAcatc  tgGACAAact  ggtcgatCTC  GCccaATTGA  CGGGCAGTGC
51  GGATGTGCAG  TgcctTTTGG  GCGGACAATG  gcATGaaacc  TTGCAACGCG
101 AAGGGCTGGT  ACACATTGTT  ACGGCGGGCA  GCGGTATCT  CTGCATCGAC
151 GCGGAACTT  CCCCgcGTCC  GGTcGGCACG  GGCGATATTG  TATTTTCCC
201 GCGCGGCTTG  GGTcATGTGT  TGAGCCACGA  CGGAAAATAC  GGAGAAAGTT
251 TACAACCGGA  CATACGACAA  AACGGCACAT  TTATGGTCAA  ACAGTGCggc
301 AACGGGCTGG  ATATGAGCCT  GTTTGCGCC  CGTTCCGCT  ACGACACCCA
351 CGCCGATTG  ATGAACGGGC  TGCCGAAAC  CGTTTTCTG  AACATTGCCC
401 ATCCAAGTTT  GCAGTATGTG  GTTCAATGC  TGCAACTGGA  AAGCGAAAAA
451 CCTTTGACGG  GGACGGTTTC  CGTGGTCAAC  GCATTACCGT  CCGTCCTGCT
501 GGTGCTTATC  CTGCGCGCCT  ATCTCGAACA  GGATAAGGAT  GTCGAACCTT
551 CGGGCGTATT  GAAAGGTTGG  CAGGACAAAC  GTTTGGGACA  TTTGATCCAA
601 AAGGTGATAG  ACAAAACCGGA  AGACGAATGG  AATATTGACA  AAATGGTTGC
651 CGCCGCCAAT  ATGTcGCGCG  CGCAACTGAT  GCGCCGCTTC  AAAAGCCAAG
701 TCGGACTCAG  CCCGcACGCC  TTTGTGAACC  ATATCCGCCT  GCAAAAAGGC
751 GCATTGCTGC  TGAAGAAAC  CCCGATTTCG  GTTTTGAGG  TCGCGCTGTC
801 GGTGGGCTTT  CAGTCGGAAC  CGCATTTCCG  CAAGCGTTC  AAACGGCAAT
851 ATCACGTTTC  GCCGGGGCAA  TACCGGAAAG  AAGGCGGGCA  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 662; ORF 160.ng>:

```

g160.pep
1  MDILDKLVDL  AQLTGSADVQ  CLLGGQWHET  LQREGLVHIV  TAGSGYLCID
51  GETSPRPVGT  GDIVFFPRGL  GHVLSHDGKY  GESLQPDIRQ  NGTFMVKQCG
101 NGLDMSLFCA  RFRYDTHADL  MNGLPETVFL  NIAHPSLQYV  VSMLQLESEK
151 PLTGTVSVVN  ALPSVLLVLI  LRAYLEQDKD  VELSGVLKGW  QDKRLGHLIQ
201 KVIDKPEDEW  NIDKMVAEAN  MSRAQLMRRF  KSQVGLSPHA  FVNHIRLQKG
251 ALLLKKTPTS  VLEVALSVGF  QSETHFGKAF  KRQYHVSPGQ  YRKEGGQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 663>:

```

m160.seq
1  ATGGACATTC  TGGACAAACT  GGTCGATTTC  GCCCAATTGA  CGGGCAGTGT
51  GGATGTGCAG  TGCCTTTTGG  GCGGACAATG  GTCGGTACGG  CATGAAACCT
101 TGCAACGCGA  AGGATTGGTA  CACATTGTTA  CATCGGCAG  CGGCTATCTC
151 TGCATCGACG  GCGAACTTC  CCCGCGTCCG  GTCAGTACAG  GGGATATTGT
201 ATTTTCCCG  CGCGGCTTGG  GTCATGTGTT  GAGCCACGAC  GGAAAATGCG
251 GAGAAAGTTT  ACAACCGGAT  ATGCGGCAGC  ACGGTGCGTT  TACGGTCAAG
301 CAGTGCGGCA  ACGGACAGGA  TATGAGCCTG  TTTTGCGCCC  GTTTCCGCTA
351 CGACACCCAC  GCCGATTGTA  TGAACGGGCT  GCCTGAAACC  GTTTTTCTGA
401 ACATTGCCCA  TCCGAGTTTA  CAGTATGTGG  TTTCAATGCT  GCAACTGGAA
451 AGCAAAAAAC  CTTTGACGGG  GACGGTTTCC  ATGGTCAACG  CATTGTGCTC

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501 CGTCCTGCTG GTGCTTATCC TGC GCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTCGCGCGC GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CCGACTCAGC CCGCAGGCCT TTGTGAACCA TATCCGCCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTGTCCGGT
801 CGCACTGTCG GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAAGA AggCGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 664; ORF 160>:

```

m160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
  51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
 101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
 151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
 201 LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
 251 QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
 301 K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m160 / g160 93.4% identity in 301 aa overlap

```

          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYLCIDGETSPRP
          |||||:|||||:||||| |||||:|||||:|||||
g160      MDILDKLV DLAQLTGSADVQCLLGGQW---HETLQREGLV HIVTAGSGYLCIDGETSPRP
          10      20      30      40      50

          70      80      90      100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          |:|||||:|||||:|||||:|||||:|||||:|||||
g160      VGTGDIVFFP RGLGHVLSHD GKYGESLQPD IRQNGTFMVKQCGNGLDMSL FCARFRYDTH
          60      70      80      90      100     110

          130     140     150     160     170     180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTVS MVNALSSVLL VLILRAYLEQ
          |||||:|||||:|||||:|||||:|||||:|||||
g160      ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SEKPLTGTVS VVNALPSVLL VLILRAYLEQ
          120     130     140     150     160     170

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          |||||:|||||:|||||:|||||:|||||:|||||
g160      DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNI DKMVA AANMSRAQLM RRFKSQVGLS
          180     190     200     210     220     230

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          |||||:|||||:|||||:|||||:|||||:|||||
g160      PHAFVNHIRL QKGALLLKN PDSVLEVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          240     250     260     270     280     290

m160.pep KX
          ||
g160      KX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 665>:

```

a160.seq
  1 ATGGACATTC TGGACAAACT GGTGATTTC GCCCAATTGA CGGGCAGTGT
 51 GGATGTGCAG TGCCTTTTGG GCGGACAATG GTCGGTACGG CATGAAACCT

```

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```

101 TGCAACGCGA AGGATTGGTA CACATTGTTA CATCGGGCAG CGGCTATCTC
151 TGCATCGACG GCGAACTTC CCCGCGTCCG GTCAGTACAG GGGATATTGT
201 ATTTTTCCTG CGCGGCTTGG GTCATGTGTT GAGCCACGAC GGAAAATGCG
251 GAGAAAGTTT ACAACCGGAT ATGCGGCAGC ACGGTGCGTT TACGGTCAAG
301 CAGTGCGGCA ACGGACAGGA TATGAGCCTG TTTTGCGCCC GTTTCGGCTA
351 CGACACCCAC GCCGATTGTA TGAACGGGCT GCCTGAAACC GTTTTCTGA
401 ACATTGCCCA TCCGAGTTTA CAGTATGTGG TTTCAATGCT GCAACTGGAA
451 AGCAAAAAAC CTTTGACGGG GACGGTTTCC ATGGTCAACG CATTGTCTGC
501 CGTCCTGCTG GTGCTTATCC TCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTGCGCGCG GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCCTG
751 CAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTTGTCTGGT
801 CGCACTGTCG GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAAGA AGGCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 666; ORF 160.a>:

```

a160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
 51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*

```

m160/a160 100.0% identity in 301 aa overlap

```

          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          |||||
a160      MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          10      20      30      40      50      60

          70      80      90     100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQMSL FCARFRYDTH
          |||||
a160      VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQMSL FCARFRYDTH
          70      80      90     100     110     120

          130     140     150     160     170     180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLES KKPLTGTV SMVNALSSVLL VLILRAYLEQ
          |||||
a160      ADLMNGLPET VFLNIAHPSL QYVVSMLQLES KKPLTGTV SMVNALSSVLL VLILRAYLEQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          |||||
a160      DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          190     200     210     220     230     240

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLLKKNP DSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          |||||
a160      PHAFVNHIRL QKGALLLKKNP DSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          250     260     270     280     290     300

m160.pep KX
          ||
a160      KX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 667>:

```

g161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTCACCGTTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTACGC TCGGTGCTGC CGCCGTATTG CGGCGCGACA CCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGAC AACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTttg GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCCG TTTACACGCA GGCGGTGCTG CTCCTTGGTT
401 TTGCCGCGCT GGTATTGCTG CTTAATCCCT CGTTCCGCAG CGGTCAAGAA
451 CCGGCGGCAC TCGCCGGGCT GGCGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGCAACC GGCGTGCGCA TGTCGTCggt ttgggcgacg
601 Ctgaccggct ggCACAcccT GTCCTTTcca tcggcagttt ATCtgtCGGG
651 CATCGGCGTG tccgcgCtgA TTGCCCAaCT GtcgatgAcg cGCGcctaca
701 aaGTCGGCGA CAAATTCACG GTTGCCTCGC tttcctaTAt gaccgtcGTC
751 TTTTCCGCCC TGTCTGCCGC ATTTTTTCTg ggcgaagagc ttttctggCA
801 GGAAATACTC GGTATGTGCA TCATTATcct CAGCGGCATT TTGAGCAGCA
851 TCCGCCCCAT TGCCTTCAAA CAGCGGCTGC AAGCCCTCTT CCGCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 668; ORF 161.ng>:

```

g161.pep
1  MDTAKKDILG SGWMLVAAAC FTVMNVLIKE ASAKFALGSG ELVFWRMLFS
51  TVTLGAAAVL RRDTFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLTTGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVVLL LNPSFRSGQE
151 PAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSAT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTV
251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPIAFK QRLQALFRQR
301 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 669>:

```

m161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTTACCATT A TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA mCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGGC CACTGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTG GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCCG TTTACACGCA GGCGGTGCTG CTCCTTGGTT
401 TTGCCGCGCT GGTATTGCTG CTTAATCCCT CGTTCCGCAG CGGTCAAGAA
451 ACGGCGGCAC TCGCCGGGCT GGCGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTCGTCGGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTCGTG
651 CATCGGCGTG TCCGCGCTGA TTGCCCAACT GTCGATGACG CGCGCTACA
701 AAGTCGGCGA CAAATTCACG GTTGCCTCGC TTTCTATAT GACCGTCGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTTTCTG GGCGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA
851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 670; ORF 161>:

```

m161.pep
1  MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMLFS
51  TVALGAAAVL RDXFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVVLL LNPSFRSGQE

```

```

151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
301 *

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m161 / g161 97.0% identity in 300 aa overlap

```

              10      20      30      40      50      60
m161.pep    MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRM LFSTVALGAAAVL
              |||||:|||||:|||||:|||||:|||||:|||||
g161        MDTAKKDILGSGWMLVAAACFTVMNVLIKEASAKFALGSGELVFWRM LFSTVTLGAAAVL
              10      20      30      40      50      60

              70      80      90     100     110     120
m161.pep    RRDXFRTPHWKNHLNRSMTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE
              |||||:|||||:|||||:|||||:|||||:|||||
g161        RRDTFRTPHWKNHLNRSMTGAMLLLFYAVTHLPLTTGVTLSTSSIFLAVFSFLILKE
              70      80      90     100     110     120

              130     140     150     160     170     180
m161.pep    RISVYTQAVLLLG FAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVREL SLAGEPG
              |||||:|||||:|||||:|||||:|||||:|||||
g161        RISVYTQAVLLLG FAGVLLLNPSFRSGQEP AALAGLAGGAMSGWAYLKVREL SLAGEPG
              130     140     150     160     170     180

              190     200     210     220     230     240
m161.pep    WRVVFYLSVTGVAMSSVWATLTGWHTLSFP SAVYLSGIGVSALIAQLSMTRAYKVGDKFT
              |||||:|||||:|||||:|||||:|||||:|||||
g161        WRVVFYLSATGVAMSSVWATLTGWHTLSFP SAVYLSGIGVSALIAQLSMTRAYKVGDKFT
              190     200     210     220     230     240

              250     260     270     280     290     300
m161.pep    VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR
              |||||:|||||:|||||:|||||:|||||:|||||
g161        VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPIAFKQRLQALFRQR
              250     260     270     280     290     300

m161.pep    X
              |
g161        X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 671>:

```

a161.seq
1   ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GCGGCCTGC TTTACCATTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTC A
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA CCTTCCGCAC
201 GCGCCATTGG AAAAACCACT TAAACCGCAG TATGGTCGGG ACGGGGCGCA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGGC CACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTG GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCCG TTACACGCA GCGGTGCTG CTCCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTTCGCGAG CGGTCAGGAA
451 ACGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCGGCG TGCGCGCTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTATCGGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTCGTG
651 CATCGGCGTG TCCGCGCTGA TTGCCAACT GTCGATGACG CGCGCCTACA
701 AAGTCGGCGA CAAATTCACG GTTGCCTCGC TTCTCTATAT GACCGTCGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTTTCTG GCCGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA

```

459

851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

This corresponds to the amino acid sequence <SEQ ID 672; ORF 161.a>:

a161.pep
1 MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMLES
51 TVALGAAAVL RRDTFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVLL LNPSFRSGQE
151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSCIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL AEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
301 *

m161/a161 99.3% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMLFSTVALGAAAVL					
a161	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMLFSTVALGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
a161	RRDTFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGFGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
a161	RISVYTQAVLLLGFGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSAVYLSCIGVSALIAQLSMTRAYKVGDKFT					
a161	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSAVYLSCIGVSALIAQLSMTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
a161	VASLSYMTVVFSALSAAFFLAEEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	250	260	270	280	290	300
m161.pep	X					
	I					
a161	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 673>:

g163.seq
1 ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTTGG TGGTATTGGT
51 TTAAACCGTG CCGGATCAGG TGCAGATGTG gctCGACCGG GCAAAAGAAG
101 TCATTTTTAC CGAGTTCAGC TGGTTTATG TTTTAACGTT TTCCATTTt
151 ctgGGTTTTc tgctGATACT CTCGGTCAGC GGTTTGGGAA ACATcagGCT
201 AGGACGGGAT GAAGATGTGC CGGAATTCGG CTCCTGTCTG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCGTGGGCC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGTCGGCG CGCCGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCGTTCACG
401 CCTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCCGGTTT

```

451 CGCTACAAAC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCGG
651 CGTGCAGGTC TTGATTATCG CCGCCGTAAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGCCTGAAGG TGTTGAGCGA GTTGAACCTG
751 GGCCCTTGGT TTTTGCTGCT GTTTTTTGTT TTGGCGGCGG ACCCCACTGT
801 TTACCTGTTG TCGGCATTCT GCGACAACAT AGGGAACCTAC CTCGGAATC
851 TGGTGCGCCT CAGTTTGAAG ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGgc
951 gcCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGg cgcaccatCc
1001 gcgagtttgt CTTGCGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAAACG CTGCTTTTAA
1151 AATTCCTTAA TTACCTCCCC CTGCCCGAAC TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CCCTGTTTTT TGTAACCTCT GCCGACTCCG GGATTATATG
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGTTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGatgtcTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTTCAGCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTCAACCC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCGGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CACCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GGCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACTG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 674; ORF 163.ng>:

g163.pep

```

1  MVILTLFFV CVLVVLVLTV PDQVQMWLDR AKEVIFTEFS WFYVLTFESIF
51  LGFLLILSVS GLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TVGAPEHRQQ QALLHTVFWH GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFGVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLEFFV LAADPTVYLL SAFGDNIGNY LGNLVRLSLK TYAYEREHKP
301 WFSWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGLV
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITSRDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVRIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 675>:

m163.seq

```

1  ATGGTTATTT TGACGACTTT GTTTTTTGTTG TGTGTTTTGG TGGTATTGGT
51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTTAC CGAGTTCAGC TGGTTTTATG TTTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT
201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTCTG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCCTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGCCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCGTTCACG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCCGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCAG

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651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GCGGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTTTGTT TTGGCGGCGG GACCCACTGT
801 TTACCTGTTG TCGGCATTCTG GCGACAACAT AGGGAACCTAC CTCGGAAATC
851 TGGTGCGCCT CAGTTTTAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTGTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTGCGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGCT
1451 TGAGTGGCGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGAGGAG CAGGATATTT TAAAATTCCT CAAACAGACT GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AAATGTTTCA TCGGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTGCGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 676; ORF 163>:

```

m163.pep
1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFSIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFWH GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFWSTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGWKER LVQIMSQTQE QDILKFLKQT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHRDE PAIEFVIRKE TMRDFMYGIK SVQDQVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQDEL
651 MAHEQVELAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m163 / g163 98.6% identity in 660 aa overlap

```

          10          20          30          40          50          60
m163.pep  MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFWYVLTFSIFLGFLILSVS
          |||
g163      MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFWYVLTFSIFLGFLILSVS
          10          20          30          40          50          60

          70          80          90          100         110         120
m163.pep  SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ
          :|||
g163      GLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITVGAPEHRQQ
          70          80          90          100         110         120

          130         140         150         160         170         180

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m163.pep	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
g163	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
	130 140 150 160 170 180
m163.pep	190 200 210 220 230 240
	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
g163	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFGVQVLIIAAVMSLAVVSAISGVGK
	190 200 210 220 230 240
m163.pep	250 260 270 280 290 300
	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
g163	GVKVLSELNLGLAFLLLFFVLAADPTVYLLSAFGDNIGNYLGNLVRLSLKTYAYEREHKP
	250 260 270 280 290 300
m163.pep	310 320 330 340 350 360
	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
g163	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
	310 320 330 340 350 360
m163.pep	370 380 390 400 410 420
	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
g163	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
	370 380 390 400 410 420
m163.pep	430 440 450 460 470 480
	ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
g163	ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
	430 440 450 460 470 480
m163.pep	490 500 510 520 530 540
	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEODILKFLKQTASPAMHELQR
g163	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVRIMSQTQEODILKFLKHTASPAMHELQR
	490 500 510 520 530 540
m163.pep	550 560 570 580 590 600
	ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
g163	ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
	550 560 570 580 590 600
m163.pep	610 620 630 640 650 660
	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
g163	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
	610 620 630 640 650 660
m163.pep	X
g163	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 677>:

```

a163.seq
1  ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTGG TGGTATTGGT
51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTAC  CGAGTTCAGC TGTTTTATG  TTTAACGTT  TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT

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201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GCGGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGC GTTCACG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTACC CCTGTGTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATAGGCTGG ATTGCCGAAA ACAGCTTCAG
651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGTGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGTCTTGGT TTTTGCTGCT GTTTTTTGTT TTGGCGGCGG GTCCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACACT CTCGGAATC
851 TGGTGCCTC CAGTTTTAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTGTG GGTGTGTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTGCGGGTT TTGCTCATCC CCGGCTGTT CGGCGTTTTC
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAGTG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCGG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTGAGCCTG TGAAAGGAT
1451 TGAGTCCGGA TAAGAAATAT TTTGAGACCC GGGTTAACC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTACAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAAGTG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 678; ORF 163.a>:

a163.pep

```

1 MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFESIF
51 LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQO QALLHTVFWH GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEIW IAENSFSVQV LIIAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGLV
351 WFTVFGNTAI WLNDGVAGGV LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQGEL
651 MAHEQVELAE *

```

m163/a163 99.4% identity in 660 aa overlap

```

10 20 30 40 50 60
m163.pep MVILTTLFFVCVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFESIF LGFLLILSVS
|||||
a163 MVILTTLFFVCVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFESIF LGFLLILSVS
10 20 30 40 50 60

70 80 90 100 110 120
m163.pep SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA EPLMHYFSDI TAGTPEHRQO

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|||||
a163      SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ
              70      80      90      100     110     120

              130     140     150     160     170     180
m163.pep  QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEISGRFGDAIDI
|||||
a163      QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEISGRFGDAIDI
              130     140     150     160     170     180

              190     200     210     220     230     240
m163.pep  MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAMSLAVVSAISGVGK
|||||
a163      MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAMSLAVVSAISGVGK
              190     200     210     220     230     240

              250     260     270     280     290     300
m163.pep  GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
|||||
a163      GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
              250     260     270     280     290     300

              310     320     330     340     350     360
m163.pep  WFESWTVLYWAWWCSWAPFVGLFIARISKGRITREFVFGVLLIPGLFGVLWFTVFGNTAI
|||||
a163      WFESWTVLYWAWWCSWAPFVGLFIARISKGRITREFVFGVLLIPGLFGVLWFTVFGNTAI
              310     320     330     340     350     360

              370     380     390     400     410     420
m163.pep  WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
|||||
a163      WLNDGVAGGVLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
              370     380     390     400     410     420

              430     440     450     460     470     480
m163.pep  ITS RDKGLSAPRWQAVMWGVLM SAVAVLLMRSGGLGNLQSM TLIVSLP FALLMLIMCFSL
|||||
a163      ITS RDKGLSAPRWQAVMWGVLM SAVAVLLMRSGGLGNLQSM TLIVSLP FALLMLIMCFSL
              430     440     450     460     470     480

              490     500     510     520     530     540
m163.pep  WKGLSADKKYFETR VNPTS VFWTGGKWKERLVQIM SQTQE QDILKFLKQTAS PAMHELQR
|||||
a163      WKGLSADKKYFETR VNPTS VFWTGGKWKERLVQIM SQTQE QDILKFLKHTAS PAMHELQR
              490     500     510     520     530     540

              550     560     570     580     590     600
m163.pep  ELSEEYGLSVRV DKMFHRDEPAIEFVIRKETMRDFMYGIK SVGQDVSDQLINDGKLPHIR
|||||
a163      ELSEEYGLSVRV DKMFHQDEPAIEFVIRKETMRDFMYGIK SVGQDVSDQLINDGKLPHIR
              550     560     570     580     590     600

              610     620     630     640     650     660
m163.pep  HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLM LDDVQGELMAHEQVELAE
|||||
a163      HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLM LDDVQGELMAHEQVELAE
              610     620     630     640     650     660

m163.pep  X
          |
a163      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 679>:

```

g164.seq (partial)
1  ..ATGAACACAT TTTTGAAAAA CAGCGAATAC GCGTATATCC TGAACGACTG
51  CAAGGCGCGC TTCCTGTTTCG CCTCGGCCGG CCTGTCAAAA GAATTGGCGG
101 GCCTGAAGGC GCAAACGCCG GTCGAAAAAA TCATTTGGAC GGACAAAAGC
151 CGGCCGCGCG GCGAAACGGC GGAAGGCGAT GCCTTTTTTG AAAACGTGCG
201 CCGCTTCCCC GAAAAACCCG ACTTGGGCCG CCAACCCCGG ATAAATGATT
251 TGGCACACAT CATCTACACC TCCGGCACGA CGGGGCATCC CAAAGGCGCG
301 CTAATCAGTT ACGCCAACCT GTTCGCCAAC CTGAACGGCA TCGAACGCAT
351 CTTtaaAATT TCCAAACGCG ACCGCTTTAT CGTTTTcctg ccgatgTTCC
401 ACAGCTTCAC GCTGACGGCT ATGGTGCTGC TGCCGATTTA TATGGCGTGT
451 TCGATTATTT TGGTCAAAtc cgttttCCCC ttttccaacG TTTTGAAACA
501 GGCCCTGCTC AAACGCGCAA CCGTGTTTTT GGGCGTACCC GCGATTTACA
551 CCGCGATGAG CAAGGCAAAA ATCCCTTGGT ATTTAGATG GTTCAACCGC
601 ATCCGCCTGT TTATCAGCGG CGGCGCGCCT TTGGCGGAAC AAACCATCCT
651 CGATTTTAAA GCCAAGTTCC CCCGCGCCAA ATTGCTGGAA GGCTACGGAC
701 TGAGCGAAGC CTCGCCCGTC GTCGCCGTCA ATACGCCCGA ACGGCAAAAA
751 GCCCGCAGCG TCGGCATCCC CCTGCCCGGT TTGGAAGCCA AAGCCGTCGA
801 TGAAGAATTG GTCGAAGTGC CGCGCGCGCA AGTGGGCGAA CTGATCGTCA
851 GGGCGGTTT GGTGATGCGG GGCTACCTCA ATATGCCTGC CGCACCGAT
901 GAAACCATCG TCAACGGCTG GTTGAAAACG GGCGATTTTC TTACCATAGA
951 CGAGGACGGC TTTATCTTTA TCGTCGACCG CAAAAAGAT TTGATTATTT
1001 CCAAAGGTCA AAACGTCTAT CCGCGCGAGA TCGAAGAAGA AATCCACAAA
1051 CTCGATGCCG TCGAAGCCGC CGCGTCATC GCGTGAAAG ACCGTTATGC
1101 CGACGAGGAA ATCGTCGCCT TCGTCCAATT GAAGGAAGGT ATGGATTTGG
1151 GCGAGGACGA aatccgccgc caccTGCCTA CCGTGCTGGC AAATTTCAAA
1201 ATCCCCAAAC AGATCCACTT TAAAGACGGG CTGCCGCGCA ACGCTACGGG
1251 CAAAGTATTG AAACGGGTGC TGAAGGAGCA GTTTGAAGGA AACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 680; ORF 164.ng>:

```

g164.pep (partial)
1  ..MNTFLKNSEY AYILNDCKAR FLFASAGLSK ELAGLKAQTP VEKIIWTDKS
51  RPAGETAEGD AFFENVRRFP EKPDLRQPR INDLAHIIT SGTTHGPKGA
101 LISYANLFAN LNGIERIFKI SKRDRFIVFL PMFHSFTLTA MVLLPIYMAC
151 SIILVKSVPF FSNVLKQALL KRATVFLGVP AIYTAMSKAK IPWYFRWFNR
201 IRLFISGGAP LAEQTILDFK AKFPRAKLE GYGLSEASPV VAVNTPERQK
251 ARSVDIPLPG LEAKAVDEEL VEVPRGEVE LIVRGGSVMR GYLNMPEATD
301 ETIVNGWLKT GDFVTIDEDG FIFIVDRKRD LIISKQONVY PREIEEIIHK
351 LDAVEAAAVI GVKDRYADEE IVAFVQLKEG MDLGEDEIRR HLRTVLANFK
401 IPKQIHFKDG LPRNATGKVL KRVLKEQFEG NK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 681>:

```

m164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTCGCCG CCGCCTGCCG
51  CAAAAACGGA AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAG GCCGAAGCCG TCGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCAC
201 AGAATTTAT ACCGCTATT TCGCCATCTC CGCCATCGGC GCGTTCGCCG
251 TACCGATGAA CACATTTTTG AAAAAACAGC AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351 GGCGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAAATCATT TGACCGGACA
401 AAAGCCGTCC GACCGGCGAA ACGGCGGAAG GCGATGCCTT TTTTGAAGAC
451 GTGCGCCGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGATATAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCCAAG
551 GCGCGCTAAT CAGTTACGCC AACCTGTTTC CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATTTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTTCGAT TATTTTGGTC AAATCCGTTT TTCCGTTTTT CAACGTTTTC
751 AAACAGACAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TACCCGCGAT
801 TTACACCGCG ATGAGCAAGG CGAAAATCCC TTGGTATTTT AGATGGTTCA
851 ACCGCATTCG CCTGTTTATC AGCGGCGGCG CGCCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGAAGGCTA

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466

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951 CGGACTGAGC GAAGCCTCTC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGG AGCCAAAGCC
1051 GTCGATGAAG AATTGGTCTG AGTGCCGCGC GCGGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TGCGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAAATG TCTATCCGCG CGAGATTGAA GAAGAAATCT
1301 ACAAACCTCGA TGCCGTCGAA GCCGCCGCCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 682; ORF 164>:

```

m164.pep
1  MNRTYANFYE MLAAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAISAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTDKSRPTGE TAEGDAFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPKGALISYA NLFANLNGIE
201 RIFKISK RDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNV L
251 KQTLK RATV FLGVP AIYTA MSKAKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEAKA
351 VDEELVEVPR GEVGELIVRG GSVMRGYLMN PAATDETIVN GWLKTGDFVT
401 IDEDGFI FIV DRKKDLISK QONVYPREIE EEIYKLD AVE AAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHLRTV LANFKIPKQI HFKDGLPRNA
501 TGKVLKRVLK EQFDGNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* m164 / g164 98.6% identity in 432 aa overlap

```

m164.pep      60      70      80      90      100      110
GDTVALAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSK
g164          10      20      30
MNTFLKNSEYAYILNDCKARFLFASAGLSK

m164.pep      120      130      140      150      160      170
ELAGLKAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPD LGRQPRINDLAHIIYT
g164          40      50      60      70      80      90
ELAGLKAQTPVEKIIWTDKSRPAGETAEGDAFFENVRRFPEKPD LGRQPRINDLAHIIYT

m164.pep      180      190      200      210      220      230
SGTTGHPKGALISYANL FANLNGIERIFKISK RDRFIVFLPMFHSFTLTAMVLLPIYMAC
g164          100      110      120      130      140      150
SGTTGHPKGALISYANL FANLNGIERIFKISK RDRFIVFLPMFHSFTLTAMVLLPIYMAC

m164.pep      240      250      260      270      280      290
SIILVKSVPF PFSNV LKQTLK RATV FLGVP AIYTA MSKAKIPWYFRWFNRIRLFI SGGAP
g164          160      170      180      190      200      210
SIILVKSVPF PFSNV LKQALLK RATV FLGVP AIYTA MSKAKIPWYFRWFNRIRLFI SGGAP

m164.pep      300      310      320      330      340      350
LAEQTILDFKAKFPRAK LLEGYGLSEASPVVAVNT PERQKARSVG IPLPGLEAKAVDEEL
g164          220      230      240      250      260      270
LAEQTILDFKAKFPRAK LLEGYGLSEASPVVAVNT PERQKARSVG IPLPGLEAKAVDEEL

m164.pep      360      370      380      390      400      410

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```

m164.pep    VEVPRGEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
            |||||
g164        VEVPRGEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
            280      290      300      310      320      330

            420      430      440      450      460      470
m164.pep    LIISKGQNVYPREIEEEIYKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRR
            |||||:|||||
g164        LIISKGQNVYPREIEEEIHKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGEDEIRR
            340      350      360      370      380      390

            480      490      500      510
m164.pep    HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX
            |||||
g164        HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFEGNKX
            400      410      420      430

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 683>:

```

a164.seq
1   ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTGACCG CCGCCTGCCG
51  CAAAAACGGC AACGGCACGG CAGTGTTCTGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAA GCCGAAGCCG TTGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 GGAATTTATT ACCGCCTATT TCGCCGTATC CGCCATCGGC GCGGTTGCCG
251 TACCGATGAA CACATTTTGT AAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGCCTGT CAAAAGAATT
351 GGCGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAAATCATT TGGACGGGCC
401 AAAGCCGTCC GGACGGCGAA ATGGCGGAAG GCGATGCCTT TTTTGAGAC
451 GTGCGCCGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGGATAAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GTCGGCTAAT CAGCTACGCC AACCTGTTCG CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATCTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTCGAT TATTTTGGTC AAATCCGTTT TCCCCTTTTC CAACGTTTGT
751 AAACAGGCAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TGCCCGCGAT
801 TTACACCGCG ATGAGCAAGA CGAAAATCCC TTGGTATTTT AGATGGTTCA
851 ACCGCATCCG CCTGTTTATC AGCGGCGGAG CACCTTTGGC GGAACAAACC
901 ATCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGGAAAGGCTA
951 CGGACTGAGC GAAGCCTCGC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAACCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGA AGTCAAAGCC
1051 GTCGATGAAG AATTGGTCTGA AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TGCGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAATG TCTATCCGCG CGAAATCGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCCGCGCCCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 684; ORF 164.a>:

```

a164.pep
1   MNRTYANFYE MLTAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAVSAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTGQSRPDGE MAEGDAFFED
151 VRRFPEKFDL GRQPRINDLA HIIYTS GTTG HPGKALISYA NLFANLNGIE
201 RIFKISKRDR FIVFLPMFHS FTLTAMVLLP IYMACSIIIV KSVFPFSNVL
251 KQALLKRATV FLGVPAIYTA MSKTKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEVKA
351 VDEELVEVPR GEVGELIVRG GSVMRGYLMN PAATDETIVN GWLKTGDFVT
401 IDEDGFIFIV DRKKDLISK QONVYPREIE EEIYKLDAVE AAAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHLRTV LANFKIPKQI HFKDGLPRNA

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468

501 TGKVLKRVLK EQFDGNK*

m164/a164 98.3% identity in 517 aa overlap

m164.pep	10	20	30	40	50	60
	MNRTYANFYEMLAACRKNNGTAVFDGKEKTAYRALKQAEAEVAAYLQNIQVKGFGDTVA					
a164	MNRTYANFYEMLAACRKNNGTAVFDGKEKTAYRALKQAEAEVAAYLQNIQVKGFGDTVA					
	10	20	30	40	50	60
m164.pep	70	80	90	100	110	120
	LAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
a164	LAVSNSTEFITAYFAVSAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
	70	80	90	100	110	120
m164.pep	130	140	150	160	170	180
	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDGRQPRINDLAHIIYTSGETTG					
a164	KAQTPVEKIIWTDKSRPDGEMAEGDAFFEDVRRFPEKPDGRQPRINDLAHIIYTSGETTG					
	130	140	150	160	170	180
m164.pep	190	200	210	220	230	240
	HPKGALISYANLFANLNGIERIFKISKDRFIVFLPMFHSFTLTAMVLLPIYMACSIILV					
a164	HPKGALISYANLFANLNGIERIFKISKDRFIVFLPMFHSFTLTAMVLLPIYMACSIILV					
	190	200	210	220	230	240
m164.pep	250	260	270	280	290	300
	KSVFPFSNVLKQTLKLRATVFLGVPAYITAMSKAKIPWYFRWFNRIRLFISGGAPLAEQT					
a164	KSVFPFSNVLKQALLKLRATVFLGVPAYITAMSKTKIPWYFRWFNRIRLFISGGAPLAEQT					
	250	260	270	280	290	300
m164.pep	310	320	330	340	350	360
	ILDFKAKFPRAKLLEGYGLSEASPVAVNTPERQKARSVGIPLPGLEAKAVDEELVEVPR					
a164	ILDFKAKFPRAKLLEGYGLSEASPVAVNTPERQKARSVGIPLPGLEVAVDEELVEVPR					
	310	320	330	340	350	360
m164.pep	370	380	390	400	410	420
	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFVDRKKDLIISK					
a164	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFVDRKKDLIISK					
	370	380	390	400	410	420
m164.pep	430	440	450	460	470	480
	GQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
a164	GQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
	430	440	450	460	470	480
m164.pep	490	500	510			
	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					
a164	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 685>:

g165.seq
 1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC


```

51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAagat gTGGCGTTGG AATCGTCAAA cGCGTGGAAC
151 AACGcCGgca CGGGGCATTC CGcGCTGTGc GAATTGAACT AtgcgccGCT
201 GGGtgccggac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctgGTCGC GGAAGGCAAG
301 TTGGAagaCA ATTCCTTCAT CAATGCcgtg ccgcatatGT Ctttggtgat
351 gAacgaagac cactgCCgtt acCTGCAAAA ACGCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtccgCTGAT TATGCGCGGC CGGgacgaaA ACCAACCCGT
501 CGCCGCCAAC TATTCCGCCG Aaggcacgga tgtcgATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCAGATTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCGCA ACCCAGACTG GCAGCTCACC CTCCGCACCC
701 GCTTCTCTT CCTCGGCGCG GCGGCGGCG CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GGCGCGCCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTCG GTCCTTACGC
951 AGGTTTCCGT TCCAAC TTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CcTGCTGGgC gAaTTGCgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 686; ORF 165.ng>:

```

g165.pep
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD VFKTQKLFEN MEFSTDRNKI
151 SDWAPLIMRG RDENQPVAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GLPVSGLFER NSNPETAEOH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFPGYAGER SNFLKQGSFM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 687>:

```

m165.seq (partial)
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGCA CGGGGCATTC CGCGCTGTG GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGgTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCAGATTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCGCA ACCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCTCTT CCTCGGCGCG GCGGCGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GGCGCGCCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTCG GCCCTTACGC
951 AGGCTTCCGT TCCAAC TTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAA...

```

This corresponds to the amino acid sequence <SEQ ID 688; ORF 165>:

```

m165.pep (partial)
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLIMRG RDENQPVAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF

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470

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201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAEQH NAKVYQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSML DLPLSIHMDN LYPMLCAGWA
351 NMPLTK...

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m165 / g165 97.2% identity in 356 aa overlap

```

              10      20      30      40      50      60
m165.pep    MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC
              |||||||
g165        MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC
              10      20      30      40      50      60

              70      80      90     100     110     120
m165.pep    ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED
              |||||:|:|:|
g165        ELNYAPLGADGVINPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED
              70      80      90     100     110     120

              130     140     150     160     170     180
m165.pep    HCSYLQKRYDAFKTQKLFENMEFSTDNRNKISDWAPLMRGRDENQPVAANYSAEGTDVDF
              || |||||:|
g165        HCRYLQKRYDVFKTQKLFENMEFSTDNRNKISDWAPLIMRGRDENQPVAANYSAEGTDVDF
              130     140     150     160     170     180

              190     200     210     220     230     240
m165.pep    GRLTRQMVKYLQGGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
              |||||||
g165        GRLTRQMVKYLQGGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDWQLTLRTRFLFLGA
              190     200     210     220     230     240

              250     260     270     280     290     300
m165.pep    GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNKAVYQASVGAPPMSPVPHL
              |||||||
g165        GGGALTLLQKSGIPEGKGYGGLPVSGLFFRNSNPETAEQHNKAVYQASVGAPPMSPVPHL
              250     260     270     280     290     300

              310     320     330     340     350
m165.pep    DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMLDLPLSIHMDNLYPMLCAGWANMPLTK
              |||||||
g165        DTRNVDGKRHLMFPGPYAGFRSNFLKQGSFMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
              310     320     330     340     350     360

g165        ELRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 689>:

```

a165.seq
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAT GGGATTATCG ATCCGCGCGC CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAAACT TTTTAAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGCGA AGGCGGTAAA AACCGAGTTC

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601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGGCCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCATTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATA CTGCTGGGC GAATTGCGTA AAACCAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGGCA AACCCGACG
1151 ACTGGGAACT CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGTT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCCGAAA GGGCGGATGA AATTATCGCC TATACGCGA
1451 AAGTGTGGA TATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 690; ORF 165.a>:

```

a165.pep
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDENQPVAA YSAEGTDVDF GRLTRQMVKY LQGKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFFVSGLFFR NSNPETAQH NAKVYGQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGS LMPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA QORVQIIKGD
401 SEKGGLVQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFFERT
451 PSWEGRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

m165/a165 99.7% identity in 356 aa overlap

```

              10      20      30      40      50      60
m165.pep    MAEATDVVLVGGGIMSATLG VLLKELEPSWEITLIERLEDVALESSNAWN NAGTGHSALC
              |||
a165         MAEATDVVLVGGGIMSATLG VLLKELEPSWEITLIERLEDVALESSNAWN NAGTGHSALC
              10      20      30      40      50      60

              70      80      90     100     110     120
m165.pep    ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED
              |||
a165         ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED
              70      80      90     100     110     120

              130     140     150     160     170     180
m165.pep    HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAAANYSAEGTDVDF
              |||
a165         HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAAANYSAEGTDVDF
              130     140     150     160     170     180

              190     200     210     220     230     240
m165.pep    GRLTRQMVKYLQGGKGVKTEFNRHVEDIKRES DGAWVLKTADTRNPDGQLT LRTRFLFLGA
              |||
a165         GRLTRQMVKYLQGGKGVKTEFNRHVEDIKRES DGAWVLKTADTRNPDGQLT LRTRFLFLGA
              190     200     210     220     230     240

              250     260     270     280     290     300
m165.pep    GGGALTLLQKSGIPEGKGYGGFFVSGLFFRNSNPETAQHNAKVYGQASVGAPPMSVPHL
              |||
a165         GGGALTLLQKSGIPEGKGYGGFFVSGLFFRNSNPETAQHNAKVYGQASVGAPPMSVPHL
              250     260     270     280     290     300

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	310	320	330	340	350
m165.pep	DTRNVDGKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTK				
a165	DTRNVDGKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG				
	310	320	330	340	350
					360
a165	ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS				
	370	380	390	400	410
					420

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 691>:

g165-1.seq

```

1  ATGGCTGAAG  CGACAGACGT  TGTCTTGGTG  GCGGCGGGCA  TTATGAGCGC
51  GACTTTGGGC  GTTTTGCTCA  AAGAACTCGA  ACCGTCTTGG  GAAATCACCC
101 TGATTGAACG  CTTGGAagat  gTGGCGTTGG  AATCGTCAAA  cGCGTGGAAC
151 AACGcCGgca  CGGGGCATTC  CGcGCTGTGc  GAATTGAACT  AtgcgcgGCT
201 GGGtgcgagac  ggcgtcatCA  ATCCGGCGCg  cgCCTGAAT  ATTGCCGAAC
251 AGTTTCATGT  CAGCCGCCAG  TTTTGGGcga  cgctggTCGC  GGAAGGCAAG
301 TTGGAAGACA  ATTCCTTCAT  CAATGCCGTG  CCGCATATGT  CTTTGGTGAT
351 GAACGAAGAC  CACTGCCGTT  ACCTGCAAAA  ACGCTATGAT  GTGTTAAAA
401 CGCAGAAACT  TTTTGAAAAT  ATGGAATTTT  CCACCGATCG  GAACAAAATT
451 TCCGATTGGG  CtcgcGTGAT  TATGCGCGGC  CGGGACGAAA  ACCAACCCGT
501 CGCCGCCAAC  TATTCGCCCG  AAGGCACGGA  TGTCGATTTC  GGACGGCTGA
551 CGCGCCAGAT  GGTGAAATAT  TTGCAGGGCA  AGGGCGTAAA  AACCAGATTTC
601 AACC GCCACG  TCGAAGACAT  CAAACGCGAA  TCCGACGGCG  CGTGGGTGCT
651 CAAAACCGCC  GATACCCGCA  ACCCAGACTG  GCAGCTCACC  CTCGCGACCC
701 GCTTCTCTTT  CCTCGGCGCG  GCGGCGGGCG  CACTGACCCT  GCTGCAAAAA
751 TCCGGCATCC  CCGAAGGCAA  AGGCTACGGC  GGCTTACCCG  TGTCCGGCCT
801 GTTCTTCCGC  AACAGCAACC  CCGAAACCGC  CGAACAACAC  AACGCCAAAG
851 TGTACGGGCA  GGCTTCCGTC  GGCGCGCCGC  CGATGTCCGT  CCCGCACCTC
901 GACACACGCA  ACGTAGACGG  CAAACGACAC  CTTATGTTTC  GTCCTTACGC
951 AGGTTTCCGT  TCCAACCTCC  TCAAGCAAGG  CTCGTTTATG  GATTTGCCGC
1001 TGTCCATCCA  TATGGACAAC  CTCTATCCTA  TGCTGCGCGC  CGGCTGGGCG
1051 AATATGCCCG  TGACCAATA  CCTGCTGGGC  GAATTGCGTA  AAACCAAGA
1101 AGAATGCTtt  gCCTCCCTGC  TGgaatacta  cccGaggcag  acccGACGAc
1151 tgg tactcat  cagcgagcnc  acGCGTcata  tcattanata  tgactCgaaa
1201 ctgcgcgtgc  tgcagttgta  cgagattgtg  ccaCGCGacg  ctcgctcgcg
1251 cattctggag  cgtcgcggcg  catcacgctn  tgcgctgata  tccgctgatg
1301 acactgctcc  gaGCGcgccc  gtcttggaat  gtgtctga

```

This corresponds to the amino acid sequence <SEQ ID 692; ORF 165-1.ng>:

g165-1.pep

```

1  MAEATDVVLV  GGGIMSATLG  VLLKELEPSW  EITLIERLED  VALESSNAWN
51  NAGTGHSALE  ELNYAPLGAD  GVINPARALN  IAEQFHVSRO  FWATLVAEGK
101 LEDNSFINAV  PHMSLMVNED  HCRYLQKRYD  VFKTQKLFEN  MEFSTDRNKI
151 SDWAPLIMRG  RDENQPVAAN  YSAEGTDVDF  GRLTRQVMKY  LQKGKVKTEF
201 NRHVEDIKRE  SDGAWVLKTA  DTRNPDWQLT  LRTRFLFLGA  GGGALTLLQK
251 SGIPEKGKYG  GLPVSGLFFR  NSNPETAEOH  NAKVYGOASV  GAPPMSPVPHL
301 DTRNVDGKRH  LMFPGPYAGFR  SNFLKQGSFM  DLPLSIHMDN  LYPMLRAGWA
351 NMPLTKYLLG  ELRKTKEERF  ASLLEYYPQ  TRRLVLITQX  TRHIIXYDSK
401 LRVLQLYEIV  PRDARSRILE  RRGASRXALI  SADDTAPSAP  VLESV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 693>:

m165-1.seq

```

1  ATGGCTGAAG  CGACAGACGT  TGTCTTGGTG  GCGGCGGGCA  TTATGAGCGC
51  GACTTTGGGC  GTTTTGCTCA  AAGAACTCGA  ACCGTCTTGG  GAAATCACCC
101 TGATTGAACG  CTTGGAAGAT  GTGGCGTTGG  AATCGTCAAA  CGCGTGGAAC
151 AACGCCGCA  CGGGGCATTC  CGCGCTGTGC  GAATTGAACT  ATGCGCCGTT
201 GGGTGCAAA  GGGATTATCG  ATCCGGCGCG  CGCCCTCAAT  ATTGCCGAAC
251 AGTTTCATGT  CAGCCGCCAG  TTTTGGGCGA  CGCTGGTCGC  GGAAGGCAAG
301 TTGGAAGACA  ATTCCTTCAT  CAATGCCGTG  CCGCATATGT  CTTTGGTGAT
351 GAATGAAGAC  CATTGTCTTT  ATCTTCAAAA  ACGTTATGAC  GCGTTTAAAA
401 CCCAAAAACT  TTTTGAAAAT  ATGGAATTTT  CCACCGATCG  GAACAAAATT
451 TCCGATTGGG  CTCCGCTGAT  GATGCGCGGC  CGGGACGAAA  ACCAACCCGT
501 CGCCGCCAAC  TACTCCGCCG  AAGGTACGGA  TGTCGATTTC  GGACGGCTGA
551 CGCGCCAAAT  GGTGAAATAT  TTGCAGGGCA  AGGGCGTAAA  AACCAGATTTC
601 AACC GCCACG  TCGAAGACAT  CAAACGCGAA  TCCGACGGCG  CGTGGGTGCT
651 CAAAACCGCC  GATACCCGCA  ACCCGACGCG  GCAGCTCACC  CTCGCTACCC
701 GCTTCTCTTT  CCTCGGCGCG  GCGGCGGGCG  CGCTGACCCT  GCTGCAAAAA
751 TCCGGCATCC  CCGAAGGCAA  AGGCTACGGC  GGCTTCCCG  TGTCCGGCCT
801 GTTCTTCCGC  AACAGCAACC  CCGAAACCGC  CGAACAACAC  AACGCCAAAG

```

```

851 TGTACGGGCA GGCTTCCGTC GGCGCGCCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGCTTATG GATTTGCCCG
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGGCA AACCCGACG
1151 ACTGGGAACT CATCACCGCA GGGCAACGCG TCCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGCGTGCT CCAGTTGGT ACGGAGATTG TCGCCACGC
1251 CGACGGCTCA CTCGCCGCAT TGCTGGGCGC GTCGCCGGC GCATCGACCG
1301 CTGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAGCGCGCC
1351 CCGTCTTGGG AAGACCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCTGAAA GGGCGGATGA AATTATCGCC TATACCGCA
1451 AAGTATTGGA TATTAA

```

This corresponds to the amino acid sequence <SEQ ID 694; ORF 165-1>:

m165-1.pep

```

1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAQH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFPGPYAGFR SNFLKQGSML DLPLSIHMDN LYPMLCAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKID
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERA
451 PSWEDRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

m165-1/g165-1 89.7% identity in 428 aa overlap

m165-1.pep	10	20	30	40	50	60
g165-1	10	20	30	40	50	60
m165-1.pep	70	80	90	100	110	120
g165-1	70	80	90	100	110	120
m165-1.pep	130	140	150	160	170	180
g165-1	130	140	150	160	170	180
m165-1.pep	190	200	210	220	230	240
g165-1	190	200	210	220	230	240
m165-1.pep	250	260	270	280	290	300
g165-1	250	260	270	280	290	300
m165-1.pep	310	320	330	340	350	360
g165-1	310	320	330	340	350	360
m165-1.pep	370	380	390	400	410	420
g165-1	370	380	390	400	410	420
	430	440	450	460	470	480

m165-1.pep LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNENPERADEIIA
:
g165-1 ILERRGASRXALISADDTAPSAPVLESVX
420 430 440

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 695>:

a165-1.seq
1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51 GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGAAC
151 AACGCCGCA CGGGGCATTG CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTCTCT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAAAT TTTTGAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCAGGTTT
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGCGCGCGC CGCTGACCTT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCACTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGGCA AACCCTGACG
1151 ACTGGGAACT CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAG GCGGCGTGTT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCCGAAA GGGCGGATGA AATTATCGCC TATACCGCA
1451 AAGTGTGGA TATTTAA

This corresponds to the amino acid sequence <SEQ ID 696; ORF 165-1.a>:

a165-1.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRO FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLLTRQVMKY LQKGKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAEOH NAKVYQASV GAPPMSVPHL
301 DTRNVGDKRH LMFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPLMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLEYYPEA NPDDWELITA GQRVQIIKKD
401 SEKGVVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

a165-1/m165-1 99.4% identity in 488 aa overlap

	10	20	30	40	50	60
a165-1.pep	MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
m165-1	MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
	10	20	30	40	50	60
	70	80	90	100	110	120
a165-1.pep	ELNYAPLGANGIIDPARALNIAEQFHVSROFWATLVAEGKLEDNSFINAVPHMSLVMNED					
m165-1	ELNYAPLGANGIIDPARALNIAEQFHVSROFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
	130	140	150	160	170	180
a165-1.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAAANYSAEGTDVDF					
m165-1	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAAANYSAEGTDVDF					
	130	140	150	160	170	180
	190	200	210	220	230	240

```

a165-1.pep  GRLTRQMVKYLGKGKGVKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
m165-1      GRLTRQMVKYLGKGKGVKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
              190      200      210      220      230      240

              250      260      270      280      290      300
a165-1.pep  GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYQASVGAPPMSVPHL
m165-1      GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYQASVGAPPMSVPHL
              250      260      270      280      290      300

              310      320      330      340      350      360
a165-1.pep  DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
m165-1      DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG
              310      320      330      340      350      360

              370      380      390      400      410      420
a165-1.pep  ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
m165-1      ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
              370      380      390      400      410      420

              430      440      450      460      470      480
a165-1.pep  LAALLGASPGASTAVPLMIRLMHQCFPERTPSWEGRLKELVPGYGIKLNENPERADEIIA
m165-1      LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNENPERADEIIA
              430      440      450      460      470      480

              489
a165-1.pep  YTAKVLDIX
m165-1      YTAKVLDIX

```

a165-1/p33940

sp|P33940|YOJH_ECOLI HYPOTHETICAL 60.2 KD PROTEIN IN ECO-ALKB INTERGENIC REGION
>gi|1736851|gnl|PID|d1016718 (D90850) ORF_ID:o372#5; similar to [SwissProt Accession Number P33940] [Escherichia coli] >gi|1788539 (AE000310) f548; This 548 aa ORF is 100 pct identical to 490 residues of YOJH_ECOLI SW: P33940 (492 aa) but contains 56 additional N-ter aa; 100 pct identical to GB: ECOHU49_33
ACCESSION: U00008 (490 aa) but contains 58 additional N-term resi... Length = 548
Score = 458 bits (1167), Expect = e-128
Identities = 233/490 (47%), Positives = 303/490 (61%), Gaps = 5/490 (1%)

```

Query: 3  EATDVVLVGGGIMSATLGVLKLEEPSWEITLIERLEDVALESSNAWNNAGTGHSALCEL 62
+ TDV+L+GGGIMSATLG L+ELEP W +T++ERLE VA ESSN WNNAGTGHSAL EL
Sbjct: 30  QETDVLIGGGIMSATLGTYLRELEPEWSMTMVERLEGVAQESSNGWNNAGTGHSALMEL 89

Query: 63  NYAPLGGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLED-NSFINAVPHMSLVMNEDH 121
NY P A+G I +A+ I E F +SRQFWA V G L SFIN VPHMS V ED+
Sbjct: 90  NYTPQNADGSISIEKAVAINAEAFQISRQFWAHQVERGVLRTPRSFINTVPHMSFVWGEDN 149

Query: 122 CSYLQKRYDAFKTQKLFENMEFSTDNRKISDWAPLMMRGRDENQPVAAANYSAEGTDVDFG 181
++L+ RY A + LF M +S D +I +WAPL+M GRD Q VAA + GTDV++G
Sbjct: 150 VNFLRARYAALQQSSSLFRGMRYSEDHAQIKEWAPLVMEGRDPQKVAATRTEIGTDVNYG 209

Query: 182 RLTRQMVKYLGKGKGVKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTXXXXXXXXXX 240
+TRQ++ LQ K + + V +KR D W + AD +N Q
Sbjct: 210 EITRQLIASLQKKSNSFLQSLSEVRALKRNDNTWTVTVADLKNGTAG-NIRAKFVFIGA 268

Query: 241 XXXXXXXXQKSGIPEGKGYGGFPVSGLFFRNSNPETAEQHNAKVYQASVGAPPMSVPHL 300
Q+SGIPE K Y GFPV G F + NP+ H AKVYG+ASVGAPPMSVPH+
Sbjct: 269 GGAALKLLQESGIPEAKDYAGFPVGGQFLVSENPDVVNHHLAKVYGKASVGAPPMSVPHI 328

Query: 301 DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG 360
DTR +DGKR ++FGP+A F + FLK GSL DL S N+ PM+ G N L KYL+
Sbjct: 329 DTRVLDGKRVLFGPFATFSTKFLKNGSLWDLMSSTTSNVMPMMHVGLDNFDLVKYLVS 388

Query: 361 ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVXXXXXX 420
++ ++E+RF +L EYYP+A +DW L AGQRVQIIK+D+EKGGVL+ GTE+V
Sbjct: 389 QVMLSEEDRFELKEYYPQAKKEDWRLWQAGQRVQIIKRDAEKGGVLRRLGTEVVSDDQGT 448

Query: 421 XXXXXXXXXXXXXXXVPLMIRLMHQCFPER--TPSWEGRLKELVPGYGIKLNENPERADEI 478

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476

P+M+ L+ + F +R +P W+ LK +VP YG KLN + +
 Sbjct: 449 IAALLGASPGASTAAPIMLNLEKVFGRVSSPQWQATLKAIVPSYGRKLNGDVAATERE 508
 Query: 479 IAYTAKVLDI 488
 + YT++VL +
 Sbjct: 509 LQYTSEVLGL 518

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 697>:

g204.seq
 1 atggcggcgg cggaaataaa acgccccctc gctgtcgatt tccagcacat
 51 agcgtccgtt ctgcacggcg gcatagccgc ttttgccctgc ctgataggg
 101 tgcaggcgcg aatgcgaaat caggtaatca gtcagtttgc cgccgtcttc
 151 ggcgatattg cccaccagtt tggcaaaaca ggtatggcac acgccgtttt
 201 ccgcccagcc cgaaggcgcg tcctttccgt cggtttccat acatttgccg
 251 acgacggctt ccaagtcgtt gggatgctt ccggtcagcc ggacggcggt
 301 ttggtccggc aagcctttaa tcggataact gatttgtttt ttgccgtcgt
 351 tggttttgcc ttcgctactt tgtcccaaag ccaaaccggc aatcgccgta
 401 ttgtcgatgt atttgacttt gaaaaccggg ttcggcgcg cttgtgccc
 451 attttgcggc tgttcgcccg tattttcggg tttgcccag gcggcaagca
 501 gcaggcagcc gcccaacacg gcaaaaggta ttttcagcat tccgcactcc
 551 tgatggtttc aaaatgccgt ctgaaatgcc gtctgaaacg tggcaggcg
 601 aggttcggac ggcattgggt ttatttcaac gggcggatgc cgaccgcac
 651 gcgtacttta tccaacaatt cgcgcgcttc tttgcgcgct ttttgcgcgc
 701 ctgcctgcaa aatctcttcg atttgcgaag gattagaggt caatgcgttg
 751 tag

This corresponds to the amino acid sequence <SEQ ID 698; ORF 204.ng>:

g204.pep
 1 MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVISQFAAVF
 51 GDIAHQFGKQ GMAHAVFRPA RRRVLSVGFH TFADDGFQVV GMLSGQPDGV
 101 LFRQAFNRIT DLFFAVVGFA FATLSQSQTG NRRIVDVDFD ENRFRRALCR
 151 ILRLFRRIFG FAAGGKQQA AOHGKRYFOH SALLMVSKCR LKRLKRGRR
 201 RFGRHVVYFN GRMPTASRTL SNNRASLRA FCAPACKISS ICEGLEVNAL
 251 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 699>:

m204.seq
 1 ATGGCGGCGG CGGAAATAAA ACGCCCCTTC GCTGTGCGATT TCCAGCACAT
 51 AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCCTGC CTGATAGGGT
 101 TGCAGGGCGG CATGCGAAAC TAGGTAATCC GTCAGTTTGC CGCCGTCTTC
 151 GGCATATTG CCCACCAGTT TGGCAAACAA GGTATGGCAC ACGCCGTTTT
 201 CTGCCCCAACC TGCCGGACTG TCCTTATCAT CGGTTTCCAT ACATTGTCGG
 251 CTGACGGCTT CCAAGTCGCC GGGATGCTTG CCGATCAGTC GGATAACATT
 301 TTGTTCCGGC AAGCCTTTAA TCGGATAACT GATTTGTTTT TTGCCGTCTG
 351 TGGTTTTGCC TTCGCTGCTT TGTCCCAAAT CCAAACCGGC AATCGCCGTA
 401 TTGTCGATAT ATATGACTTT GAAAACCGGT TTCGGCGCGC TTTGTACCGC
 451 GTTTTGCGGC TGTACCGCCG TATTTwCGGA TTTGCCGCaC GGCaArGCAG
 501 CAGGCAGCGG CCAATACGG CAAAaArAwGT wTTCAGCATT CCACaYTCCT
 551 GATGGTTTCA AAATGCCGTC TGAAACGCGG CAGGCGGAGG TTCGGACGGC
 601 ATCGGGTTCA TTTCAACGGG CGGATGcCGA CCGCATCgGT ACTTTGTCCA
 651 ATAATTCGCG TGCTTCTTTA CGCGCTTTTC CCGCGCCTGC CTGCAAAATC
 701 TCTTCGATTT GCGAAGGGTC GGCGGTCAGC TCGTTGTAG

This corresponds to the amino acid sequence <SEQ ID 700; ORF 204>:

m204.pep
 1 MAAAEIKRPF AVDFQHIASV LHGGIAAFAC LIGLQGGMRN *VIRQFAAVF
 51 GDIAHQFGKQ GMAHAVFCPT CRTVLIIGFH TFAADGFQVA GMLADQSDNI
 101 LFRQAFNRIT DLFFAVVGFA FAALSQIQTG NRRIVDIYDF ENRFRRALYR
 151 VLRLYRRIxG FAATAXQQA AYGKXXXQH STXLMVSKCR LKRGRRRFGR
 201 HRVHFNGRMP TASGTLNNS RASLRAFAAP ACKISSICEG SAVSSL*

Computer analysis of this amino acid sequence gave the following results:

m204/g204

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 701>:

This corresponds to the amino acid sequence <SEQ ID 702; ORF 204.a>:

a204.pep

1	MAAAEIKRPL	AVDFQHIASV	<u>LHGGIAAFAC</u>	<u>LIGLQGGMRN</u>	QVIRQFAAVF
51	GDIAHQFGKQ	GMAHAVCRPA	RRRALSFGFH	TFADDGFQVV	GMLAQGPDDV
101	LFRQAF....
151KRFRGR
201	HWVYFNGRIP	TASRTLPNNS	RASLRAFCAP	ACKISSICEG	SAVSSL*

m204/a204 54.5% identity in 246 aa overlap

	10	20	30	40	50	60
m204.pep	MAAAEIKRPFVDFQHIASVLHGGIAAFACLIQLQGGMNRNXVIRQFAAVFGDIAHQFGKQ					
a204	MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIQLQGGMNRNQVIRQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204.pep	GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
a204	GMAHAVCRPARRRALSVGFHTFADDGFQVVGMLAGQPDVLFQAF-----					
	70	80	90	100		
	130	140	150	160	170	180
m204.pep	FAALSQIQTNRRIVDIYDFENRFRRALYRVLRLYRRIXGFAATAXQQAAYGKXXXQH					
a204	-----					
	190	200	210	220	230	240
m204.pep	STXLMVSKCRLKGRRRFGRHRVHFNGRMPTASGTLNNSRASLRAFAAPACKISSICEG					
a204	-----KRFGRHWVYFNGRIPTASRTLPNNSRASLRAFCAPACKISSICEG					
	110	120	130	140	150	
m204.pep	SAVSSLX					
a204	SAVSSLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 703>:

```

g205.seq
1  atgctgaaaa taccttttgc cgtgttgggc ggctgcctgc tgcctgccgc
51  ctgcgcaaaa tccgaaaaata cggcggaaca gccgcaaaat gcggcacaaa
101 gcgcgccgaa accggttttc aaagtcaaat acatcgacaa tacggcgatt
151 gccggttgg ctttgggaca aagtagcgaa ggcaaaacca acgacggcaa
201 aaaacaaatc agttatccga ttaaaggctt gccggaacaa aacgccgtcc
251 ggctgaccgg aaagcatccc aacgacttgg aagccgtcgt cggcaaatgt
301 atggaaaccg acggaaagga cgcgccttcg ggctgggagg aaaacggcgt
351 gtgccatacc ttgtttgcca aactggtggg caatatcgcc gaagacggcg
401 gcaaaactgac tgattacctg atttcgcatt ccgccctgca accctatcag
451 gcaggcaaaa gcggtatgac cgccgtgcag aacggacgct atgtgctgga
501 aatcgacagc gagggggcgt tttatttccg ccgccgcat tattga

```

This corresponds to the amino acid sequence <SEQ ID 704; ORF 205.ng>:

```

g205.pep
1  MLKIPFAVLG GCLLLAACGK SENTAEQPQN AAQSAPKPVF KVKYIDNTAI
51  AGLALGQSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGDAPS GWAENGVCHT LFAKLVGNI A EDGKLT DYL ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFFRRRH Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 705>:

```

m205.seq
1  ATGCTGAaW A CwTyTTTTGC CGTATTGGGC GGCTGCCTGC TGCyTtGCCG
51  tGCGGCAaAT CCGwAAATAC GGCGGTACAG CCGCAAAACG CCGTACAAAG
101 CGCGCCGAAA CCGGTTTTCA AAGTCATATA TATCGACAAT ACGGCGATTG
151 CCGGTTTTGA TTTGGGACAA AGCAGCGAAG GCAAAACCAA CGACGGCAAA
201 AAACAAATCA GTTATCCGAT TAAAGGCTTG CCGGAACAAA ATGTTATCCG
251 ACTGATCGGC AAGCATCCCG GCGACTTGGA AGCCGTCAGC GGCAAAATGTA
301 TGGAaACCGA TGATAAGGAC AGTCCGGCAG GTTGGGCAGA AAACGGCGTG
351 TGCCATACCT TGTTTGCCAA ACTGGTGGGC AATATCGCCG AAGACGGCGG
401 CAAACTGACG GATTACCTAG TTTCGCATGC CGCCCTGCAA CCTATCAGG
451 CAGGCAAAAG CGGCTATGCC GCCGTGCAGA ACGGACGCTA TGTGCTGGAA
501 ATCGACAGCG AAGGGGCGTT TTATTTCGC CGCCGCCATT ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 706; ORF 205>:

```
m205.pep
  1  MLXTXFAVLG GCLLXCRCGK SXNTAVQPQN AVQSAPKPVF KVIYIDNTAI
 51  AGLDLGQSSE GKTNDGKKQI SYPIKGLPEQ NVIRLIGKHP GDLEAVSGKC
101  METDDKDSPA GWAENGVCHT LFAKLVGNIA EDGGKLTDLV VSHAALQPYQ
151  AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 205 shows 88.4% identity over a 181 aa overlap with a predicted ORF (ORF 205.ng) from *N. gonorrhoeae*:

```
m205/g205

      10      20      30      40      50      60
m205.pep  MLXTXFAVLGGCLLXCRCGKSXNTAVQPQNNAVQSAPKPVFKVIYIDNTAAGLDLGQSSE
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g205       MLKIPFAVLGGCLLLAACGKSENTAEQPQNAASAPKPVFKVKYIDNTAAGLALGQSSE
          10      20      30      40      50      60

      70      80      90     100     110     120
m205.pep  GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDSPAAGWAENGVCHT
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g205       GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT
          70      80      90     100     110     120

      130     140     150     160     170     180
m205.pep  LFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g205       LFAKLVGNIAEDGGKLTDLVISHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
          130     140     150     160     170     180

m205.pep  YX
          |
g205      Y
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 707>:

```
a205.seq (partial)
  1  TCCGAACCTC TTAAAGGCTT GCCGGAACAA AACGTCGTCC GGCTGACCGG
 51  CAAGCATCCC AACGACTTGG AAGCCGTCGT CGGCAAATGT ATGGAAACCG
101  ACGGAAAGGG CGCGCCTTCG GGCTGGGCGG CAAACGGCGT GTGCCATACC
151  TTGTTTGCCA AACTGGTGGG CAATATCGCC GAAGACGGCG GCAAACCTGAC
201  GGATTACCTG ATTCGCATT CCGCCCTGCA ACCCTATCAG GCAGGCAAAA
251  GCGGCTATGC CGCCGTGCAG AACGGACGCT ATGTGCTGGA AATCGACAGC
301  GAGGGGGCGT TTTATTTCCG CCGCCGCCAT TATTGA
```

This corresponds to the amino acid sequence <SEQ ID 708; ORF 205.a>:

```
a205.pep (partial)
  1  SEPLKGLPEQ NVVRLTGKHP NDLEAVVGKC METDGKGAPS GWAANGVCHT
 51  LFAKLVGNIA EDGGKLTDLV ISHSALQPYQ AGKSGYAAVQ NGRYVLEIDS
101  EGAFYFRRRH Y*
```

m205/a205 88.3% identity in 111 aa overlap

```
      50      60      70      80      90     100
m205.pep  KVIYIDNTAAGLDLGQSSEGKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKC
          | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
a205       SEPLKGLPEQNVVRLTGKHPNDLEAVVGKC
          10      20      30

      110     120     130     140     150     160
m205.pep  METDDKDSPAAGWAENGVCHTLFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQ
```

```

a205      ||||| | : : ||| ||||| ||||| ||||| ||||| ||||| ||||| : : ||| ||||| ||||| |||||
          METDGKGAPSGWAANGVCHTLFAKLVGNIADGGKLT DYLI SHSALQPYQAGKSGYAAVQ
              40          50          60          70          80          90

m205.pep      170      180
              NGRYVLEIDSEGAFYFRRRHYX
a205          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
              NGRYVLEIDSEGAFYFRRRHYX
              100      110

```

1	ATGCTGAAAA	TAcCTTTTGC	CGTGTGGGCG	GGCTGCCTGC	TGCTTGCCGC
51	CTGCGGCAAA	TCCGAAAAAT	CGCGGCAACA	CGCGCAAAAT	CGCGGCAAAA
101	GCGCGCGCAA	ACCGGTTTTC	AAAGTCAAA	ACATCGACAA	TACGGCGATT
151	CGCGGTTTGG	CTTTGGGACA	AAGTAGCGAA	GGCAAAACCA	ACGACGGCAA
201	AAAACAAATC	AGTTATCCGA	TTAAAGGCTT	GCGGCAACAA	AACGCCGTTC
251	GGTGACCCG	AAAGCATCCC	AACGACTTTG	AAGCCGTCGT	CGGCAAAATG
301	ATGGAACAAC	ACGGAAGAAG	CGCGCCTTCG	GGCTGGGCGG	AAACCGCGCT
351	GTGCCATACC	TTGTTTGCCA	AACTGGTGGG	CAATATCGCC	GAAGACGGCG
401	GCAAACTGAC	TGATTACCTG	ATTTGCGATT	CCGCCCTGCA	ACCTATCAG
451	GCAAGCAAA	GCGGCTATGC	CGCCGTGCAG	AACGGACGCT	ATGTGCTGGA
501	AATCGACAG	GAGGGGCGGT	TTTA		

1	<u>MLKIPFVAVLC</u>	<u>GCLLLAACGK</u>	SENTAEQPQN	AAQSAPKPVF	KVKYIDNTAI
51	AGLALQGSSE	GKTNDGKKQI	SYPIKGLPEQ	NAVRLTGKHP	NDLEAVVGKC
101	METDGDAPDS	GWAENGVCHT	LFALKLVGNIA	EDGGKLT DYL	ISHSALQPYQ
151	AKSGSYAAVQ	NGRYVLEIDS	EGAF		

1	ATGCTGAAAA	CATCTTTTGC	CGTATTGGGC	GGCTGCCTGC	TGTTTGC CGC
51	CTGCGCGCAA	TCCGAAAAAT	CGCGCGAACA	CGCGCAAAAC	CGCGGTACAAA
101	GCGCGCGCAA	ACCGGTTTTT	AAAGTCAAAT	ATATTCGACA	TACGGCGGATT
151	CGCGGTTTGG	ATTTGGGACA	AAGCAGCGAA	GGCAAAACCA	ACGACGGCAA
201	AAAACAAATC	AGTTATCCGA	TTAAAGGCTT	GCCGCGAACA	AATGTTTATCC
251	GACTGATCGG	CAAGCATCCC	GGCAGCTTGG	AAGCCGTCAG	CGGCAAAATGT
301	ATGGAATACG	ATGATAAGGA	CAGTCCGGCA	GGTTGGGCAG	AAAACGGCGT
351	GTGCCATACC	TTGTTTGCCA	AACTGGTGGG	CAATATCGCC	GAAGACGGCG
401	GCAAACGTAC	GGATTACCTA	GTTCGCGATG	CCGCGCTGCA	ACCCATTCGA
451	CGAGGCAAAA	GCGGCTATGC	GGCCGTGCAG	AACGGACGCT	ATTGTCTGGA
501	AATCGACAGC	GAGGGGCGGT	TTTATTTCGG	CCGCGCCCAT	TATTGA

1	MLKTSFAVLG	GCLLLAACGK	SENTAEQPQN	AVQSAPKPVF	KVKYIDNTAI
51	AGLDLGQSSE	GKTNDGKKQI	SYPIKGLPEQ	NVIRLIGKHP	GDLEAVSGKC
101	METDDKDSQA	GWAENGVCHT	LFALGVGNIA	EDGKGLTDYL	VSHAALQPYQ
151	AGKSGYAAVQ	NGRYVLEIDS	EGAFVYRRRH	Y*	

	10	20	30	40	50	60
g205-1.pep	MLKIPFAVLGGCLLLAACGKSENTAEQPQNAAQSA	PKPVFKVKYIDNTA	IAAGLALGQSSE			
m205-1	MLKTSFAVLGGCLLLAACGKSENTAEQPQNAVQSA	PKPVFKVKYIDNTA	IAAGLDLGQSSE			
	10	20	30	40	50	60
	70	80	90	100	110	120
g205-1.pep	GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAV	VGKCMETDGKDAPSGWAENG	VCHT			
m205-1	GKTNDGKKOISYPIKGLPEONVIRLIGKHPGDLEAV	SGKCMETDDKDS	PAGWAENG	VCHT		

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```

              70      80      90      100      110      120
          130      140      150      160      170
g205-1.pep  LFAKLVGNIAEDGGKLT DYLVSHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAF
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m205-1      LFAKLVGNIAEDGGKLT DYLVSHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
          130      140      150      160      170      180

m205-1      YX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 713>:

```

a205-1.seq (partial)
  1  CCTCTTAAAG GCTTGCCGGA ACAAACGTC GTCCGGCTGA CCGGCAAGCA
 51  TCCCAACGAC TTGGAAGCCG TCGTCGGCAA ATGTATGGAA ACCGACGGAA
101  AGGGCGCGCC TTCGGGCTGG GCGGCAACG GCGTGTGCCA TACCTTGTTT
151  GCCAAACTGG TGGGCAATAT CGCCGAAGAC GCGGCAAC TGACGGATTA
201  CCTGATTTCC CATTCGCCCC TGCAACCTTA TCAGGCAGGC AAAAGCGGCT
251  ATGCCGCCGT GCAGAACGGA CGTATGTGC TGGAAATCGA CAGCGAGGGG
301  GCGTTTATT TCCGCCGCG CCATTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 714; ORF 205-1.a>:

```

a205-1.pep (partial)
  1  PLKGLPEQNV VRLTGKHPND LEAVVGKCM ETDGKGAPSGW AANGVCHTLF
 51  AKLVGNIAED GGKLT DYLVSHSALQPYQAG KSGYAAVQNG RYVLEIDSEG
101  AFYFRRRHY*

```

m205-1/a205-1 89.0% identity in 109 aa overlap

```

              50      60      70      80      90      100
m205-1.pep  KYIDNTAIAGLDLGQSSEKTN DNGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCM E
          |||:|||||:|||||:|||||:|||||:|||||
a205-1      PLKGLPEQNVVRLTGKHPNDLEAVVGKCM E
              10      20      30

              110      120      130      140      150      160
m205-1.pep  TDDKDSPAGWAENGVCHTLF A KLVGNIAEDGGKLT DYLVSHSALQPYQAGKSGYAAVQNG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a205-1      TDGKGAPSGWAENGVCHTLF A KLVGNIAEDGGKLT DYLVSHSALQPYQAGKSGYAAVQNG
              40      50      60      70      80      90

              170      180
m205-1.pep  RYVLEIDSEGAFYFRRRHYX
          |||:|||||:|||||:|||||
a205-1      RYVLEIDSEGAFYFRRRHYX
              100      110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 715>:

```

g206.seq
  1  atgttttccc ccgacaaaac ccttttcctc tgtctcggcg cactgctcct
 51  cgcctcatgc ggcacgacct ccggcaaaca ccgccaaccg aaacccaaac
101  agacagtccg gcaaatccaa gccgtccgca tcagccacat cggccgcaca
151  caaggctcgc aggaactcat gctccacagc ctcggactca tcggcacgcc
201  ctacaaatgg ggcggcagca gcaccgcaac cggcttcgac tgcagcggca
251  tgattcaatt ggtttacaaa aacgccctca acgtcaagct gccgcgcacc
301  gcccgcgaca tggcggcggc aagccgcaaa atcccgcaca gccgcctcaa
351  ggccggcgac atcgtattct tcaacaccgg cggcgcacac cgctactcac
401  acgtcggact ctacatcggc aacggcgaa tcatccatgc ccccggcagc
451  ggcaaaaacca tcaaaaccga aaaactctcc acaccgtttt acgccaaaaa
501  ctaccttggg gcgcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 716; ORF 206.ng>:

```

g206.pep
  1  MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT

```

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51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPR
 101 ARDMAAASRK IPDSRLKAGD IVFFNTGGAH RYSHVGLYIG NGEFIHAPGS
 151 GGTIKTEKLS TPFYAKNYLG AHTFFTE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 717>:

m206.seq
 1 ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
 51 CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
 101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
 151 CAAGGCTCGC AGGAATCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
 201 CTACAAATGG GCGGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
 251 TGATTCAATT CGTTTACAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC
 301 GCCCGCGACA TGGCGCGGC AAGCCGSAAT ATCCCGGACA GCCGCTTCAA
 351 GGCCGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
 401 ACGTCGGACT CTACATCGGC AACGGCGAAT TCATCCATGC CCCAGCAGC
 451 GGCAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
 501 CTACCTCGGC GCACATACTT TTTTACAGA ATGA

This corresponds to the amino acid sequence <SEQ ID 718; ORF 206>:

m206.pep.
 1 MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
 51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR
 101 ARDMAAASRK IPDSRXKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
 151 GGTIKTEKLS TPFYAKNYLG AHTFFTE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
g206	MFSPDKTLFLCLGALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRXKAGD					
g206	LGLIGTPYKWGGSSTATGFD CSGMIQLVYK NALNVKLPR TARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
	:					
g206	IVFFNTGGAHRYSHVGLYIGNGEFIHAPSGKTIKTEKLSTPFYAKNYLGAHTFFTE					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 719>:

a206.seq
 1 ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
 51 CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
 101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
 151 CAAGGCTCGC AGGAATCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
 201 CTACAAATGG GCGGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
 251 TGATTCAATT CGTTTACAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC
 301 GCCCGCGACA TGGCGCGGC AAGCCGCAAA ATCCCGGACA GCCGCTTAA
 351 GGCCGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
 401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCAGCAGC
 451 GGCAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
 501 CTACCTCGGC GCACATACTT TCTTTACAGA ATGA

483

This corresponds to the amino acid sequence <SEQ ID 720; ORF 206.a>:

```
a206.pep
  1 MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
  51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT
 101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
 151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
a206	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYKNALNVKLPRTARDMAAASRKIPDSRXKAGD					
a206	LGLIGTPYKWGGSSTATGFD CSGMIQFVYKNALNVKLPRTARDMAAASRKIPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLPFYAKNYLGAHTFFTEX					
a206	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 721>:

```
g209.seq
  1 atgctgcggc atttaggaaa cgacttcgcc ttgggcgcgt tgtttttcga
  51 tgctgcggtt gatgtgccac tgctgggcga tggtcaggag gttgttgacc
 101 acccagtaga gaaccaaacc ggcagggaag aagaagaaca tgacggagaa
 151 aaccaacggc atgattttca tcattttcgc ctgcatcggg tcggtcggcg
 201 gcgggttcag ataggtttgg gcgaaacatc ttgccgccat aatgatgggc
 251 aggatgtagt aggggtcggc gcggctgagg tcggtaatcc agcccagcca
 301 aggtgcctgg cgcaattcta cggaggcgaa caatgcccag tacaagccga
 351 tgaagacggg gatttgcaac agcataggca gacagccgcc cagcgggttg
 401 atttcctcgt cttcgaaaag ctgcatcatc gcttgctgtt gcgccatacg
 451 tcgctgcggc tatttttctt tgatggctct cagttcgggt gcggcggcac
 501 gcattttcgc catcgaaagg taggaggcgt tggtaaatgg atacagtacg
 551 gctttgacga tgatggtcaa aacgacgatt gcccagcccc agttgccgat
 601 aatgttggtc agttggttca ggagccagaa gaggcgcgat gcgaaccagt
 651 gtactttacc gtagtctttt gccagttgca gggtgtcggc gatgtttcgg
 701 ataacggatg tggtttcgg accggcatac aggttgaccg ccattttcgg
 751 ttttggcccc cgggttgga tagcgggtaa
```

This corresponds to the amino acid sequence <SEQ ID 722; ORF 209.ng>:

```
g209.pep
  1 MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDHPVENQT GREEEEHDGE
  51 NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGDVVGVG AAEVGNPAQP
 101 RCLAQFYGGE QCPVQADEDG DLQQHRQTAA QRVDLFLFEK LHHRLRLRHT
 151 VVAVFFFDGL QFGCGGTHFR HRTVGGVGQW IQYGFDDDGQ NDDCPAPVAD
 201 NVVQLVQEPE ERRCEPVYFT VFVCQLQVVG DVCDNGCGLR TGIQVDRHFR
 251 FWPPGWDSG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 723>:

```
m209.seq
  1 ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGgGCGTT GTTTTTTCGAT
  51 GCTGCGGTTG ATGTGCCATT GCTGGGCGAT GGTCAGGAGG TTGTTGACTA
 101 CCCAGTACAA TACCAGACCG GCAGGAAGA AGAAGAACAT GACGGAGAAA
 151 ACCAACGGCA TGATTTTCAT CATTTTCGCC TGCATCGGGT CGGTCGGCGG
 201 CGGGTTCAGA TAAGTTTGGG CGAACATCGT TGCCGCCATA ATGATGGGCA
 251 GGATGTAGTA GGGGTCGGCG CGGCTGAGGT CGGTAATCCA ACCCAGCCAA
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301 GGTGCCTGGC GCAATTCTAC GGAGCGGAAC AATGCCCAAT ACAATCCGAT
351 GAAGACGGGG ATTTGCAACA GCATAGGCAG GCAGCCGCCC AGCGGGTTGA
401 TTTTCTCGTC TGTGTAAAGC TGCATCATCG CCTGTTGTTG CGCCATACGG
451 TCGTCGCCGT ATTTCTCTTT GATGGCTTGC AGTTTGGGTG CGGCGGCACG
501 CATTTTCGCC ATAGAGCGGT AAGAGGCGTT GGTCAATGGA TACAGTACGG
551 CTTTGACGAT GATGGTTAAA ACGATAATCG CCCAGCCCCA GTTGCCGATG
601 ATGTTGTGCA GTTGGTTCAG GAGCCAGAAG AGCGGGGAGG CGAACCAGTG
651 TACTTTGCCG TAGTCTTTGG CCAGTTGCAG GTTGTCGGCG ATGTTTGCGA
701 TGACGGATGT GGTCTGCGGG CCGGCGTAGA GGTGATGGA GGCTTCGgTT
751 TCGCGCCGTT TTGGATGGCG GCTAAAGGCA CGCTGACGCT GGTGCTGTAC
801 AGCTTGTCGT TCGGCGCTTT GATGTCGATG TTGCACTCGC CTGCGGCGCA
851 AACGCTTTGT CTGCCTTTAG GTTGGAGAAT CCAGGTGGAC ATGAAGTGGT
901 GTTCAATCAT GCCGAGCCAG CCGGTCGGGG TTTGCGGAT GTATTCGGCC
951 TCGGATTTGC CGGATTTGGC ATCGTCGTCC AAGTCGAAA AGCTGACTTT
1001 TTGGAAGTTG CCTTCAGGGG TATAA

```

This corresponds to the amino acid sequence <SEQ ID 724; ORF 209>:

```

m209.pep
1 MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDYPVQYQT GREEEEHDGE
51 NQRHDFHHFR LHRVGRRRVQ ISLGEHRCRH NDGQDVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDG DLQQRQAAA QRVDFLVCVK LHRLLLRHT
151 VVAVFLFDGL QFGCGGTHFR HRAVRGVGQW IQYGFDDDG* NDNRPAPVAD
201 DVVQLVQEP EERGEPVYFA VVFGQLQVVG DVCDDGCGLR AGVEVDGGFG
251 FAPFWMAAKG TLTLVLYSL LRLMSMLHS PAAQTLCLPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSG V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 209 shows 88.5% identity over a 253 aa overlap with a predicted ORF (ORF 209.ng)

from *N. gonorrhoeae*:

```

m209/g209

      10      20      30      40      50      60
m209.pep MLRHLGNDFA LGALFFDAAVDVPLLGDGQEVVDYPVQYQTGREEEEHDGENQRHDFHHFR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g209      MLRHLGNDFA LGALFFDAAVDVPLLGDGQEVVDHPVENQTGREEEEHDGENQRHDFHHFR
          10      20      30      40      50      60

      70      80      90     100     110     120
m209.pep LHRVGRRRVQISLGEHRCRHNDGQDVVGVGAAEVGNPTQPRCLAQFYGGEQCPIQSDG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g209      LHRVGRRRVQIGLGEHRCRHNDGQDVVGVGAAEVGNPAQPRCLAQFYGGEQCPVQADEG
          70      80      90     100     110     120

      130     140     150     160     170     180
m209.pep DLQQRQAAAQRVDFLVCVKLHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g209      DLQQRQTAQAQRVDFLVFEKLHRLLLRHTVVAVFFFDGLQFGCGGTHFRHRTVGGVGQW
          130     140     150     160     170     180

      190     200     210     220     230     240
m209.pep IQYGFDDDGXNDNRPAPVADDVVQLVQEP EERGEPVYFAVVGQLQVVGDVCDGCGLR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g209      IQYGFDDDGQNDDCPAPVADNVVQLVQEP EERRCEPVYFTVVCQLQVVGDVCDNGCGLR
          190     200     210     220     230     240

      250     260     270     280     290     299
m209.pep AGVEVDGGGFGF-APFWMAAKGTLTLVLYSLRLMSMLHSPAAQTLCLPLGWRIQVDMK
          :|:|:| | | | |
g209      TGIQVDRHFRFWPPGWD SG
          250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 725>:

```

a209.seq
1 ATGCTGCGGC ATTTAGGAAA CCACTTCGCC TTGGGCGCGT TGTTTTTCGA

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51  TGCTGCGGTT GATGTGCCAT TGCTGGGCGA TGGTCAGGAG GTTGTTGATC
101  ACCCAGTACA ATACCAGACC GGCAGGGAAG AAGAAGAACA TGACGGAGAA
151  AACCAAAGGC ATGATTTTCA TCATTTTCGC CTGCATCGGG TCGGTCGGCG
201  GCGGGTTCAG ATAGGTTTGG CCGAACATCG TTGCCGCCAT AATGATGGGC
251  AGGATGTAGT AGGGGTCGGC GCGGCTGAGG TCGGTAATCC AACCCAGCCA
301  AGGTGCCTGG CGCAATTCTA CGGAGGCCAA CAATGCCCAA TACAATCCGA
351  TGAAGACGGG GATTTGCAAC AGCATAGGCA GGCAGCCGCC CAGCGGGTTG
401  ATTTTCTCGT CTGTGTAAAG CTGCATCATG GCTTGTGCT GCGCCATACG
451  GTCGTCGCGG TATTTCTCTT TGATGGCTTG CAGTTTGGGC GCGGCGGCAC
501  GCATTTTCGC CATCGAACGG TAAGAGGCGT TGGTCAATGG ATACAGTACG
551  GCTTTGACGA TGATGGTTAA AACGATAATC GCCCAGCCCC AGTTGCCGAT
601  GATGTTGTGC AGTTGGTTCA AAAGCCAAAA GAGGGGGGAG GCGAACCACT
651  GTACTTTGCC GTAGTCTTTG GCCAGTTGCA GGTTGTCGGC GATGTTTGCG
701  ATAACGGATG TGGTCTGTGG GCCGGCGTAG AGGTTGATGG AGGCTTCGGT
751  TTCGCACCGT TTTGGATAGC GGCTAAAGGC ACGCTGACGC TGGTGCTGTA
801  CAGCTTGTCG TTGCGGCGTT TGATGTCGAT ACGGCAGTCG CCAGCGGCGC
851  AAACGCTTTG TCCGCCTTTG GGTGGAGGA TCCAGGTGGA CATGAAGTGG
901  TGTTCATCA TGCCGAGCCA GCCGGTCGGG GTTTTGCGGA TGTATTCGGC
951  CTCGGATTG CCGGATTG CATCGTCGTC CAAGTCGGAG AAGCTGACTT
1001 TTTGGAAGTT GCCTTCAGGG GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 726; ORF 209.a>:

```

a209.pep
1  MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEHHDGE
51  NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGQDVVGVGAAEVGNPTQP
101  RCLAQFYGGE QCPIQSDG DLQQHRQAAA QRVDFLVCVK LHHGLLLRHT
151  VVAVFLFDGL QFGRGGTHFR HRTVRGVGQW IQYGFDDDG* NDNRPAPVAD
201  DVVQLVQPK EGGGEPVYFA VVFGQLQVVG DVCDNGCGLW AGVEVDGGFG
251  FAPFWIAAKG TLTLVLYSL LRRLMSIRQS PAAQTLCPPL GWRIQVDMKW
301  CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSG V*

```

m209/a209 95.6% identity in 341 aa overlap

```

m209.pep      10      20      30      40      50      60
MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEHHDGENQRHDFHHFR
|||||
a209          10      20      30      40      50      60
MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEHHDGENQRHDFHHFR

m209.pep      70      80      90      100     110     120
LHRVGRRRVQISLGEHRCRHNDGQDVVGVGAAEVGNPTQPRCLAQFYGGEQCPIQSDG
|||||:|||||
a209          70      80      90      100     110     120
LHRVGRRRVQIGLGEHRCRHNDGQDVVGVGAAEVGNPTQPRCLAQFYGGEQCPIQSDG

m209.pep      130     140     150     160     170     180
DLQQHRQAAAQRVDFLVCVKLHHRLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW
|||||:|||||
a209          130     140     150     160     170     180
DLQQHRQAAAQRVDFLVCVKLHHGLLRHTVVAVFLFDGLQFGCGGTHFRHRTVRGVGQW

m209.pep      190     200     210     220     230     240
IQYGFDDDGXNDNRPAVADDVVQLVQEPGEGGEPVYFAVVFGQLQVVGDVCDGCGLR
|||||:|||||
a209          190     200     210     220     230     240
IQYGFDDDGXNDNRPAVADDVVQLVQKPEGGEPVYFAVVFGQLQVVGDVCDGCGLR

m209.pep      250     260     270     280     290     300
AGVEVDGGFGFAPFWMAAKGTLTLVLVLYSLRRLMSMLHSPAAQTLCLPLGWRIQVDMKW
|||||:|||||
a209          250     260     270     280     290     300
AGVEVDGGFGFAPFWIAAKGTLTLVLVLYSLRRLMSIRQSPAAQTLCPPLGWRIQVDMKW

m209.pep      310     320     330     340
CSIMPSQPVGVLRMYSASDL PDLASSSKSEKLTFWKLPSGVX

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|||||
a209 CSIMPSQPVGVLRMYASDLPDLASSKSEKLTFWKLP SGVX
      310      320      330      340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 727>:

```

g211.seq
  1 atgttgcgga ttgctgctgc caatcagttg ggcggtcgaa atgggtcggc
 51 ggtgggaaac ggggtcgata agtttggcg tggtgctgat aatcaggttg
101 agtttttga aggaacactg attgtagtcg gcgcgtccgg gcgtgccgct
151 gtaacggtag ccgtggcgca attcgagcgt gcgtttgttg tccttcagcg
201 agaagttacc ttctttggcg aagatgatgt tgcgccgcc gttttgtcc
251 tggtcgcgca ggaacagggt ttcatgatg ccggttcgg tgtcaaagg
301 ttcgacgaaa taaacctgc cgttgcgctt gcccagtta ttgaactcgc
351 cggcttcac caaagacaat tcctgcttct gttcaaaat ttcggcatat
401 tcgcggtgc gcagctctgc ccacggatc acccaaagct gcagacggc
451 aatcaggatg gcaaacggca cggcaaactg catgacgggg cgtatccact
501 gtttcaacgc caatccgcag gatag

```

This corresponds to the amino acid sequence <SEQ ID 728; ORF 211.ng>:

```

g211.pep
  1 MLRIAAANQL GGRNGAAVGN GVDFKFRGAD NQVEFLEGNL IVVGASGRAA
 51 VTVAVAQFER AFVVLQREVT FFGEDDVVAA VFVLFAQEQV FHDAGFGVKG
101 FDEINPAVAL AQVIELAGFH QRFLLLLQN FGIFAAALC PRYHPKLHDG
151 NQDGKRHGKL HDGAYPLFQR QSAG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 729>:

```

m211.seq
  1 ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGTCGGA ATGGTACGGC
 51 GGTGGGAAAC GGGGTCGATG AGTTTGGGCG TGGTGTGAT AATCAGTTG
101 AGTTTTTGA AGGAAACCTG ATTGTAGTCG GCGCGTCCGG GCGTGCCGCT
151 GTAACGGTAG CCGTGGCGCA ATTCGAGCGT GCGTTTGTG TCGTTCAGCG
201 AGAAGTTACC TTCTTTGGCG AAGATGATGT TGTCGCCGCC GTTTTTGTCC
251 TGTTGCGGCA GGAACAGGTT TTTCATGATG CCGGATTCGG TATCGAAGGT
301 TTCGACAAAA TAAACCCTGC CGTTGCGCTT GCCCAAATG TTGAACTCGC
351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451 AACCAAAACG GCAAACGGCA CGGCAAATG CATCACCGGG CGTATCCATT
501 GTTCAATGC CAATCCGCAg GATAG

```

This corresponds to the amino acid sequence <SEQ ID 730; ORF 211>:

```

m211.pep
  1 MLRVAAANQL GGRNGTAVGN GVDEFGRGAD NQVEFLEGNL IVVGASGRAA
 51 VTVAVAQFER AFVVVQREVT FFGEDDVVAA VFVLFAQEQV FHDAGFGIEG
101 FDKINPAVAL AQTVELACLH QRFLLLLQD FSVFAAAXLC PRYHPKLHDG
151 NQNGKRHGKL HHRAYPLFQC QSAG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 211 shows 89.1% identity over a 174 aa overlap with a predicted ORF (ORF 211.ng) from *N. gonorrhoeae*:

```

m211/g211
      10      20      30      40      50      60
m211.pep MLRVAAANQLGGRNGTAVGNVDFEFGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g211 MLRIAAANQLGGRNGAAVGNVDFKFRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER
      10      20      30      40      50      60
m211.pep AFVVVQREVTFFGEDDVVAAVFVLFAQEQVFHDAGFGIEGFDKINPAVALAQTVELACLH
      70      80      90     100     110     120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 731>:

This corresponds to the amino acid sequence <SEO ID 732; ORF 211.a>:

m211/a211 99.4% identity in 174 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 733>:

g212.seq (partial)						
1	atggacaatc	tcgatgghga	cggtattccc	gacatccgca	cactcgacca	
51	aaccatccgc	aaacacgcac	accggtctaa	cctgattgtc	tgctctcccg	
101	ataatcagat	tcccgatttt	caaaccgcac	aagatgcttc	ggactcggaa	
151	tgccgtctga	agcaccggtt	ggatcaggca	accagtgcc	tccagttcga	
201	cagcatcaac	ctcatcgaac	acatcctgcc	cgatgtccgc	ttctggtctg	
251	ttcccccttc	acgcacccgc	cgctcgacg	aaacattcca	ccacattctc	
301	tggcagaccg	aagccatccc	gcaaaccgag	agcaagtccg	acaaaccttc	
351	qtttgcaact	ccacaacaat	ccgaacqaaa	aaaaccqaaa	cacgtcctcc	

```

401 tcatcgggtgc aggcattgcc ggcgcacgca cgcgccacgc cttagcatca
451 cacggcatttt ccgttaccgt attggaagcc cgaaaagccg ctcaagccgc
501 cagcggcaac cggcaagggc tgctttacgc caaaatctcg ccgcacgaca
551 ccggacagac cgaactgctg cttgccggct acggctacac caaacgcctg
601 ctccggacaca tcctgcccga ctccgacact tggggcggca acggcatcat
651 ccacctcaat tacagccgca ccgaacaaca acgcaatcac gaattggggtt
701 tgcaaaaaca ccataaccac ctctaccgca gcatcacgtc tgcagaagcc
751 gaaaaaatcg ccggcatccc gctgaacacg ccctacgccg aaccattatg
801 cggactctac tggcaacacg gcgtatggct caatccgccg gcattcgctc
851 gcaccctcct cagccatccg ctgatcgaac tatatgaaaa cacaacgtta
901 accggcatttt cccacgacgg agaaaagtgg attgcaagca cgccaaacgg
951 cacatttacc gccacacaca tcatctactg caccggcgcg cacagcccct
1001 gcctgcccga aaccaacctc gccgccctac ccctcaggca aatacgcgga
1051 caaacccggc tcacaccgtc caccgccgtt tccgaacaac tgcgttgcgc
1101 cgtttcaggc gaaagctaca tcagcccgtc gtggcacgga ctgcactgct
1151 acggcgcgag ttttattccc aacagcagca ataccggatg gaacgaagcc
1201 gaagaagcct caaacgccca agcattggca caccctaacc ccgcccttgc
1251 cgaatcattg ttt...

```

This corresponds to the amino acid sequence <SEQ ID 734; ORF 212.ng>:

g212.pep (partial)

```

1 MDNLVWDGIP DIRTLDQIR KHAHPLNLIV CLPDNQIPDF QTAQDASDSE
51 CRLKHLRDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKSDKPWFAL PQTSEKKPE HVLVIGAGIA GASTAHALAS
151 LGHISVTLEA RKAQAASGN RQGLLYAKIS PHDTGQTELL LAGYGYTKRL
201 LGHILPDSDT WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA
251 EKIAGIPLNT PYAEPLCGLY WQHGVLNPP AFVRTLLSHP LIELYENTTL
301 TGISHDGEKW IASTPNGTFT ATHIIYCTGA HSPCLPETNL AALPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LH CYGASFIP NSSNTGWNEA
401 EEASNRQALA HLNPALAESL F...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 735>:

m212.seq

```

1 ATGGACAATC TCGTATGGGA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AGCCATCCGC AAACACGCAC CCCCGCTCAA CCTGATTATC TGCCTCCCGG
101 ATAATCAGAT TCCCATTGTT CAAACCGCAC AAGATGCTTC GGACGCGGAA
151 TGCCGTCTGA AGCACCCTTT GGATCAGGCA ATGCAGTGCC TCCAGTTCGA
201 CAGCATCAAC CTCATCGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCAC CACCTGCACG AACATTTCCA CCACATTTC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGCAAGCCCG ACAAAACCTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGCGC GGGCATATCC GCGCGGGCAA CCGCCCACGC CTTAGCATCA
451 CACGGCATT TCCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCCAAGCCGC
501 CAGCGGCAAC CGCCAAGGGC TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAGAC CGAACTTTTG CTTGCCGGCT ACGGCTACAC CAAACGCCGTG
601 CTCGGACACA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACATC TGCAGAAGCC
751 GAAAAAATCG CCGGTATCCC ACTGTCCGTC CCATACGACC ACCCTTATG
801 CGGACTCTAC TGGCAACACG GCGTATGGCT CAATCCACCC GCATTCTGCC
851 GCACCTCTCT CAACCATCCG CTCATTGGAC TACACGAAGA CACACCTTG
901 ACCGACATT CCCACGACGG GGA AAAAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCCT
1001 ACCTACCCGA AACCACCTC GCCGCCCTGC CTCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TGC GTTGC GC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCACGGA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTCCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCCA ACCCAAACCC CCAAAAACAC CAAGGGCAGC
1301 CCGCCATACG CTGCGACAGC CCCGACCACC TTCCCTAGT CCGGCGCACTC
1351 GCGGACATTG CCGCCATGCG GCAGACCTAC ACCAAACTCG CGCTGGACAA
1401 AAATACCGC ATCGACACCC CATGCCATA CCTGCCTAAT GCCTACGTCA
1451 ACACCGCGCA CCGCACCCGC GGA CTGCCA CCGCCCCAT CTGCGCCGCC

```

1501 GmCAwTGCAG CCCAAATCsT AGGCyTGCCC CATCCCTTTT yAcAAcGCCT
 1551 gCGCCACGCC cTAcACCCCA ACCGCACCAT CATCCGCGCC ATCGTCAGAA
 1601 GGAAGGATCT AACCCCTTAA

This corresponds to the amino acid sequence <SEQ ID 736; ORF 212>:

m212.pep
 1 MDNLVWDGIP DIRTLDQAIR KHAPPLNLII CLPDNQIPDF QTAQDASDAE
 51 CRLKHLRDQA MQCLQFDSIN LIEHILPDVR FWLVPPSRTH HLHEHFHHIS
 101 WQTEAIPQTE SKPDKPWFAL PQTSERQKPE HILVIGAGIS GAATAHALAS
 151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL
 201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA
 251 EKIAGIPLSV PYDHPSGLY WQHGVWLNPP AFVRTLLNHP LIGLHEDTPL
 301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL AALPLRQIRG
 351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSHTGWNEA
 401 EEASNRQALA HLNPALESSE FAANPNPQKH QGHAAIRCDS PDHPLVLGAL
 451 GDIAAMRQTY TKLALDKNYR IDTPCPYLPN AYVNTAHGTR GLATAPICAA
 501 XXAAQIXGLP HPFXQRLRHA LHPNRTIIRA IVRRKDLTP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 212 shows 92.9% identity over a 421 aa overlap with a predicted ORF (ORF 212.ng) from *N. gonorrhoeae*:

m212/g212

	10	20	30	40	50	60
m212.pep	MDNLVWDGIPDIRTLDQAIRKHAPPLNLIIICLPDNQIPDFQTAQDASDAECRLKHLRDQA					
	: : : : :					
g212	MDNLVWDGIPDIRTLDQIRKHAHPLNLIVCLPDNQIPDFQTAQDASDSECRLKHLRDQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m212.pep	MQCLQFDSINLIEHILPDVRFWLVPPSRTHHLHEHFHHISWQTEAIPQTESKPDKPWFAL					
	: : : : :					
g212	TQCLQFDSINLIEHILPDVRFWLVPPSRTRLHEHFHHISWQTEAIPQTESKSDKPWFAL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m212.pep	PQTSERQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
	: : : : :					
g212	PQTSERKKPEHVLVIGAGIAGASTAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m212.pep	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIIHLNYSRTEQQRNHELGLQKHHNH					
	: : : : :					
g212	PHDTGQTELLLAGYGYTKRLLGHILPDSDTWGGNGIIHLNYSRTEQQRNHELGLQKHHNH					
	190	200	210	220	230	240
	250	260	270	280	290	300
m212.pep	LYRSITSAEAEKIAGIPLSVPYDHPSGLYWQHGVWLNPPAFVRTLLNHP LIGLHEDTPL					
	: : : : :					
g212	LYRSITSAEAEKIAGIPLNTPYAEPLCGLYWQHGVWLNPPAFVRTLLSHPLIELYENTTL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m212.pep	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPLYLPETNL AALPLRQIRGQTGLTPSTPF					
	: : : : :					
g212	TGISHDGEKWIASTPNGTFTATHIIYCTGAHSPCLPETNL AALPLRQIRGQTGLTPSTPF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m212.pep	SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSHTGWNEAE EASNRQALAH LNPALSES					

	:
g212	SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSNTGWNEAEEASNROALAHLPALAESL
	370 380 390 400 410 420
	430 440 450 460 470 480
m212.pep	FAANPNPQKHQGHAAIRCDSPDHLPLVGALGDIAAMRQTYTKLALDKNYRIDTPCPYLPN
g212	F

a212.seq

1	ATGGACAATC	TCGCATGGAA	CGGCATTCCC	GACATCCGCA	CACTCGACCA
51	AACCATCCGC	AAACACGCAC	ACCCGCTCAA	CCTGATTGTC	TGCCCTCCCG
101	ATAATCAGAT	TCCCAATTTT	CAAACCGCAC	AAGATGCTTC	GGCCTCGGAA
151	TGCCGTCTGA	AGCACC GTT	GGATCAGGCA	ACCCAGTGCC	TCCAGTTCTGA
201	CAGCATCAAC	CTGATTGAAC	ACATCCTGCC	CGATGTCCGC	TTCTGGCTGG
251	TTCCCCCTTC	ACGCACCCGC	CGCCTGCACG	AACACTTCCA	CCACATTTCC
301	TGGCAGACCG	AAGCCATCCC	GCAAACCGAA	AGTAAGCCCG	ACAAACCTCG
351	GTTTGCACTT	CCACAACATC	CCGAACGGCA	AAACACGGAA	CACATCCTCG
401	TTATCGGAGC	GGGCATATCC	GGCGCGGCAA	CCGCCACGC	CTTAGCATCA
451	TACGGCATTT	CCGTTACCGT	ATTGGAAGCC	CGAAAAGCCG	CCCAAGCCGC
501	CAGCGGCAAC	CGCCAAGGCG	TGCTCTACGC	CAAATCTCTG	CCGCACGACA
551	CCGAACAAAC	CGAATCTGCT	CTTGCCGGCT	ACGGCTACAC	CAAAACGCTG
601	CTCGGACATA	TCTGCCCCGA	ATCCGAAACC	TGGGCGCGCA	ACCGCATCAT
651	CCACCTCAAT	TACAGCCGCA	CCGAACAACA	ACGCAATCAC	GAATTGGGTT
701	TGCAAAAACA	CCATAACCAC	CTCTACGCA	GCATCAGCA	GGCAGAAGCC
751	GAAAAAATCG	CCGGCATCCC	TCTGAACACG	CCCTACGCCG	AACCATTATG
801	CGGACTGTTT	TGGCAGTAGC	CGGTATGGCT	CAATCCTCCC	ACATTCTGTC
851	CGCCCTCCTT	CAGCCATCCG	CTCATTGGAC	TACACGAAGA	CACACCGTTA
901	ACCGACATTT	CCCACGACGG	GGAAAAGTGG	ATTGCAAGCA	CGCCAAACGG
951	CACATTTACC	GCCACACACA	TCATCTACTG	CACCGTGCG	AACAGCCCCT
1001	ACCTACCCGA	AACCAACCCT	GCCACCTCTG	CCCTCAGGCA	AATACGCGGA
1051	CAAACCGGCC	TCACACCGTC	CACCCCGTTT	TCCGAACAAC	TGCGTTGCGC
1101	CGTTTCAGGC	GAAAGCTACA	TCAGCCCGTC	GTGGCAGGGA	CTGCACTGCT
1151	ACGGCGCGAG	TTTTATTCCC	AACAGCAGCC	ATACCGGATG	GAACGAAGCC
1201	GAAGAAGCCT	CAAACCGCCA	AGCATTGGCA	CACCTTAACC	CCGCCCTTTC
1251	CGAATCATTG	TTTGCCGCCA	ACCCAAACCC	CCAAAAACAC	CAAGGGCACG
1301	CGGCCATACG	CTGCGACAGC	CCCGACCACC	TTCCCTTAGT	CGGCGCACTC
1351	GGCGACATTG	CCGCTATGCA	ACAAACTTAC	GCCAAACTCG	CGCTGGACAA
1401	AAACTATCGC	ATCGATGCCC	CCTGCCCGTA	CCTGCCCAAT	GCCTACGCCA
1451	ACACCGCCCA	CGGCACACGC	GGGCTTGCCA	CCGCCCCCAT	CTGCGCCGCC
1501	GCCGTTGCAG	CCGAAATCCT	AGGCTTGCCC	CATCCCCTCT	CAAAACGCCT
1551	CGGCCACGCC	CTACACCCCA	ACCGCGCCAT	CATCCGCGCC	ATCGTCAGAA
1601	GGAAGGATCT	AACCCCTTAA			

```
a212.pep
1 MDNLAWNGIP DIRTLDQ TIR KHAHPLNLIV CLPDNQIPNF QTAQDASDAE
51 CRLKHLRLDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKAPDKPWFAL PQTSEKQKPE HILVIGAGIS GAATAHALAS
151 YGISVTVLEA RKAQQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL
201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYSRTQAEA
251 EKIAGIPLNT PYAEPLCGLF WQYGVWLNPP TFVRALLSHP LIGLHEDTPL
301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL ATLPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCGYASFIP NSSHTGWNEA
401 EEASNRRQAL HNLPALESIL FAANPNPQKH QGHAAIRCDS PDHPLPLVGA
451 GDIAAMQQA QY AKLALDKNYR IDAPCPYLPN AYANTAHGTR GLATAPICAA
501 AVAAEILGLP HPLSKRLRHA LHPNRAIIRA IVRRKDLTP*
```

m212.pep MDNLVWGIPIDIRTLDOAIRKHAPPLNLIICLPDNPQIPDFQTAAQDASDAECLRKHLRDLQA
|||||:|||||:|||||:|||||:|||||:
a212 MDNLAWNGIPIDIRTLDOTIRKHAHPLNLIVCLPDNOIPNFOTAAQDASDAECLRKHLRDLQA

491

	10	20	30	40	50	60
m212.pep	70	80	90	100	110	120
a212	70	80	90	100	110	120
m212.pep	130	140	150	160	170	180
a212	130	140	150	160	170	180
m212.pep	190	200	210	220	230	240
a212	190	200	210	220	230	240
m212.pep	250	260	270	280	290	300
a212	250	260	270	280	290	300
m212.pep	310	320	330	340	350	360
a212	310	320	330	340	350	360
m212.pep	370	380	390	400	410	420
a212	370	380	390	400	410	420
m212.pep	430	440	450	460	470	480
a212	430	440	450	460	470	480
m212.pep	490	500	510	520	530	540
a212	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 739>:

```

g214.seq
1  atgatacaaa agatatgtaa gctatttgtt ttaattgtaa tttttgcaac
51  ttctcccgtt tttgcccttc aaagcgacag cagacggccc atccaaatcg
101 aagccgacca aggttcgctc gatcaagcca accaaaggac cacatttagc
151 ggcaatgtca tcatcagaca gggtagcttc aacatttcgc cctcgtgtgt
201 caacgtcaca cgcggcaggc aaaggcggcg aatccgtgag ggcggaaggt
251 tcgcccgtcc gcttcagcca aacgttggac gggggcaaa ggcaggtgcg
301 cggtcaggca aacaacgtta cctattcctc cgcaggaagc actgtcgttc
351 tgaccggcaa tgccaaagtg cagcgcggcg gcgacgttgc cgaagggtcg
401 gtcattacct acaacaccaa aaccgaagtc tataccatca acggcagcac
451 gaaatcgggt gcgaaatccg cttccaaaac cggcagggtc agcgtcgtca
501 tccagccttc aagcacacaa aaaaccgaat aaccccgatg ccgtctgaaa
551 cggaaacgca gtccagacgg catttgccga ccgaaatgcc gagaagagat
601 tattga

```

This corresponds to the amino acid sequence <SEQ ID 740; ORF 214.ng>:

```
g214.pep
```

492

```

1  MIQKICKLV LIVIFATSPA FALQSDSRP IQIEADQGS L DQANQRTTFS
51  GNVIIRQGT L NISASCVNVT RGRQRRRIE GGRFARPLQ NVGRGQRDGA
101 RSGKQRYLF L RRKHCRSDRQ CQSAARRRR RRCGHYLQHQ NRSLYHQHQH
151 EIGCEIRFQ N RQGQRRHPAF KHTKNRITPM PSETETQFRR HLPTEMPRRD
201 Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 741>:

```

m214.seq (partial)
1  ATGATACAAA AGATATGTAA GCTATTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTCCG CCGCCCGCGT
201 CAATGTTACA CGCGGCGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGC GC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGCGCG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATT...

```

This corresponds to the amino acid sequence <SEQ ID 742; ORF 214>:

```

m214.pep (partial)
1  MIQKICKLV LIAFFSASPA FALQSDSRP IQIEADQGS L DQANQSTTFS
51  GNVIIRQGT L NISAARVNVT RGRQRRRIE GGRFASPLQ DIGRRQRHGA
101 RTGKQRCLF I CRQHRSLNR* CQSTARRRCR RRCGDYIQHQ NRSLYHQHQH
151 KI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 214 shows 80.3% identity over a 152 aa overlap with a predicted ORF (ORF 214.ng) from *N. gonorrhoeae*:

```

m214/g214

      10      20      30      40      50      60
m214.pep  MIQKICKLVLIAFFSASPALQSDSRPIQIEADQGS LDQANQSTTFSGNVIRQGT L
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g214      MIQKICKLV LIVIFATSPA FALQSDSRRPIQIEADQGS LDQANQRTTFSGNVIRQGT L
          10      20      30      40      50      60

      70      80      90     100     110     120
m214.pep  NISAARVNVT RGRQRRRIE GGRFASPLQ PDIGRRQRHGARTGKQRCLFICRQHRSLNRX
          |||: |||||:|||||:|||||: |||: || |||: ||| ||: ||: |
g214      NISASCVNVT RGRQRRRIE GGRFARPLQ PNVGRGQRDGARS GKQRYLF LRRKHCRSDRQ
          70      80      90     100     110     120

      130     140     150
m214.pep  CQSTARRRCRRRCGDYIQHQNRSLYHQHQHKI
          |||: ||| ||| |: |||||: |||||: |||: |
g214      CQSAARRRCRRRCGHYLQHQNRSLYHQHQEIGCEIRFQNRQGQRRHPAFKHTKNRITPM
          130     140     150     160     170     180

g214      PSETETQFRRHLPTMPRRDY
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 743>:

```

a214.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTCCG CCGCCCGCGT
201 CAATGTTACA CGCGGC.GGC AAAGGCGGCG AATCCGTGAG GGCGGAAGGT
251 TCGCCAGTCC GCTTCAGCCA GACATTGGAC GGCGGCAAAG GCACGGTGCG
301 CGGACAGGCA AACAACGTTG CTTATTCATC TGCAGGCAGC ACCGTAGTCT

```


493

```

351 TAACCGGTAA TGCCAAAGTA CAGCGCGGCG GCGATGTCGC CGAAGGTGCG
401 GTGATTACAT ACAACACCAA AACCGAAGTC TATACCATCA GCGGCAGCAC
451 AAAATCCGGC GCAAAATCCG CTTCCTCAATC CGGCAGGGTC AGCGTCGTTA
501 TCCAGCCTTC GAGTACGCAA AAATCCGAAT AATCCCAATG CCGTCTGAAA
551 CATAAACCTG GTTCGGACGG CATTTGCCGA CCGAAATATT GAAGAGATAT
601 TTATGA

```

This corresponds to the amino acid sequence <SEQ ID 744; ORF 214.a>:

```

a214.pep
1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISAARVNV T RGXQRRRI R GGRFASPLQ P DIGRRQRHGA
101 RTGKQRCLE F CRQHRSLNR* CQSTARRRC R RCGDYIQH Q NRSLYHQ RQH
151 KIRRKIRFQ I RQGQRRYP AF EYAKIRIIP M PSET*TWFG R HLPTEILKRY
201 L*

```

m214/a214 99.3% identity in 152 aa overlap

	10	20	30	40	50	60
m214.pep	MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L					
a214	MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L					
	10	20	30	40	50	60
m214.pep	NISAARVNV TRGRQRRRI REGGRFASPLQ PDIGRRQRH GARTGKQRCLE FICRQHRSLNR X					
a214	NISAARVNV TRGXQRRRI REGGRFASPLQ PDIGRRQRH GARTGKQRCLE FICRQHRSLNR X					
	70	80	90	100	110	120
m214.pep	NISAARVNV TRGRQRRRI REGGRFASPLQ PDIGRRQRH GARTGKQRCLE FICRQHRSLNR X					
a214	NISAARVNV TRGXQRRRI REGGRFASPLQ PDIGRRQRH GARTGKQRCLE FICRQHRSLNR X					
	70	80	90	100	110	120
m214.pep	CQSTARRRC RRCGDIYI QHNRSLYHQ RHQHKI					
a214	CQSTARRRC RRCGDIYI QHNRSLYHQ RHQHKI RIRKIRFQ I RQGQRRYP AF EYAKIRIIP M					
	130	140	150	160	170	180
m214.pep	CQSTARRRC RRCGDIYI QHNRSLYHQ RHQHKI					
a214	CQSTARRRC RRCGDIYI QHNRSLYHQ RHQHKI RIRKIRFQ I RQGQRRYP AF EYAKIRIIP M					
	130	140	150	160	170	180
m214.pep	PSETXTWFG RHLPTEILKRY L X					
a214	PSETXTWFG RHLPTEILKRY L X					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 745>:

```

g214-1.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATTGTAA TTTTGC AAC
51  TTCTCCCGCT TTTGCCCTTC AAAGCGACAG CAGACGGCCC ATCCAAATCG
101 AAGCCGACCA AGGTTCGCTC GATCAAGCCA ACCAAAGTAC CACATTTAGC
151 GGCAATGTCA TCATCAGACA GGGTACGCTC AACATTTCCG CCTCGCGCGT
201 CAACGTCACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCCGTCCG CTTACGCCAA ACGTTGGACG GGGGCAAAGG GACGGTGCGC
301 GGTCAGGCAA ACAACGTTAC CTATTCTCTC GCAGGAAGCA CCGTCGTTCT
351 GACCGGCAAT GCCAAAGTGC AGCGCGGCGG CGACGTTGCC GAAGGTGCGG
401 TCATTACCTA CAACACCAA ACCGAAGTCT ATACCATCAA CCGCAGCACG
451 AAATCGGGTG CGAAATCCGC TTCCAAAACC GGCAGGGTCA GCGTCGTCAT
501 CCAGCCTTCA AGCACACAAA AAACCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 746; ORF 214-1.ng>:

```

g214-1.pep
1  MIQKICKLFV LIVIFATSPA FALQSDSRRP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISASRVNV T RGGKGGESVR AEGSPVRF S Q TLDGGKGTVR
101 GQANNVTYSS AGSTVVL TN AKVQRGGDVA EGAVITYNT K TEVYTINGST
151 KSGAKSASKT GRVSVVIQPS STQKTE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 747>:

```

m214-1.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGCG
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTCGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTTCCG CCGCCCGCGT

```

494

```

201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTCAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACC GGTAAT GCCAAAGTAC AGCGGCGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 748; ORF 214-1>:

m214-1.pep

```

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51 GNVVIRQGT L NISAARVNV T RGGKGGESV R AEGSPVRF S Q TLDGGKGT V R
101 GQANNVAY S S AGSTVVLT G N AKVQRGGD V A EGAVITYN T K TEVYTISG S T
151 KSGAKSAS K S GRVSVVIQ P S STQKSE*

```

m214-1/g214-1 93.8% identity in 176 aa overlap

	10	20	30	40	50	60
m214-1.pep	MIQKICKLFV	LIAFFSASPA	FALQSDSRQP	IQIEADQGS	LDQANQSTTFS	GNVVIRQGT
g214-1	MIQKICKLFV	LIVIFATSP	AFALQSDSR	RPIQIEADQ	GS L DQANQSTTFS	GNVVIIRQGT
	10	20	30	40	50	60
	70	80	90	100	110	120
m214-1.pep	NISAARVNV	TRGGKGGES	VRAEGSPV	RFSQ TLDGGK	GT V R GQANNV	AYSSAGSTV
g214-1	NISASRVN	TRGGKGGES	VRAEGSPV	RFSQ TLDGGK	GT V R GQANNV	TYSSAGSTV
	70	80	90	100	110	120
	130	140	150	160	170	
m214-1.pep	AKVQRGGD	VAEGAVITY	NKTEVYTIS	SGSTKSGAK	SASKSGRVS	VVIQPSSTQ
g214-1	AKVQRGGD	VAEGAVITY	NKTEVYTING	STKSGAKS	ASKTGRVS	VVIQPSSTQ
	130	140	150	160	170	

g214-1/p38685

sp|P38685|YHBN_ECOLI 17.3 KD PROTEIN IN MURA-RPON INTERGENIC REGION PRECURSOR (ORF185)
>gi|551336 (U12684) orf185 [Escherichia coli] >gi|606139 (U18997) ORF_o185 [Escherichia coli]
>gi|1789592 (AE000399) orf, hypothetical protein [Escherichia coli] Length = 185
Score = 97.1 bits (238), Expect = 6e-20
Identities = 57/126 (45%), Positives = 74/126 (58%), Gaps = 3/126 (2%)

Query: 19 PAFALQSDSRQPIQIEADQGS L DQANQSTTFS GNVVIRQGT L NISAARVNVTR--GGKGG 76
PAFA+ D+ QPI IE+DQ SLD TF+GNV++ QGT+ I+A +V VTR G +G
Sbjct: 24 PAFAVTGD TDQPIHIESDQQLDMQGNVVTFTGNVIVTQGTIKINADKVVVTRPGGEQ GK 83

Query: 77 ES VRAEGSPVRF SQTLDGGKGT V R GQANNVAYSSAGSTV VLTGN AKVQRGGDVAEGAVIT 136
E + G P F Q D GK V G A + + Y A V VLTGNA +Q+ +G IT
Sbjct: 84 EVIDGYGKPATFYQM QDN GK-PVEGHASQMHYELAKDFV VLTGNAYLQQVDSNIKGDKIT 142

Query: 137 YNTKTE 142
Y K +
Sbjct: 143 YLVKEQ 148

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 749>:

a214-1.seq

```

1 ATGATACAAA AGATATGTAA GCTATTGTT TTAATAGCAT TTTTTCGGC
51 GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTTCGCTC GATCAAGCCA ACCAAAGCAC CACATTTCAGC
151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTTCCG CCGCCCGCGT
201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTCAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACC GGTAAT GCCAAAGTAC AGCGGCGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 750; ORF 214-1.a>:

a214-1.pep

```

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS

```

495

51 GNVVIRQGTI NISAARVNVT RGGKGGESVR AEGSPVRFSSQ TLDGGKGTVR
 101 GQANNVAYSS AGSTVVLGTN AKVQRGGDVA EGAVITYNTK TEVYTISGST
 151 KSGAKSASKS GRVSVVIQPS STQKSE*

a214-1/m214-1 100.0% identity in 176 aa overlap

	10	20	30	40	50	60
a214-1.pep	MIQKICKLFLVLI	AFSSAPAFALQSDSRQPIQIEADQGS	LDQANQSTTFSGNVVIRQGTI			
m214-1	MIQKICKLFLVLI	AFSSAPAFALQSDSRQPIQIEADQGS	LDQANQSTTFSGNVVIRQGTI			
	10	20	30	40	50	60
a214-1.pep	NISAARVNVT	RGGKGGESVRAEGSPVRFSSQ	TLDGGKGTVRGQANNVAYSSAGSTVVLGTN			
m214-1	NISAARVNVT	RGGKGGESVRAEGSPVRFSSQ	TLDGGKGTVRGQANNVAYSSAGSTVVLGTN			
	70	80	90	100	110	120
a214-1.pep	NISAARVNVT	RGGKGGESVRAEGSPVRFSSQ	TLDGGKGTVRGQANNVAYSSAGSTVVLGTN			
m214-1	NISAARVNVT	RGGKGGESVRAEGSPVRFSSQ	TLDGGKGTVRGQANNVAYSSAGSTVVLGTN			
	70	80	90	100	110	120
a214-1.pep	AKVQRGGDVAEGAVITYNTKTEVYTISGSTKSGAKSASKSGRVS	SVVIQPSSTQKSEX				
m214-1	AKVQRGGDVAEGAVITYNTKTEVYTISGSTKSGAKSASKSGRVS	SVVIQPSSTQKSEX				
	130	140	150	160	170	
a214-1.pep	AKVQRGGDVAEGAVITYNTKTEVYTISGSTKSGAKSASKSGRVS	SVVIQPSSTQKSEX				
m214-1	AKVQRGGDVAEGAVITYNTKTEVYTISGSTKSGAKSASKSGRVS	SVVIQPSSTQKSEX				
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 751>:

g215.seq
 1 atgaaagtaa gatggcggtta cggaattgag ttccattga tattggcggt
 51 tgccttgggc agcctgtcgg catggttggg ccgtatcagc gaagtcgaaa
 101 tcgaggaagt caggctcaat cccgacgaac ctcaatacac aatggacggc
 151 ttggacggaa ggcggtttga cgaacagggga tacttgaaag aacatttgag
 201 cgcgaaagt gcgaaacagt ttccgaaaa cagcgacatc cattttgatt
 251 cgccgcacat cgtgttcttc caagaaggca ggctgttgta cgaagtcggc
 301 agcgatgaag cgtttacca taccgaaaac aaacaggttc ttttataaaa
 351 caacgttgtg ctgacaaaaa ccgcccagcg cagcgggcag gcgggtaaa
 401 tcgaaaccga aaaactgcac gtcgataccg aatctcaata tgcccaaacc
 451 gatacgctg tcagtttcca atatggcgcg tcgcacgggc aggcggggcg
 501 tatgacctac aaccacaaaa caggcatgtt gaacttctca tctaaagtga
 551 aagccgcgat ttatgataca aaagatatgt aa

This corresponds to the amino acid sequence <SEQ ID 752; ORF 215.ng>:

g215.pep
 1 MKVRWRYGIA FPLILAVALG SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS
 51 LDGRRFDEQG YLKEHLSAKG AKQFPENSDI HFDSPLVFF QEGRLLYEVG
 101 SDEAVYHTEN KQVLFKNNVV LTKTADGRRQ AGKVETEKLN VDTESQYAQT
 151 DTPVSFQYGA SHGQAGGMTY NHKTGMLNFS SKVKAAYDT KDM*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 753>:

m215.seq (partial)
 1 ..AGCCTGTCGG CATGGTTGGG TCGTATCAGC GAAGTCGAGA TTGAAGAAGT
 51 CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACAGC TTGGACGGCA
 101 GGCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTGAG CGCGAAGGGC
 151 GCGAAACAGT TTCCGAAAAG CAGCGACATC CATTTTGATT CGCCGCATCT
 201 CGTGTCTTCT CAAGAAGGCA GGTGTGTGTA CGAAGTCGGC AGCGACGAAG
 251 CCGTTTACCA TACCGAAAAC AAACAGGTTT TTTTAAAAA CAACGTTGTG
 301 CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG TTGAAGCCGA
 351 AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAACC GATACGCCTG
 401 CAGTTTCCA ATATGGTGCA TCGCACGGTC AGGCGGGCGG CATGACTTAC
 451 GACCACAwA CAGGCATGTT GAACTTCTCA TCTAAAGTGA AAGCCACGAT
 501 TTATGATACA AAAGATATGT AA

This corresponds to the amino acid sequence <SEQ ID 754; ORF 215>:

m215.pep (partial)
 1 ..SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS LDGRRFDEQG YLKEHLSAKG
 51 AKQFPENSDI HFDSPLVFF QEGRLLYEVG SDEAVYHTEN KQVLFKNNVV
 101 LTKTADGKRQ AGKVEAEKLN VDTESQYAQT DTPVSFQYGA SHGQAGGMTY

151 DHXTGMLNFS SKVKATIIDT KDM*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 215 shows 96.0% identity over a 173 aa overlap with a predicted ORF (ORF 215.ng) from *N. gonorrhoeae*:

m215/g215

		10	20	30	40
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG			
		:			
g215	MKVRWRYGIAFPLILAVALGSLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG	10	20	30	40
		50	60	70	80
m215.pep	YLKEHLSAKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV	50	60	70	80
		:			
g215	YLKEHLSAKGAKQFPENSIDHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV	70	80	90	100
		110	120	130	140
m215.pep	LTKTADGKRQAGKVEAEKLHVDTESQYAQTDPVSFQYGASHGQAGGMTYDHXTGMLNFS	110	120	130	140
		:			
g215	LTKTADGRRQAGKVETEKHVDTESQYAQTDPVSFQYGASHGQAGGMTYNHKTGMLNFS	130	140	150	160
		170			
m215.pep	SKVKATIIDTKDMX	170			
		:			
g215	SKVKAATIIDTKDM	190			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 755>:

a215.seq

1	ATGAAAGTAA	GATGGCGGTA	CGGAATTGCG	TTCCCATTTGA	TATTGGCGGT
51	TGCCTTGGGC	AGCCTGTCTG	CATGGTTGGG	ACGCATCAGC	GAAGTCGAGA
101	TTGAAGAAGT	CAGGCTCAAT	CCCGACGAAC	CGCAATACAC	AATGGACGGA
151	TTGGATGGCA	GGCGGTTTGA	CGAACAGGGA	TACTTGAAAG	AACATTTGAG
201	TTCGAAGGCG	GCGAAACAGT	TTCCCGAAAG	CAGCGACATT	CATTTCGACT
251	CACCGCATCT	CGTGTCTTTC	CAAGAAGGCA	GGTTGTTGTA	CGAAGTCGGC
301	AGCGATGAAG	CCGTTTACCA	TACCGAAAAC	AAACAGGTTC	TTTTTAAAAA
351	CAACGTTGTG	CTGACCAAAA	CCGCCGACGG	CAAACGGCAG	GCGGGTAAAG
401	TTGAAGCCGA	AAAGCTGCAC	GTCGATACCG	AATCTCAATA	TGCCCCAAACC
451	GATACGCCTG	TCAGTTTCCA	ATATGGTGCA	TCGCACGCTC	AGGCGGGCGG
501	CATGACTTAC	GACCACAAAA	CAGGCATGTT	GAACCTCTCA	TCTAAAGTGA
551	AAGCCACGAT	TTATGATACA	AAAGATATGT	AA	

This corresponds to the amino acid sequence <SEQ ID 756; ORF 215.a>:

a215.pep

1	MKVRWRYGIA	FPLILAVALG	SLSAWLGRIS	EVEIEEVRLN	PDEPQYTMDS
51	LDGRRFDEQG	YLKEHLSSKG	AKQFPESSDI	HFDSPHLVFF	QEGRLLYEVG
101	SDEAVYHTEN	KQVLFKNNVV	LTKTADGKRQ	AGKVEAEKLH	VDTESQYAQT
151	DTVPVSFQYGA	SHGQAGGMTY	DHKTGMLNFS	SKVKATIIDT	KDM*

m215/a215 98.3% identity in 173 aa overlap

		10	20	30	40
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG			
		:			
a215	MKVRWRYGIAFPLILAVALGSLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG	10	20	30	40
		50	60	70	80
m215.pep	YLKEHLSAKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV	50	60	70	80

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```

a215      |||||:|||||
          YLKEHLSSKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
          70      80      90      100      110      120

          110      120      130      140      150      160
m215.pep  LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHXTGMLNFS
a215      LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHKTGMLNFS
          130      140      150      160      170      180

          170
m215.pep  SKVKATIIYDTKDMX
          |||||
a215      SKVKATIIYDTKDMX
          190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 757>:

```

g216.seq (partial)
1  ..atgatatcga ttctgagctc ggtacccagc gacgaaatca cgcctcatcat
51  ccccgcactc aaacgcaaag acattaccct cgtctgcatc accgcccgcg
101 ccgattcaac catggcgcg ccatgccgata tccacatcac cgcctcggtt
151 tcgcaagaag cctgcccgtt ggggcttgcc ccgaccacca gcaccaccgc
201 cgttatggct ttgggcgacg cgttgccggt cgtcctgctg cgcgcccgcg
251 cgttcacgcc cgacgacttc gccttgatcc accctgccgg cagcctcggc
301 aaacgcctgc ttttgccgct tgccgacatt atgcacaaag gcggcgccct
351 gcccgccgct cgactcggca cgcccttgaa aggagccatc gtcagcatga
401 gcgagaaaag tttgggcatg tgggcgggaa cggacgggca aaggctgtct
451 gaaaggcctt ttactga

```

This corresponds to the amino acid sequence <SEQ ID 758; ORF 216.ng>:

```

g216.pep (partial)
1  ..MISISSVPS DEITAIIPAL KRKDITLVC I TARPDSTMAR HADIHITASV
51  SQEACPLGLA PTTSTTAVMA LGDALAVLL RARAFTPDDF ALIHPAGSLG
101 KRLLLRVADI MHKGGGLPAV RLGTPLKGA I VSMSEKGLGM WAGTDGQRLS
151 ERPFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 759>:

```

m216.seq
1  ATGGCAATGG CAGAAAACGG AAAATATCTC GACTGGGCAC GCGAAGTGT
51  GCACGCCGAA GCGGAAGGCT TCGCGGAAAT TGCAGCGGAA TTGsACAAAA
101 ACTTCGTCTT TCGGCGAGAC GCGTTGTTGC ACTGCAAGGG CAGGGTCGTT
151 ATCACGGGCA TGGTCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 TATGGCCTCG ACCGGCACGC CTGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGCGCA TTTGGGTATG ATTGTGGACA rCGACGTGGT CGTCGCGATT
301 TCCAATTCCG GCGAAAGCGA CGAAATCGCC GCCATCATCC CCGCACTCAA
351 ACGCAAAGAC ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACGCGCG TCATGGCTTT
501 GGGCGATGCG TTGGCGGTCG TCCTGCTGCG CgcACGCGCG TTCACGCCCC
551 ACGATTTTCG CTTGAGCCAT CCTGCCGGCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GGCGGCCTGC CTGCCGTCCG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGCG
701 TGGGCATGTT GCGGTAACG GACGGGCAAG GCCGTCTGAA AGCGGTATTC
751 ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAACC ATCTCCGCCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTG CTGGCGGCAC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 760; ORF 216>:

```

m216.pep
1  MAMAENGKYL DWAREVLHAE AEGLREIAAE LXKNFVLAAD ALLHCKGRVV

```

498

```

51  ITGMVKSGHI GRKMAATMAS TGTPAFFVHP AEAHGDLM IVDXDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAPPTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRL
201 LRVADIMHKG GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQGRLLKGVF
251 TDGDLRRLFQ ECDNFTGLSI DEVMHTHPKT ISAERLATEA LKVMQANHVN
301 GLLVTDADGV LIGALNMHDL LAARIV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 216 shows 91.8% identity over a 147 aa overlap with a predicted ORF (ORF 216.ng) from *N. gonorrhoeae*:

m216/g216

```

              70      80      90      100      110      120
m216.pep      TMASTGTPAFFVHPAEAAHGDLMIVDXDVVAISNSGESDEIAAIIPALKRKDITLVC
              ::|||:| ||||:|||||
g216           MISISSVPSDEITAIIPALKRKDITLVC
              10      20      30

              130     140     150     160     170     180
m216.pep      TARPDSMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPD
              |||||:|||||
g216           TARPDSMARHADIHITASVSQEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPD
              40      50      60      70      80      90

              190     200     210     220     230     240
m216.pep      ALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLEAIVSMSEKGLGMLAVTDGQGR
              |||||:|||||
g216           ALIHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLEAIVSMSEKGLGMWAGTDGQRL
              100     110     120     130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 761>:

```

a216.seq
1  ATGGCGATGG CAGGAAACGA AAAATATCTT GATTGGGCAC GCGAAGTGTT
51 GCACACCGAA GCGGAAGGCT TCGCGCAAAT TCGCGCGGAT TTGGACGAAA
101 ACTTCGCCCT TCGCGCGGAC GCGTTGTTGC ACTGCAAAGG CAGGGTCGTT
151 ATCACGGGCA TGGGCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 CATGGCCTCG ACCGGCACGC CCGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGGCGA TTTGGGCATG ATTGTGGACA ACGACGTGGT CGTCGCGATT
301 TCCAATTCCG GTGAAAGCGA CGAAATCGCC GCCATCATCC CCGCGCTCAA
351 ACGCAAAGAT ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACCGCCG TTATGGCTTT
501 GGGCGATGCG TTGGCGGTTG TCCTGCTGCG CGCCCGCGCG TTCACGCCCG
551 ACGACTTCGC CTTGAGCCAC CTTGCGGCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GCGCGCTGCG CTGCCGTCCG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GGCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGCCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTT TTGGCGGCGC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 762; ORF 216.a>:

```

a216.pep
1  MAMAGNEKYL DWAREVLHTE AEGLEIAAD LDENFALAAD ALLHCKGRVV
51  ITGMVKSGHI GRKMAATMAS TGTPAFFVHP AEAHGDLM IVDNDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAPPTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRL
201 LRVADIMHKG GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQGRLLKGVF
251 TDGDLRRLFQ ECDNFTGLSI DEVMHTHPKT ISAERLATEA LKVMQANHVN

```

499

301 GLLVTDADGV LIGALNMHDL LAARIV*

m216/a216 97.2% identity in 326 aa overlap

	10	20	30	40	50	60
m216.pep	MAMAENKYL	DWAREVLHAE	AEGLREIAAE	LXKNFVLAAD	ALLHCKGRVV	ITGMVKS
a216	MAMAGNEKYL	DWAREVLHTE	AEGLEIAADL	DENFALAAD	ALLHCKGRVV	ITGMKSGHI
	10	20	30	40	50	60
	70	80	90	100	110	120
m216.pep	GRKMAATMA	STGTPAFFV	HPAEAAHGD	LGMIVDXDV	VVAISNSGE	SDEIAAII
a216	GRKMAATMA	STGTPAFFV	HPAEAAHGD	LGMIVDNDV	VVAISNSGE	SDEIAAII
	70	80	90	100	110	120
	130	140	150	160	170	180
m216.pep	ITLVCITAR	PDSTMARHA	DIHITASVS	KEACPLGLA	PTTSTTAV	MALGDALAV
a216	ITLVCITAR	PDSTMARHA	DIHITASVS	KEACPLGLA	PTTSTTAV	MALGDALAV
	130	140	150	160	170	180
	190	200	210	220	230	240
m216.pep	FTPDDFALS	HPAGSLGKR	LLLRVADIM	HKGGGLPAV	RLGTPPLKE	AIIVSMSEK
a216	FTPDDFALS	HPAGSLGKR	LLLRVADIM	HKGGGLPAV	RLGTPPLKE	AIIVSMSEK
	190	200	210	220	230	240
	250	260	270	280	290	300
m216.pep	DGQGRILK	GVFTDGD	LRRLFQEC	NFTGLSIDE	VMHHPKTIS	AEALATEAL
a216	DGQGRILK	GVFTDGD	LRRLFQEC	NFTGLSIDE	VMHHPKTIS	AEALATEAL
	250	260	270	280	290	300
	310	320				
m216.pep	GLLVTDADG	VLIGALNMH	DLLAARIVX			
a216	GLLVTDADG	VLIGALNMH	DLLAARIVX			
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 763>:

g217.seq

```

1  atggcggatg acggtttgtt gcggcaactg tccgaaaaac ccagccaaag
51  tgctctcttc ctgccatttg acccattcgt ttcgaggtt ttggactgcc
101 ttttggtcac cgggcccggc ttgaaacaat gtttcaagca aatcccggca
151 acgcgccacc cattcgccga ccgtcgcagg ttgccgccat atccgggcaa
201 tatccgacag ggtttcgagg aaggcggcaa aacgtccgaa catggcggtt
251 tgattcacgt cggcatacca cgcgctgaca tcctgccaca tcgggttgcc
301 gccttcgggc agcatccagc ccaatatcat acggtctgcc gcctgcttcc
351 aggtaaacag ctgatccgtg ccgcccgcga tttctccgtc caatcccca
401 tggacgttca aatcggcaac catatcgtgc aaaagcggca aatcgtcccc
451 ggtcagtcag aaacggcgca acacgggcgc ggtttccaaa agcgcgagca
501 ctttgccgac ttcaaaacgg ctttcagca agtcggacac gactccaac
551 gcataaaaaa acggttgccg gcggctgatt ttcacgtccg aaacggaata
601 cggcaatgcc tgcgcgccgg gttgcgcctg tccgaacacg gcttccataa
651 aaggcgtata gggttcgata ttcgggggta a

```

This corresponds to the amino acid sequence <SEQ ID 764; ORF 217.ng>:

g217.pep..

```

1  MADDGLLRQL SEKPSQSALF LPFDPFVFEV LDCLLVIGPG LKQCFKQIPA
51  TRHPFADRRR LPPYPGNIRQ GFEEGGKTSE HGGLIHVGIP RADILPHRVA
101 AFGQHPAQYH TVCRLLPGKQ LIRAAAHFSV QSPMDVQIGN HIVOKRQIVP
151 GQSETAQHGR GFQKREHFAD FKTAFOQVGH ALQRIKRLP AADFHVNRGI

```

500

201 RQCLRAGLRL SEHGFKRRI GFDIRG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 765>:

m217.seq

```

1  ATGGCGGATG ACGGTGTGCG GCGGCAACTG TCCGAAAAAT TGCGCCAATT
51  CGGTTTCCGC CTrCCATTG ACCCATTCGT TTTCAAGGTT TTGGACTGAC
101 TTTTGGTCAT CGGCTTCAGC TTGGAACAAT GTTCAAGCA AATCCCGGCA
151 ACGCGCCACC CATTCCGCCA CCGTTGCGGG CTGCCGCCAT ATCCGTACAA
201 TATCCGTCAG GGTTCGAGG AAGGCGGCAA AACGTCCGAA CATGGCGGTT
251 TGATTACAGT CGGCATACCA CGCGCTGACA TCCTGCCACA TCGGATTGCC
301 GCCTTTGGGC AGCATCCAGC CCAATATCAT GCGTTCTACC GCCTGCTTCC
351 AGGTGAACAG CTGATCCGTG CCGCCGCGCA TTTCTCCGTC CAAACCCAG
401 TGGACGTTCA AATCGGCAAC CATGTCGTGC AAAAGCGGTA AATCGTCCTC
451 AGTCAGTCCG AAACGGCGCA ACACGGGCGC GGTTCCTAAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAAACA GCGGTTGGCG GCGGCTGATT TTCACGTCG ACACGGAATA
601 CGGCAATGCC TGCGCACCgG GctGCGCCTG TCCGAACACG GCTTCGATAA
651 AAGCGGTATA GGATTCGATA TTCGGGGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 766; ORF 217>:

m217.pep

```

1  MADDGVRRL SGKLRQFGFR LPFDPFVFKV LDXLLVIGFS LEQCFKQIPA
51  TRHPFADRCG LPPYPYNIQ GFEEGKTSE HGGLIHVGIP RADILPHRIA
101 AFGQHPAQYH AFYRLPGEQ LIRAAAHFSV QTPVDVQIGN HVVQKRXIVL
151 SQSETAQHGR GFXXKHKFID FKSAFQVEQ AXQSMKQRLA AADFHVXHGI
201 RQCLRTGLRL SEHGFDKRI GFDIRG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 217 shows 80.5% identity over a 226 aa overlap with a predicted ORF (ORF 217.ng) from *N. gonorrhoeae*:

m217/g217

	10	20	30	40	50	60
m217.pep	MADDGVRRLSGKLRQFGFRLPFDPFVFKVLDXLLVIGFSLEQCFKQIPATRHFPADRCG					
	: : : : :					
g217	MADDGLLRQLSEKPSQSALFLPFDPFVFEVLDCLLVIGPGLKQCFKQIPATRHFPADRRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m217.pep	LPPYPYNIQGFEEGKTSEHGGLIHVGIPRADILPHRIA AFGQHPAQYHAFYRLPGEQ					
g217	LPPYPGNIRQGFEEGKTSEHGGLIHVGIPRADILPHRVA AFGQHPAQYHTVCRLLPGKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m217.pep	LIRAAAHFSVQTPVDVQIGNHVQKRXIVLSQSETAQHGRGFXXKHKFIDFKSAFQQVEQ					
g217	LIRAAAHFSVQSPMDVQIGNHIVQKQIVPGQSETAQHGRGFQKREHFADFKTAFQQVGH					
	130	140	150	160	170	180
	190	200	210	220		
m217.pep	AXQSMKQRLAAADFHVXHGI RQCLRTGLRLSEHGFDKRRIGFDIRGX					
	: : : :					
g217	ALQRIKKRLPAADFHVRNGIRQCLRAGLRLSEHGFKRRIGFDIRG					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 767>:

a217.seq

```

1  GTGGCGGATG ACGGTGTGCA GCGGCAACTG TCCGAAAAAT TGCGCCAATT
51  CGGTTTCCGC CTGCCATTG ACCCATTCGT TTTGAGGCT TTGGACTGCC
101 TTTTGGTCAT CGCCTTCGAC TTGGAACAAT GTTCAAGCA AATCCCGGCA
151 ACGCGCCACC CATTCTCAA CCGTCGAGG TTGCCGCCAT ATCCGTACAA

```